Medieval Ichthyoarchaeology and Historical Ecology of *Salmo* sp. Fishes Across the North Sea Basin

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Abstract

This doctoral thesis research is primarily concerned with the medieval history of human exploitation of fishes belonging to the *Salmo* genus, investigated through the study of archaeological material recovered from sites surrounding the North Sea. A large-scale review of ichthyoarchaeological material from North Sea medieval sites provides insight into long-term trends in presence and absence of *Salmo* sp. fishes, as well as providing a framework for targeted sampling of fish bones for further analysis. An assemblage of fish bone material from archaeological sites located in the Netherlands, England, Scotland and Denmark has been subjected to osteological, bulk stable isotope (SI), and collagen peptide barcoding (ZooMS) analysis. A total of 286 samples with associated ZooMS and/or SI data are presented here, 194 from *Salmo* sp. fish and 92 from comparative marine, migratory and freshwater fish species. In addition to archaeological datasets and bone material, a complementary review of medieval and historical documents ranging from tax records and purchase orders, to bestiaries and monastic texts was conducted to assess medieval conceptions of salmon and trout.

This interdisciplinary research provides a series of observations about the status of *Salmo* sp. fishes in the medieval North Sea basin, as well as resulting in a new combined biomolecular approach to identifying behavioural ecotypes of these fish in the archaeological record– specifically migratory Atlantic salmon, migratory sea trout, and freshwater brown trout. This thesis demonstrates that there is a higher-than-expected presence of migratory sea trout within the medieval North Sea archaeological record, and the ecotype data reported here highlights the complex archaeobiogeography of the *Salmo* genus in the region. It also discusses regional variations in *Salmo* ecotype exploitation and isotopic characteristics, as well as socially-stratified procurement trends which demonstrate changes in cultural and economic "value" of *Salmo* sp. fish throughout the region and through time.

*Þanne [he] were set, and bord leyd, And þe beneysun was seyd, Biforn hem com þe beste mete Þat king or cayser wolde ete; Kranes, swannes, ueneysun, **Lax**, lampreys, and god sturgun, Pyment to drinke, and god clare, Win hwit and red, ful god plente.*

TR: When they were seated, the table set and grace said, they were served the best food that king or emperor would eat: cranes, swans, venison, **salmon**, lampreys and sturgeon, and plenty of fine wine.

"The Lay of Havelok the Dane"
Geffrei Gaimar, c. 1136-1140

Author's Declaration

I declare that this thesis is a presentation of original work and I am the sole author. This work has not previously been presented for a degree or other qualification at this University or elsewhere. All sources are acknowledged as references. The work carried out as part of this thesis has resulted in the following papers in the process of being prepared for submission in some format or another, with the following prospective co-authors:

1.CHAPTER 6 - **Liz M. Quinlan**, James Barrett, Jen Harland, Hans Christian Küchelmann, Inge van der Jagt, Anton Ervynck, Wim van Neer, Anne Karin Hufthammer, Michelle Alexander, and David Orton. A Review of *Salmo* sp. Remains from the Medieval North Sea Basin. Submission pending publication of Northern Seas Synthesis Dataset (Barrett et al.).

- Contributions for the planned author list are as follows: LQ - conception of the paper, final dataset preparation, statistical analysis, data visualization, and all writing; JB, JH, HCK, IVDJ, AE, WVN, AKH - organization of original Northern Seas Synthesis datasets; DO and MA - SeaChanges principal investigators, commentary and substantive feedback on LQ's work throughout the research process, guidance on paper development.

2. CHAPTER 7 - **Liz M. Quinlan**, Samantha Presslee, Matthew von Tersch, Jen Harland, Colleen Batey, David Orton, and Michelle Alexander. A Combined Biomolecular Method for the Identification of *Salmo* sp. Ecotypes within Ichthyoarchaeological Assemblages. Planned submission to *Proceedings of the Royal Society: B*.

- Contributions for the planned author list are as follows: LQ - sample collection and preparation, collagen extraction, data cleaning and organization, statistical analysis, data visualization, and all writing; SP and MVT - ZooMS and bulk stable isotope technician support, including sample runs and training; JH and CB - archaeological site background on Earl's Bu and Coppergate, as well as sampling assistance; DO and MA - SeaChanges principal investigators, commentary and substantive feedback on LQ's work throughout the research process, guidance on paper development.

3. CHAPTER 8 - **Liz M. Quinlan**, Matthew von Tersch, Maria Fontanals-Coll, David Orton, and Michelle Alexander. Regional Variation in Isotope Characteristics of Archaeological *Salmo* sp. Remains and Comparative Taxa from the North Sea Basin. Several submission possibilities at present.

- Contributions for the planned author list are as follows: LQ - sample collection and preparation, collagen extraction, data cleaning and organization, statistical analysis, data visualization, and all writing; MVT and MFC - bulk stable isotope technician support, including sample runs and training; DO and MA - SeaChanges principal investigators, commentary and substantive feedback on LQ's work throughout the research process, guidance on paper development.

A collaboration with Daniel Farbowitz, a data scientist and physicist currently based at the Danmarks Tekniske Universite, resulted in a program written in Python to average raw ZooMS data, extract sample names from run sheets and plate maps, identify sample peaks, compare them against trypsin constants, and extract peak data

and intensities from TXT files and save the resulting data in spreadsheet format. This resulted in the data seen in Appendix C. The program does not automate sample identification, but it does prepare the data for manual ID confirmation, and make it easier to pull out individual samples for verification using a spectra viewer like mMass. The program in question will likely be published as part of publication 1 (Chapter 6), with Farbowitz as an additional co-author.

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Chapter 1

Introduction

1.1 Research Context

This thesis research was conducted as part of the SeaChanges Marie Skłodowska-Curie actions (MSCA) Innovative Training Network (ITN), funded through the Horizon2020 program of the European Union. As such, this thesis project was one of fifteen interdisciplinary research projects included within the SeaChanges ITN, connecting the fields of archaeology, marine biology, and conservation ecology. Two of the key overarching goals of the SeaChanges ITN were to "improve understanding of the time depth of human use of and impact on key European marine species" and "increase cross-disciplinary and cross-sectoral awareness of the potential of long-term perspectives in marine ecology" (European Commission 2023). In order to achieve these two goals, individual research projects were proposed focusing on archaeologically and historically significant marine species, ranging from walruses to sea turtles– and everything in between; including dolphins, whales, grouper, herring, cod, flatfish, sturgeon, hake, tuna, and, of course, salmon. This research project was initially proposed as a way to track historical declines in Atlantic salmon populations in the North Sea, using archaeological material from around the North Sea basin region to investigate identification methods for salmon and trout and explore human mercantile and environmental impacts on these fish (European Commission 2023). Initial plans to develop a geometric morphometrics-based identification protocol to differentiate between salmon and trout had to be abandoned due to the impact of the COVID-19 pandemic, but the spirit of the original research proposal remains. This project is a truly interdisciplinary one, bringing together aspects of stable isotope ecology, zooarchaeology, proteomics, and documentary analysis to explore the complex history of human interactions with fish belonging to the species *Salmo trutta* and *Salmo salar*.

1.2 Aims and Objectives

The principal aim of this thesis is to gain a deeper understanding of the ecological, economic, and cultural status of migratory salmon and trout during the broadly Medieval Period (c. 500-1500 CE) in the North Sea basin area. A suite of methodological approaches were used to realize this aim, with four primary objectives:

1. **Review** published ichthyoarchaeological material to gain an understanding of the breadth of *Salmo* sp. exploitation across the North Sea basin area and throughout the broadly Medieval Period. This review will also identify archaeological assemblages to target for biomolecular analysis of fish remains.

2. **Sample** fish remains, including *Salmo* sp. and comparative taxa, from archaeological sites located in England, Scotland, the Netherlands, and Denmark. The remains are then cleaned, collagen extracted, and a combination of bulk stable isotope analysis and collagen peptide fingerprinting is applied to the archaeological samples.

3. **Integrate** the results of these biomolecular results to investigate various aspects of isotope ecology, archaeobiogeography, human-animal interactions, and regional differences in *Salmo* sp. exploitation and population characteristics across the North Sea basin area.

4. **Review** documentary, historical, and artistic references and records of Atlantic salmon and sea trout throughout the broadly Medieval Period in order to understand perceptions of these fish within the study area by people from varying social and cultural groups, using an ethnoicthyological approach.

The underlying research questions informing these objectives fit into two broad research topics: interactions between past groups of humans and *Salmo* sp. fishes in the medieval North Sea basin area; and characteristics

of past populations of *Salmo* sp. fishes in the same region. The main underlying research question about these two topics centres on why we would want to identify *Salmo* sp. bones in the first place, and what researching fish like salmon and trout can tell us about past groups of people in the North Sea basin area. The simplest goal of researching these topics is to differentiate correctly between the two species in the *Salmo* genus– *Salmo salar* (Atlantic salmon) and *Salmo trutta* (Brown/sea trout), so we can gain a deeper understanding of how and why humans from different regions made the decision to exploit the species they did. The goal of this thesis research, then, is to explore how human groups interacted with, managed, consumed, and affected salmon and trout during the broadly medieval period. To reach this goal, a wide variety of questions need to be answered, which fit broadly into three main groupings and which are addressed throughout the body of the thesis.

1. **How can archaeological *Salmo* sp. bones be identified?** Are traditional zooarchaeological methods based on morphology reliable? What are the unique osteological characteristics of *Salmo* sp. fishes that differentiate them from other commonly exploited fish in North Sea region? Is ZooMS analysis a more reliable method of identification? Can ecotypes of *Salmo* sp. fishes be differentiated using a combination of ZooMS and bulk stable isotope analysis? What are the isotopic differences between *Salmo* sp. fishes and other taxa, and are they as expected?

2. **How did human exploitation of these fish change over time in the North Sea basin area?** Are there regional differences in exploitation visible through time? Are there different cultural or economic perceptions of Atlantic salmon, sea trout, and brown trout in the study area? Did human activity impact wild *Salmo* sp. populations through time, and are reported declines in population visible in the archaeological record? What does the archaeological "landscape" of identified *Salmo* sp. remains look like in the medieval North Sea basin area?

3. **What differences are observable between ancient populations of *Salmo* sp. fish and modern populations?** Are these differences regionally or temporally dependant? Can they be quantified isotopically? What benefit is there to understanding past population baselines for *Salmo* sp. fishes? Can archaeological fish remains contribute to modern conservation efforts for threatened species?

1.3 Structure of the Thesis

The following section provides a brief overview of each of the 9 chapters that make up the body of this thesis, covering archaeological context and materials (Chapter 2), analytical and research methods (Chapter 3), background reviews of key topics (Chapters 4 and 5), results (Chapters 6-9), and concluding remarks (Chapter 10). Additionally, brief descriptions of the five appendices are presented following those of the chapters.

The introduction to this thesis (Chapter 3) focuses primarily on the archaeological materials and contexts of the study assemblages, as well as the sampling approach taken. The aim of the chapter is to situate the fish bone materials within not only the site-specific historical and archaeological contexts, but also the wider North Sea region, looking at large scale cultural and political shifts in power across a roughly 1000-year time period. The site summaries– which cover excavation history, phasing, and relevant historical details– provide important background information for answering broader research questions about regional and class differences in *Salmo* sp. fish exploitation, which are investigated more thoroughly in Chapters 6-9. Chapter 3 of this thesis outlines the methods used to address the overarching research goals and aims of the thesis, covering research, analytical, and statistical methods. The chapter covers laboratory methods for zooarchaeological analysis, bulk stable isotope analysis, and zooarchaeology by mass spectrometry analysis. Additionally, archaeological assemblage

review and documentary research methods are outlined and described. Statistical methods and open research methods are also explained, including a discussion of open access goals for the research. Together these methods provide the direct analytical means for answering higher-level research questions relating to fish species identification and isotopic characteristics. Furthermore, the methods chapter itself explores questions of reliability of morphological identification methods for differentiating between *Salmo salar* and *Salmo trutta*, providing a brief summary of known skeletal differences between the two species. Chapters 4 and 5 are extended literature reviews focusing specifically on the biomolecular methods used in this thesis (Chapter 4) and the specifics of *Salmo* sp. fish ecology and biology. Chapter 4 provides an in-depth review of the underlying theory and history of bulk stable isotope analysis and zooarchaeology by mass spectrometry in archaeological research, focusing specifically on it's applications in icthyoarchaeological contexts. Chapter 5 covers the ecological and biological characteristics of *Salmo salar* and *Salmo trutta* fishes, with particular focus on the differences between the two species and their ecotypes. This provides key contextual information for later research questions surrounding ecotype identification, past biogeography of *Salmo* sp. ecotypes, and applications to modern conservation efforts. The chapter also discusses bulk stable isotope ecology of *Salmo* sp. fish, as understood from modern stable isotope ecology research data. This modern isotope data is especially relevant for answering questions related to differences between modern and ancient populations of *Salmo* sp. fishes, regional and temporal differences in isotope characteristics, and modern conservation ecology. The final sections of this chapter cover the known historical ecology of *Salmo* sp. fishes in the medieval, historical, and modern periods, providing important background information for questions relating to both isotope ecology and population declines.

Following on from these background and methodological chapters are the four results-focused chapters, presented as interrelated, but ultimately standalone, case studies covering the results of the documentary, artistic, zooarchaeological, isotopic, and proteomic analysis. Chapters 6-9 are presented generally in article format, althought none have been submitted for publication at this time. The first results chapter (Chapter 6) is a synthesis of documentary, historical, and representative analysis looking at perceptions of *Salmo* sp. fishes across the North Sea region and throughout the broadly Medieval Period. It includes the results of a preliminary documentary analysis pilot study focused on tax and purchase records from ecclesiastical and mercantile contexts. This documentary analysis answers questions relating to changing economic values and culinary/preservative preparations of salmon in England. Additionally, reviews of early literary references to salmon and trout, as well as later recipe collections and proto-cookbooks, are presented to provide further context for understanding how the fish species were perceived during the time period by people from varying cultural groups and social classes. Finally, a brief review of artistic representations of salmon and trout is presented, looking at medieval carvings, illustrations, and heraldic imagery. Chapter 7 presents the results of a comprehensive review of published and unpublished icthyoarchaeological material from the North Sea basin area, and directly addresses questions surrounding the frequency of *Salmo* sp. finds across the region, differing levels of access to these species by different social groups, and the impacts of collection methods on fish identifications. This chapter also contains the results of targeted ZooMS analysis conducted on *Salmo* sp. fish remains sampled from 16 North Sea archaeological sites identified during the review of archaeological materials. This ZooMS study is the first large-scale investigation into the frequency of *Salmo salar* and *Salmo trutta* remains across the region, and is used to discuss the efficacy and reliability of identification methods for *Salmo* sp. fishes in the archaeological record.

Chapter 8 is presented as a methods paper describing a novel combined biomolecular approach to identifying behavioral ecotypes of archaeological *Salmo salar* and *Salmo trutta* fish remains. This chapter uses two sites, 16-22 Coppergate (York, England) and Earl's Bu (Orkney, Scotland) to illustrate the efficacy of this method, and directly answers questions about bast biogeography, archaeological ecotype identification, and cultural prefer-

ences for salmon and sea trout. This chapter is presented in article format and will be submitted with several co-authors, but all data analysis, interpretation, and writing included in this thesis chapter is my sole work. Chapter 9 is focused on the larger bulk isotope dataset, consisting of fish bone material from 14 medieval North Sea sites from *Salmo* sp. and comparative fish taxa. The assemblage includes bulk carbon and nitrogen isotope results for archaeological remains from four modern day countries (England, Scotland, the Netherlands, and Denmark), and fish from the Gadidae, Anguillidae, Esocidae, Cyprinidae, Percidae, Clupediae, Coregoninae, Rajidae, Pleuronectiformes, and *Salmo* taxonomic groups. These results of the bulk stable isotope analysis are interpreted using several methods, including the application of isotope niche space analysis to understand regional and population-level differences in fish foraging ecology. The chapter answers questions about regional and temporal differences in isotope characteristics and human exploitation of *Salmo* sp. fishes. It presents a large dataset of past isotopic baselines which can be used for further study, and is presented in article format in the same way as Chapter 8.

Finally, Chapter 10 synthesizes the results and commentary of the previous four chapters in a final discussion of patterns in *Salmo* sp. exploitation across the medieval North Sea basin area. This discussion chapter covers both the strengths and limitations of the datasets presented, while also connecting the four results chapters together to answer remaining questions about differences in *Salmo* sp. fishes through time, the reported "prestige" of salmon and sea trout, and how archaeological information can be integrated with modern ecological research. The chapter ends on a discussion of future work and considerations, as well as presenting a concise summary of the key findings of this thesis. Appendices A-E follow Chapter 10, and contain the zooarchaeological review data from Chapter 7, isotopic data from Chapters 8 and 9, ZooMS data from Chapters 7 and 8, documentary record data from Chapter 6, as well as all R code produced. Appendix A consists of basic site data from the 146 medieval archaeological sites reporting identifications of *Salmo* sp. fishes from eight modern day North Sea countries. Appendix B contains isotopic data from 246 archaeological fish samples with associated bulk carbon and nitrogen data, including all samples within a basic 3.00-3.60 C:N ratio range. Appendix C contains a spreadsheet of 198 archaeological fish samples with associated ZooMS identifications, while Appendix D has a spreadsheet of 150 entries of documentary records relating to salmon, trout, and other fish species found in medieval tax and purchase records. Finally, Appendix E is a PDF version of an rMarkdown file that can be used to run all statistical analysis and data visualization code produced for this thesis.

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Chapter 2

Archaeological Materials and Background

2.1 Introduction

This chapter will be focused on describing the complex archaeological and historical contexts of the 17 archaeological sites included within the scope of this thesis research. This chapter will also discuss the materials used for study throughout this PhD research, in order to better understand the variety of methodological approaches taken (see Chapter 3). A major purpose of this chapter is to detail the sampling strategies used for choosing and collecting fish bone material from the 17 archaeological sites across the study area. No modern fish bone was used in this study, and all fish bone was from the broadly Medieval Period, with midpoint dates for the sites/contexts studied ranging between 550-1545 CE. A brief note on dating; throughout this thesis the terms "Early", "High", and "Late" medieval have been used when broad classifications are necessary, but specific date ranges and local cultural period descriptions have also been used wherever possible. In the context of this thesis, "Early Medieval" refers to period between approximately 500-950 CE, "High Medieval" to between 950-1300 CE, and "Late Medieval" to between 1300-1550 CE. The following sections will detail the sampling strategy applied for each taxonomic group involved in this study, discussing desired characteristics of the archaeological material collected. Additionally, the sampled assemblages from each of the 17 sites included in this research will be described with site background, information on site phasing, total fish NISPs, and conclusions made by previous zooarchaeologists about the studied assemblages all presented. Finally, there will be an historical overview of the medieval North Sea Basin area, covering the shifting cultural, geographic, political, and economic situations across time and space in the study assemblage. This will cover selected periods of English, Dutch, Scottish, and Danish archaeological and historical contexts.

2.2 Materials

2.2.1 Sampling Strategy

The sampling strategy employed for this research was intended to compile an assemblage of archaeological fish bones which could be used for a diachronic and geographic study of bulk stable isotope values, with a complementary application of zooarchaeology by mass spectrometry (ZooMS). Samples were identified by reviewing a combination of published and unpublished archaeological fish bone data, and compiling information from these datasets into a master database which could be used to identify archaeological sites to target. This database eventually formed the basis of the North Sea Archaeological *Salmo* sp. review (Chapter 7), and contained fish bone data from 410 archaeological sites. Within this master database were 146 sites with confirmed identifications of *Salmo* sp. fish, and the first step in data sorting was to exclude sites which contained fewer than 20 identified *Salmo* sp. bones. This number was chosen to ensure that a targeted site would have a robust enough *Salmo* sp. assemblage to sample for bulk stable isotope analysis, which would provide insight into a meaningful subsample of the *Salmo* sp. assemblage, without destroying it completely. This sorting excluded approximately 93% of all *Salmo* sp. sites, leaving just 18 sites in England, Belgium, the Netherlands, Norway, Scotland, Germany and Denmark. The next planned step was to contact the relevant stewards for these archaeological sites, however the rapid onset of the ongoing Covid-19 pandemic required plans to be changed. As this PhD research was based at the University of York it was decided that the 16-22 Coppergate site from York would be targeted for a pilot study, and additional sites were added as pandemic restrictions ebbed and flowed. From the original list, only four sites were sampled – 16-22 Coppergate (York, UK), Nieuw Rhijngeest-zuid (Oegsgeest, NL), Earl's Bu (Mainland, Orkney, UK) and ASR 9 Posthuset (Ribe, DK). While making inquiries about the Dutch and Danish sites from the original list, additional sites were identified in discussions with collections managers from regional storage

depots and added to the target list.

A total of 20 sites were initially targeted for this thesis research (Table 1; Fig. 1), which involved in-person review of osteological assemblages by the author prior to sampling for biomolecular analysis. This involved visits to regional collections, commercial archaeological storage depots, and museums, all of which was restricted at various times by local Covid-19 regulations. A total of 748 fish bones were recorded during reviews of available assemblages on sampling trips, and a total of 382 of these fish bones were selected for biomolecular analysis (bulk stable isotope, zooarchaeology by mass spectrometry analysis, or both). Biomolecular analysis results were successfully obtained from a total of 327 samples from 17 sites, with 53 samples either lost during demineralization, or not yielding adequate collagen for further analysis, including the five samples from the Achlum, Oosterbeintum, and Stenen Kamer/Linge sites. The total biomolecular sample of 327 samples was narrowed to 300 samples after quality control criteria were applied (see Chapters 4, 8, and 9 for more information). Of this final dataset of 300 samples from 17 sites: 132 have only bulk stable nitrogen and carbon isotope data, 88 have only ZooMS data, and 107 have both ZooMS and isotopes data.

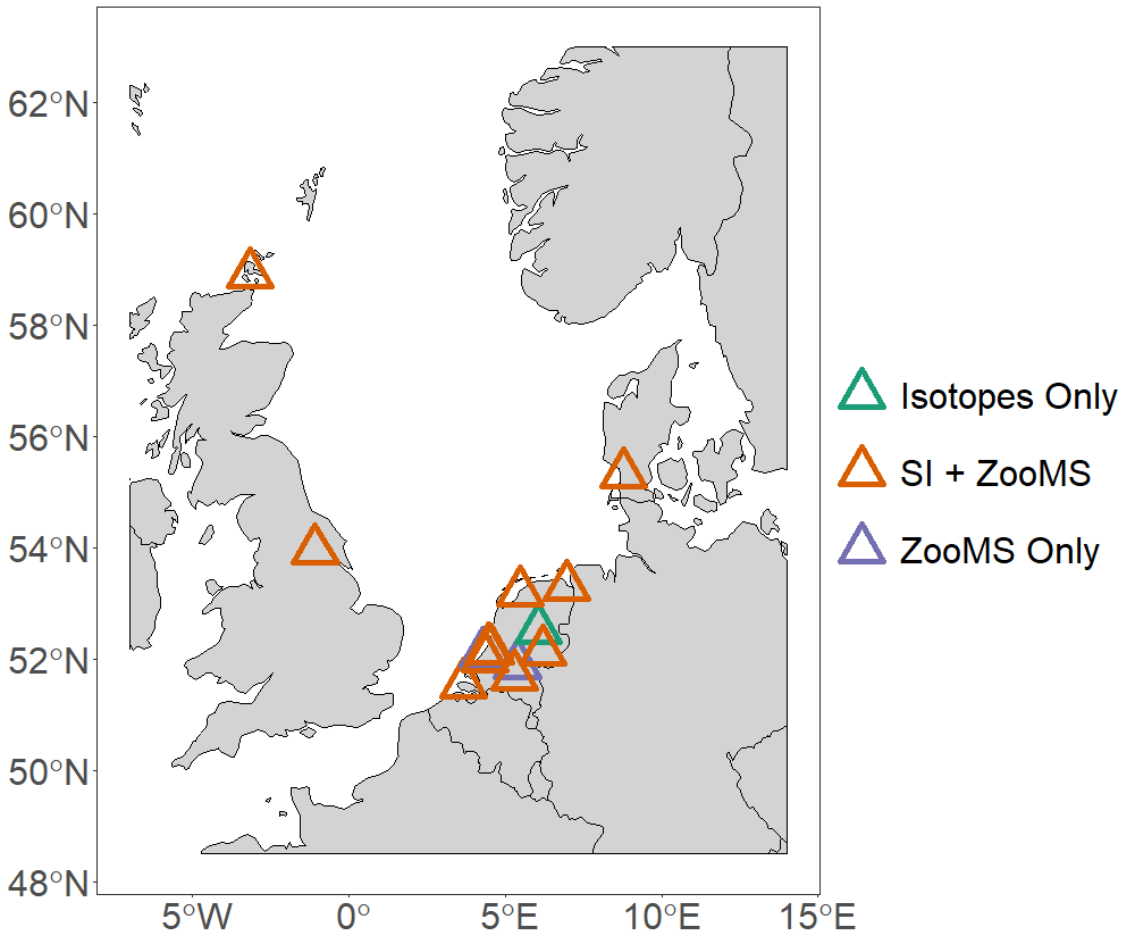


FIGURE 2.1: Site locations of bone material sampled for biomolecular analysis. Legend color corresponds to whether data from bulk stable isotope analysis, ZooMS, or both methods is available.

For most visits the entire bone assemblage was made available and site records were used to search out *Salmo*

Site	Country	Date Range (CE)	Site Fish NISP	Initial Biomol. Sample NISP
16-22 Coppergate	England	400-1720	32015/20463*	84
ASR 13 Lindegården	Denmark	1200-1300	245	4
ASR 2090 von Støckens Plads	Denmark	1000-12000	203	11
ASR 9 Posthuset	Denmark	700-1200	3071	83
Earl's Bu	Scotland	750-1200	18957	59
Achlum	Netherlands	50-1400	UNK	1
Heveskesklooster	Netherlands	1300-1500	UNK	1
Huis Malburg	Netherlands	900-1049	110	1
Huize van den Kasteele	Netherlands	950-1100	425	1
In den Struys	Netherlands	1425-1500	2797	4
Johan van Oldenbarneveltlaan	Netherlands	450-700	547	2
Kasteel Voorst	Netherlands	1280-1362	83	2
Minderbroedersklooster	Netherlands	1175-1500	3464	59
Nieuw Rhijngeest-zuid	Netherlands	475-725	6567	44
Ooosterbeintum	Netherlands	300-800	UNK	2
Oude en nieuwe Gasthuis	Netherlands	1400-1450	690	4
Plantage Leiderdorp	Netherlands	650-850	2734	7
Stadhuis Zutphen	Netherlands	1125-1175	4346	1
Stenen Kamer/Linge	Netherlands	900-1050	UNK	1
Tjitsma Wijnaldum	Netherlands	550-950	3967	11
TOTAL				382

TABLE 2.1: Complete list of biomolecular samples and their archaeological contexts

sp. bones to verify quantities, morphological identification, and preservation. There were two overall categories of archaeological bone material collected from these sites, *Salmo* sp. and comparatives. The *Salmo* sp. category includes all bones identified as Atlantic salmon (*Salmo salar*), brown trout (*Salmo trutta*), and a variety of catch-all terms that indicated uncertainty about the exact taxonomic identification, but confidence that the bone was from either a salmon or trout. The comparative category includes all other fish species sampled in order to provide freshwater, marine and diadromous baseline bulk stable isotope data.

Salmo sp. fishes

The sampling procedure for *Salmo* sp. fish bones first involved morphological identification, based both on cranial elements, which can be differentiated by species, and vertebral features, which can only differentiate *Salmo* sp. fish from other taxa. Identifiable features of the dentary, premaxilla, maxilla, supraethmoid, vomer, and atlas vertebra are described in Chapter 3, but of the 230 suspected *Salmo* sp. elements sampled for biomolecular analysis, only 21 (9.1%) were non-vertebral elements. The vast majority (90.9%) of the suspected *Salmo* sp. bones were vertebral elements, consisting of precaudal (n=68) and caudal (n=90) vertebrae, first vertebrae (n=5), and vertebral fragments (n=46). Identification of *Salmo* sp. vertebral elements is based primarily on the presence of a characteristic "honeycomb" pattern across the centrum (Figure 2), with smooth anterior and posterior margins (Watt, Pierce, and Boyle 1997, pg. 161). While other taxa may display honeycomb-like patterning, none show the same consistency of form. This honeycomb pattern is a key diagnostic feature when differentiating between the vertebra of other large marine fish and *Salmo* sp. fish. Other features of *Salmo* sp. vertebrae which contribute to a positive identification are the steep angle seen in the zygapophyses (articular surfaces which interlock with other vertebrae) and the overall squared shape with a lack of a distinct waist (Watt, Pierce, and Boyle 1997, pg. 161). The appearance of the characteristic honeycomb pattern remains fairly consistent across the other two categories of salmonids exploited by humans in the study area, migratory whitefish (subfamily *Coregoninae*) and Arctic char (*Salvelinus alpinus*). The freshwater grayling (*Thymallus thymallus* and vendace (*Coregonus vandesius*) both do not display the honeycomb pattern, and are therefore easily distinguished from other salmonids.

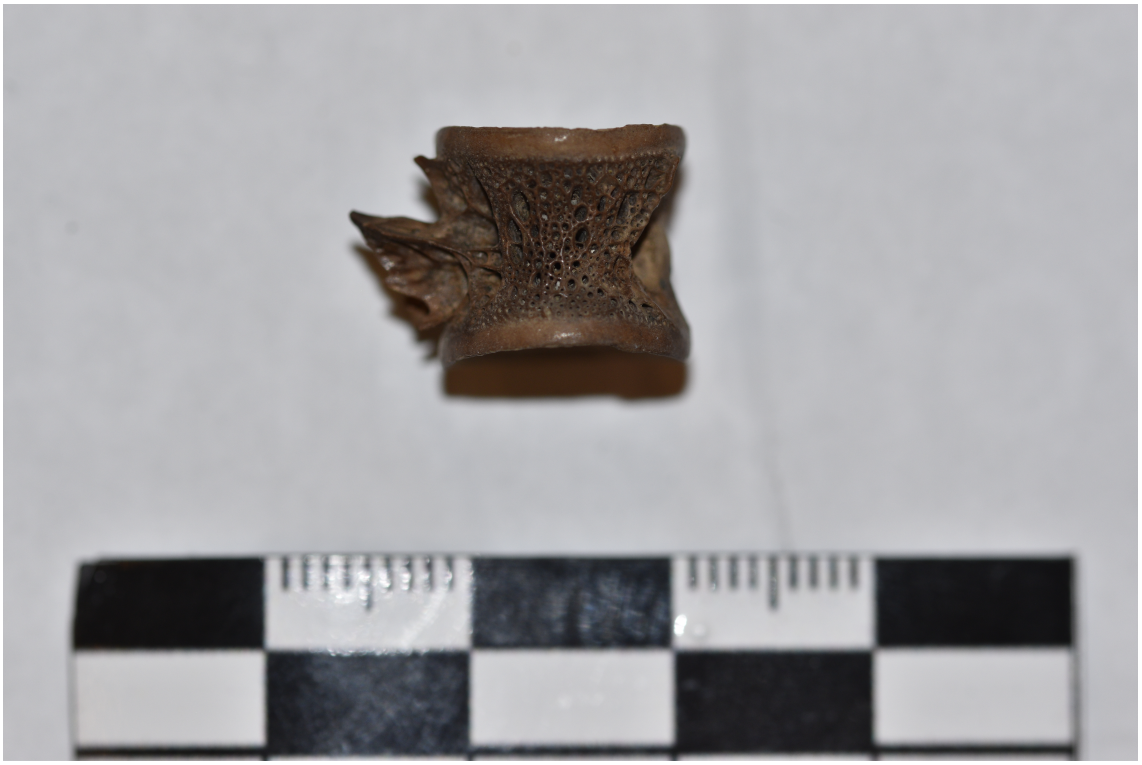


FIGURE 2.2: Photo of a *Salmo* sp. precaudal vertebra designated as NL_salmo_002 and identified via ZooMS as belonging to the species *Salmo salar*, sampled from the 15th-century Oude en nieuwe Gasthuis site in Delft. The characteristic honeycomb pattern of *Salmo* sp. fish vertebrae is visible on the lateral aspect.

Site	Published Fish NISP	Published Salmo sp. NISP	Recorded Salmo sp. NISP	SI-only Sample	ZooMS-only Sample	SI ZooMS Sample	Notes
16-22 Coppergate	32015/20463	394/115	256	3	5	55	29 samples previously unidentified; * = indicates a discrepancy in the 2 published records of fish remains from the site; 4 samples with "isotopes only" due to recording errors
ASR 13 Lindegården	245	2	2			2	
ASR 2090 von Støckens Plads	203	4	2			4	
ASR 9 Posthuset	3071	200	100	1	29	16	only 100 bones present in the sample made available for study; 2 samples with ïsotopes only" due to recording errors
Earl's Bu	18957	79	38	2	15	16	13 samples previously unidentified; only 23 of original 79 found upon review; 3 samples with "isotopes only" due to recording errors
Heveskesklooster	UNK	1	1			1	total site NISP unknown, records unavailable
Huis Malburg	110	1	1		1		
Huize van den Kasteele	425	1	1			1	
In den Struys	2797	6	14			4	Additional 8 samples found in bags of unidentified fish remains
Johan van Oldenbarneveltlaan	547	8	6		2		1 sample unaccounted for
Kasteel Voorst	83	4	3	2			1 sample unaccounted for; 2 samples with "isotopes only" due to recording errors
Minderbroedersklooster	3464	30	26	1	13	7	7 samples previously unidentified; only 17 of original 30 found upon review; 1 sample with "isotopes only" due to recording errors
Nieuw Rhijngeest-zuid	6567	111	31	1	12	3	majority of bone material unavailable for review; 1 sample with "isotopes only" due to recording errors
Oude en nieuwe Gasthuis	690	1	4		1	2	3 additional Salmo sp. bones found in bag of Gadidae remains
Plantage Leiderdorp	2734	8	9			2	7 samples previously unidentified; only 2 of original 8 found upon review
Stadhuis Zutphen	4346	1	1			1	
Tjitsma Wijnaldum	3967	42	21		3	3	2 samples previously unidentified; only 21 of original 42 found upon review;
TOTALS			**518**	**10**	**81**	**117**	

TABLE 2.2: Summary table of published, recorded, and sampled material from all sites

Site	Location	Date Range (CE)	Fish NISP	Salmo sp. NISP	% of Fish NISP	Biomolecular Salmo sp. Sample	% of Salmo sp. NISP
16-22 Coppergate	York, UK	400-1720	20463	256	1.25	63	24.60
ASR 13 Lindegården	Ribe, UK	1200-1300	245	2	0.82	2	100.00
ASR 2090 von Støckens Plads	Ribe, UK	1000-1200	203	4	1.97	4	100.00
ASR 9 Posthuset	Ribe, UK	700-1200	3071	100	3.26	47	47.00
Earl's Bu	Orphir, UK	750-1200	18957	38	0.20	33	86.80
Heveskesklooster	Eemsdelta, NL	1300-1500	UNK	1	NA	1	100.00
Huis Malburg	Kerk-Avezaath, NL	900-1049	110	1	0.90	1	100.00
Huize van den Kasteele	Zutphen, NL	950-1100	425	1	0.24	1	100.00
In den Struys	Veere, NL	1425-1500	2797	14	0.50	4	28.57
Johan van Oldenbarneveltlaan	s'-Gravenhage, NL	450-700	547	6	1.10	2	33.33
Kasteel Voorst	Zwolle, NL	1280-1362	83	3	3.61	2	66.66
Minderbroedersklooster	's-Hertogenbosch, NL	1175-1500	3464	26	0.69	23	95.83
Nieuw Rhijngeest-zuid	Oegstgeest, NL	475-725	6567	31	0.47	24	77.41
Oude an nieuwe Gasthuis	Delft, NL	1400-1500	690	4	0.58	3	75.00
Plantage Leiderdorp	Leiderdorp, NL	650-850	2734	9	0.47	6	66.66
Stadhuis Zutphen	Zutphen, NL	1125-1175	4346	2	0.05	1	50.00
Tjitsma Wijnaldum	Wijnaldum, NL	550-950	3967	21	0.53	11	52.38

TABLE 2.3: Summary table of proportions and characteristics of biomolecular sample of *Salmo* sp. remains

Selection of *Salmo* sp. elements for biomolecular testing was assessed on a site-by-site basis during in-person sampling visits. For sites where identified bones had been separated out by taxa, previous identifications were confirmed first. Then, wherever possible, large bags of unsorted fish bone or fish bone identified as simply "Gadids" was sorted through by hand to look for any missed *Salmo* sp. bones, and approximately 19.1% (n=99) of all *Salmo* sp. bones recorded during these reviews (n=517) were either previously not identified or identified as unspecified gadids. Of the original 20 archaeological sites sampled for biomolecular analysis, eight provided both *Salmo* sp. subsamples and comparative fish taxa (Table 4), and 12 only provided a *Salmo* sp. sample. *Salmo* sp. bones destined to be used for bulk stable isotope analysis were preferably kept whole and transported to the University of York where anywhere from 200-500mg of bone material was sampled for destructive analysis, but in some cases (described more in detail in following subsections) bones were split using wire snips or a hand dremel on location. *Salmo* sp. bones which were intended to only be used for ZooMS identification required much less bone material (between 10-30mg), and were usually sampled on-site using the same methods. When sampling whole bones which were the only identified *Salmo* sp. sample from a site, nondiagnostic portions of bone were targeted for sampling, such as neural and hemal spines.

Comparatives

The selection of comparative taxa for biomolecular analysis followed a fairly similar procedure, with most bones being collected whole and brought to the University of York for further sampling for bulk stable isotope analysis. A total of 140 bones from ten taxonomic groups or species were used as comparative samples for biomolecular analysis (Table 4) from 8 archaeological sites, with taxa from diadromous, marine, and freshwater environments. The original preferred diadromous comparative species was the catadromous Euopean eel (*Anguilla anguilla*), however substitutions were required at sites with no eel presence, or those which only had eel elements smaller than 100mg. Substitute taxa included anadromous *Coregonus sp.* elements, anadromous Twait shad (*Alosa fallax*, and situationally-catadromous Thinlip mullet (*Chelon ramada*). Freshwater species sampled included Northern pike (*Esox lucius*), European perch (*Perca fluviatilis*), and fish from the Cyprinidae family including common bream (*Abramis brama*). While there were several sites which necessitated the use of flatfish (family *Pleuronectidae*) and a single Thornback ray (*Raja clavata*) element as marine comparatives, the vast majority were from the Gadidae family. Atlantic haddock (*Melanogrammus aeglefinus*) were preferentially selected from gadidae assemblages, as they are generally from local fisheries and both cranial and vertebral elements can be assumed to belong to a locally processed fish. Conversely, cod and other gadids preserved as stockfish were generally dried and cured using methods which removed the head of the fish around the cleithrum, usually causing damage to it and the supracleithrum. This results in cranial cod elements generally being found in primary processing locations, while the vertebral elements can be found anywhere the dried stockfish was imported and consumed (Barrett 1997; Orton et al. 2014). To circumvent this issue, the majority of the Gadidae sample (n=50) were haddock elements of all kinds (n=41), while the remaining elements were Gadidae cranial elements like dentaries, maxillae, and parasphenoids.

Site	Anguillidae	Clupeidae	Coregonidae	Cyprinidae	Esocidae	Gadidae	Mugilidae	Percidae	Pleuronectidae	Rajidae	TOTAL
16-22 Coppergate	7			1	6	7					21
DANISH SITES											
ASR 13 Lindegården						2					2
ASR 2090 von Støckens Plads				3		4					7
ASR 9 Posthuset	1			10	3	3	10	1	8		36
Earl's Bu	3					20			1	1	25
DUTCH SITES											
Minderbroedersklooster			6	7	11	12					36
Nieuw Rhijngeest-zuid	2	1	2	1		2		5			13
TOTAL	13	1	8	22	19	50	10	6	9	1	140

TABLE 2.4: Breakdowns of comparative taxa sampled for biomolecular analysis from all archaeological sites

2.3 Archaeological Assemblages and Background

The first subsection introduces some of the more general characteristics of the various medieval periods across the study area, as well as describing issues of periodisation and comparison across such broad spatial and temporal scales. After this overview of the medieval North Sea, the following subsections will discuss the characteristics of each sampled site's (n=17) fish bone assemblage and selected biomolecular samples, in as detailed a manner as possible, as well as site phasing and cultural/historical context. The following sites all have publications and grey literature available which contain fish bone data, site phasing and contexts, and even some interpretive comments by the original analysts; 16-22 Coppergate, ASR 9 Posthuset, ASR 2090 Lindegården, ASR 13 von Støckens Plads, Earl's Bu, Heveskesklooster, Huis Malburg, In den Struys, Johan van Oldenbarneveltlaan, Kasteel Voorst, Plantage Leiderdorp, and Tjitsma Foarryp-Wijnaldum (Batey 2023; Besteman and Nieuwhof 1999; Croix 2015; Dijkstra, Verhoeven, and Straten 2016; Enghoff 2006; E. Esser 2000; Feveile 2006; Feveile and S. Jensen 2000; R. A. Hall 2014; R. A. Hall and Hunter-Mann 2002; J. Harland 2006; J. F. Harland, Jones, and Orton 2016; IJzereef 1983; Laarman and Lauwerier 1996; Magendans and Waasdorp 1989; Mainland and Batey 2018; T. O'Connor 1989; Prummel, K. Esser, and Zeiler 2013; Slippe, Sogn, and Sovso 2006; Søvsø 2006; Sovso and T. B. Jensen 2016). The fish remains from the Oude en Nieuw Gasthuis site in Delft were included in archaeozoologist Kinie Esser's 1992 unpublished master's thesis (E. Esser 1992). The Nieuwe Rhijngeest-zuid site from Oegstgeest, NL does have preliminary data published from earlier excavations in 2009, but all additional interpretive information is taken from personal correspondence and data provided by University of Leiden zooarchaeologist Dr. Laura Llorente-Rodriguez and Rijksdienst voor het Cultureel Erfgoed Staff Zooarchaeologist Inge van den Jagt (Bruin, Bakels, and Theuws 2021). The fish remains from both the Huize van de Kasteele and Stadhuis sites in Zutphen were the subject of a preliminary internal report by Bob Beerenhout for commercial post-excavation company Archaeo-

zoo (Bob Beerenhout 2011). Finally, the fish remains from the Minderbroedersklooster site in 's-Hertogenbosch have not been fully recorded at this time, so only a limited view of the full assemblage is presented here.

2.3.1 The Medieval North Sea - c. 500-1500 CE

The North Sea basin is a geological basin spanning approximately 750,000 square kilometers and encompassing an area that stretches from the east coast of the UK, the coastline of southern Norway, western Sweden and Denmark, to the coastlines of northern France, the Netherlands and northwestern Germany (Milner et al. 2008). The North Sea is a highly productive marine environment with a cool-to-temperate climate, rapid nutrient cycling due to cyclical weather systems, and a shallow sea bed (Milner et al. 2008). This marine productivity has greatly benefited human settlements in the area going back at least 10,000 years (Milner et al. 2008), and the Medieval Period, spanning from roughly 500-1500 CE, was no different. This thesis is concerned with archaeologically-derived fish remains recovered from sites in four modern-day North Sea basin countries; England, Scotland, the Netherlands and Denmark (Figure 3). The medieval settlements in this study area were heavily reliant on the North Sea not only for marine resources, but for social and political connection across it's basin area (Ayers 2016; Milner et al. 2008).

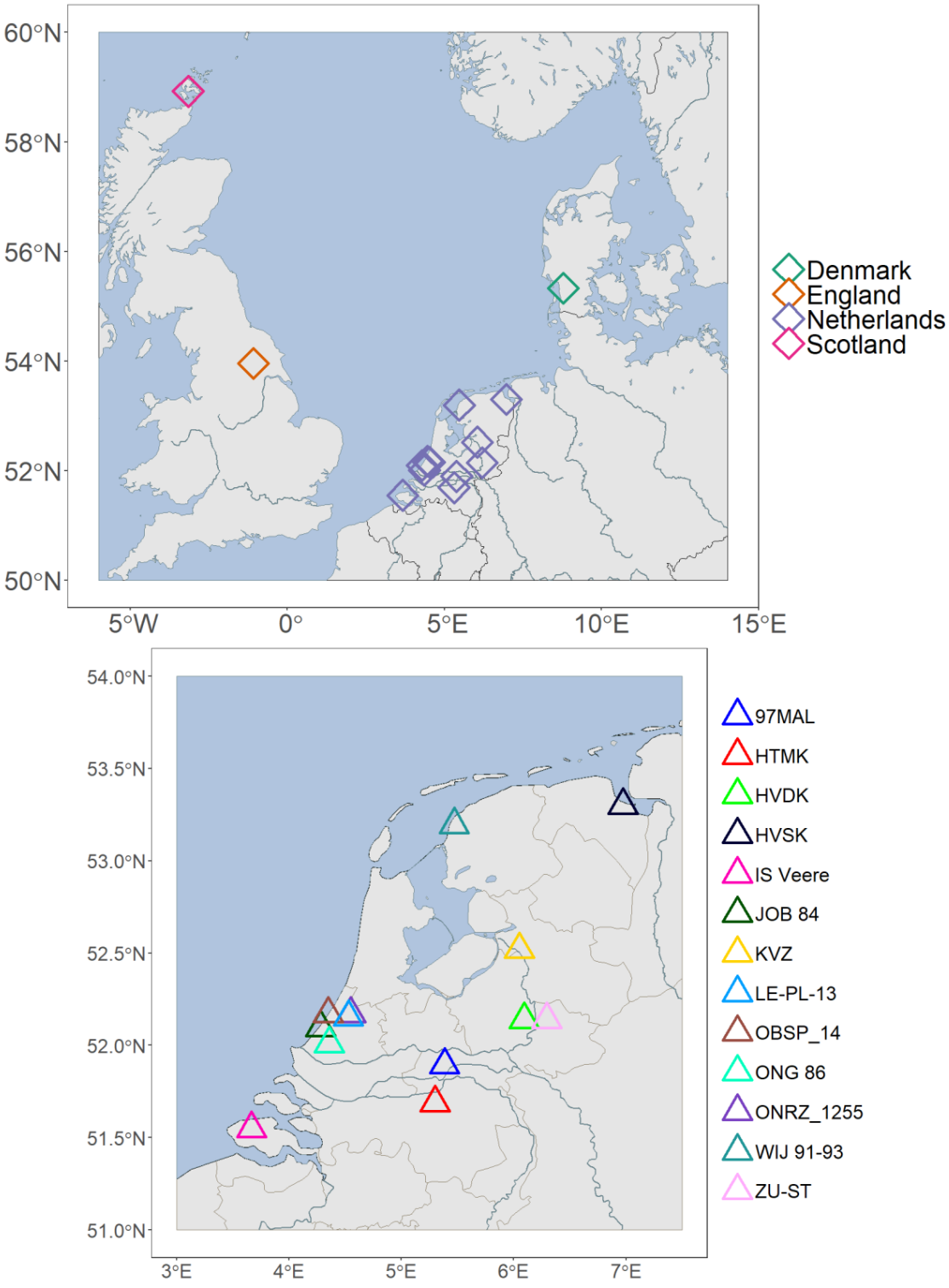


FIGURE 2.3: Top: locations of the 17 archaeological sites included within this study. Bottom: Locations of the 12 Dutch sites within the Netherlands.

Throughout the roughly 1000-year period this thesis focuses on, there were significant shifts in social, political, and cultural control of the areas that would become the UK, Netherlands and Denmark. One of the more

difficult aspects of summarizing this Medieval Period in the North Sea basin area is that it is simultaneously a geographically broad, but closely connected area. Subdividing this Medieval Period into meaningful units for discussion and comparison is an ongoing debate within medieval studies, with regional chronologies reflecting the unique periodisation of each area as well as the influences of modern identity construction (Graham-Campbell et al. 2007; Rambaran-Olm 2021). There is a traditional division of the "ages" of Europe into Classical, Medieval, and Modern which, while it can be a useful starting point to understand some of the shifting cultural and social identities of the period, does obscure the complexities of the era (Rambaran-Olm 2021). The legacy of Roman occupation and society is evident in the way that medieval chronology in the Netherlands and England are defined, but has less impact on those of Scotland and Denmark (Graham-Campbell et al. 2007). What is considered the "Early Medieval" in England, for example, is still firmly in the Danish "Late/Germanic Iron Age" (Näsman 1989), and the Norse period in Orkney extends well into what is called the "high" and "late" medieval periods in York (Anderson 1873; Barrett, Beukens, et al. 2000; J. Harland 2019). The influence of Roman occupation in York is still evident today, with much of the modern city built directly on top of the Roman military encampment, but other influential trading centres, like that seen at Oegstgeest, were constructed away from nearby former Roman towns (Graham-Campbell et al. 2007; Loveluck 2017; Parker 2019). Similarly, the impacts of Christianity in medieval Europe were evident at an institutional level, but were not all encompassing, and cannot be the only lens through which these complex narratives of social, political and economic change are understood (Graham-Campbell et al. 2007; Loveluck 2017).

It is for this reason that the following descriptions of site phasing and broader cultural context will be discussed in terms of locally relevant periodisation, with consideration for the influence of wider geographic, cultural and political entities on the settlements in question. What unites all of these sites is the presence of *Salmo* sp. remains and, therefore, an implied importance of aquatic resources to the human occupants of the site. One of the major known periods of intensification of marine resource exploitation, the so-called "fish event horizon", is described by Barett et al. and centres around a transition in fishing from freshwater to marine species on either side of the 11th-century CE (Barrett 2016; Barrett, Locker, and Roberts 2004). These shifts in fishing practice are reflected in the archaeological assemblages from around the North Sea basin, and are one of the major interpretive frameworks for this thesis research. While cultural, political and social drivers of these fishing practice changes may have differed across the study area and occurred on different timelines, the changes were ultimately observable and had long-lasting impacts.

2.3.2 16-22 Coppergate - York, England - 450-1720 CE

Phasing and Background

Between 1976-1981 the archaeological site at 16-22 Coppergate, York was excavated by the York Archaeological Trust (YAT) (R. A. Hall 2014; R. A. Hall and Hunter-Mann 2002). Throughout the years of excavation an exceptional amount of soil was sampled for later analysis by the York Environmental Archaeology Unit (Bond and T. P. O'Connor 1999; Kenward and A. R. Hall 1995; T. O'Connor 1989). A total of 375 bulk soil samples were wet sieved through 1mm mesh, air dried, and then dry-sieved through 2mm mesh to aid in recovery of small animal bone fragments (T. O'Connor 1989). These collection efforts yielded a fish bone assemblage spanning well over 1300 years of occupation with an approximate NISP of between 22,000-32,000 (see following section for discussion of Coppergate fish bone assemblage). The broadly medieval chronology of the Coppergate site runs from the 5th-century CE to approximately 1500 CE, with the densest periods of occupation beginning in the mid-late 900s (Table 5). The majority of the recovered fish bones were from contexts described generally as

"Anglo-Scandinavian" (Periods 3, 4A , 4B, 5A, and 5B) and "Medieval" (Periods 5Cf, and 5Cr) with the former fitting generally into the years c. 850-1050CE, and the latter from c. 1050-1500CE. Both the Anglo-Scandinavian and medieval periods at the Coppergate site contain rich cultural, osteological, architectural and faunal deposits which have been explored in various publications over the years (Bond and T. P. O'Connor 1999; R. A. Hall 2014; R. A. Hall and Hunter-Mann 2002; MacGregor, Mainman, and Rogers 1999; Mainman 1990). Two volumes produced by the York Archaeological trust describe the Anglo-Scandinavian period of occupation (R. A. Hall 2014) and a post-Norman medieval occupation (R. A. Hall and Hunter-Mann 2002). These volumes establish the original chronology of the distinct occupations at Coppergate (Table 5), which breaks the site down into 6 periods.

The general characteristics of the Coppergate site, and the city of York itself, fluctuated through time depending upon the cultural and social attributes of the occupants, but throughout it's use it remained a busy urban settlement. York's status as an important political and economic settlement is generally ascribed to the formal establishment of a Roman military outpost circa 70/71 CE, with official designation of Eboracum as a civilian *colonia*, or high status Roman outpost, dating to the end of the 2nd-century CE (Parker 2019). There is evidence for survival of active and somewhat "normal" civilian life in York during the long decline of the Roman empire and after the formal hiatus of central Roman governance in the area circa 410 CE (Frere 1998). There are scant references to a post-Roman reclamation of the town of York by Britons prior to the arrival of the Angles and Saxons, mainly based on Nennius' reference to a settlement called *Cair Ebrauc* which may have been a continuation of Roman *Eboracum* (Nennius and Gildas 1841). The late 5th-9th centuries in York are generally referred to as the "Anglo-Saxon" period, but this term has been criticized for it's lack of specificity, homogenization of a complex influx of Germanic settlers during this period, and is sometimes considered an anachronistic appellation– as Myres put it in his 1970 Raleigh Lecture; "Bede invented the Angles, the Saxons and the Jutes" (Frere 1998; Myres 1972; Wilton 2020). Archaeological excavations in the York area now show an alternative view of the post-Roman town as a polyfocal urban area, with evidence for Anglian and Saxon burials, multi-use domestic features, and commercial operations characterizing a *wic*, or trading emporia, situated around the former Roman core during the late 5th-early-7th centuries (R. Hall 2011; Palliser 2014; Spall and Toop 2008). Centralization of power into a unified Northumbria occurred as the 7th-century progressed, with York as a central location in this kingdom stretching from the Humber to the Clyde and Forth (Loyn 2009; Rollason 2007). The archaeological evidence from York supports the notion of York as a bustling commercial centre in Northumbria, growing from a loosely affiliated collection of *wics* on the outer edges of the former Roman fortress to *Eoforwic*, a robust settlement with distinct administrative, industrial and domestic spaces by the mid-9th-century CE (R. Hall 2011; Spall and Toop 2008).

The mid-9th-century CE is significant for two reason– it is when evidence for renewed occupation of domestic and commercial contexts appears at Coppergate in Period 3 (see Table 5), and is when the Scandinavian raiding parties that had been landing along the British coast since the late 780s CE unified into large colonial forces from 865 CE onward (R. A. Hall 2014; R. A. Hall and Hunter-Mann 2002; Richards 2013). The "Viking Great Army", a confederation of most-likely Danish forces that overwintered in England for the first time in 865 CE, gained control of York in 866CE, and would go on to establish a short-lived, but influential, Scandinavian colonial kingdom up and down the eastern coast of the UK (R. A. Hall 2014; Palliser 2014; Richards 2013). York was under Scandinavian rule from 867-954 CE, but it appears that the ethnic composition of the town remained diverse, with those who could be described as Northumbrians living side by side with Danish and Norse newcomers (Palliser 2014). There is no widespread destruction layer from the 860s in York, and it seems that after a brief disruption life in York continued on a relatively normal path of urbanization, with pockets of intensive reorganization and

Period	Dating	Characteristics
1	late-1st to late 4th-century or later	Roman timber and stone buildings; Late Roman cemetery. Limited survival of organic material.
2	5th to mid-9th century	Apparent desertion. Homogenous loamy deposits which did not preserve organic materials.
3	mid 9th-late 9th/early 10th-century	Rubbish disposal, suggesting occupation close by. Post/stake and wattle alignments, possibly boundaries. Organic materials preserved in pit cuts.
4A	late 9th/early 10th-century- c. 930/5	Realignment of boundaries, suggesting that Coppergate was laid out by this period. Possible buildings at Coppergate frontage. Organic materials preserved mainly in pit cuts.
4B	c. 930/5 - c. 955/6	Four tenements distinguishable, with post and wattle buildings at Coppergate frontage. Evidence for ironworking and other trades on a commercial scale. Organic-rich deposits nearer to Coppergate; organic content thinning to zero towards River Foss.
5A	c. 955/6	Near Coppergate frontage only. Layers between structures of Periods 4B and 5B; probably mixture of occupation deposits, dump deposits and soil from 5B semi-basements.
5B	c.955/6-early/mid 11th-century	Perpetuation of boundaries. Introduction of sunken-featured structures in double row at street frontage. Organic-rich deposits as in Period 4B.
5Cf	mid-later 11th-century	Organic rich deposits at street frontage, associated with buildings which survived only in Tenement D.
5Cr	mid-later 11th-century	Post-built structures closest to River Foss sealed by earliest in a succession of dump deposits. Little organic material surviving.
6	later-11th to 16th-century	No remaining structures surviving at street frontage, but area to rear increasingly built up above later dump deposits. New methods of building and rubbish disposal, leading to reduction in organic content of debris.

TABLE 2.5: Table of Original Coppergate Phasing (after Hall et al. 2014)

infrastructure changes centering around modern-day streets like Micklegate, Ousegate, and the Pavement (R. A. Hall 2014). The evidence from Coppergate shows a thriving domestic and trade centre that was under administrative control of Scandinavian leaders, but remained in close contact with southern British kingdoms (R. A. Hall 2014; Palliser 2014). As the southern Anglian and Saxon kingdoms were consolidated under Athelstan in 927CE, the struggle for York began and it passed between Saxon and Scandinavian control until it was finally seized and incorporated into the Kingdom of England in 954 CE (Palliser 2014).

The Coppergate site, and York itself, continued to demonstrate a mixed cultural and ethnic identity even after English control of the town was firmly established in the mid-10th-century, with material culture evidence suggesting continued Scandinavian influence and connection with Denmark and Norway through trade (Hadley 2003; R. A. Hall 2014; Palliser 2014). By the mid-11th-century there had been renewed Scandinavian efforts to retake York and reestablish permanent settlements within the former Danelaw, culminating in the turbulent 1066-1069 period involving the Battles of, among others, Stamford Bridge, Fulford, and Hastings, as well as William the Conqueror's eventual retaking of York in 1069 CE (Hadley 2003; Palliser 2014). Archaeological evidence in York, and elsewhere in the North does not necessarily support the alleged severity of the "Harrying of the North" as reported by Oderic and Geoffrey of Monmouth (Palliser 2014). While York likely lost about 30% of its inhabitants and/or housing between 1066-1068, archaeological and linguistic evidence implies that the wealthy may have fled the town, but most inhabitants remained (Palliser 2014). Throughout the remainder of the 11th and into the 12th centuries, the lands and people of York were fully encapsulated under Norman rule as part of William's centralized English state, with the town remaining an ecclesiastical and administrative centre of power in the North (Palliser 2014). Along with it's religious and political importance, York's position as a powerful trading town only expanded as the Medieval Period continued, with successive periods of economic and population growth from the 1200s to the mid 1400s (Palliser 2014). During this "Late Medieval" period York was second only to London in terms of economic importance and sheer variety of trade, industry, and occupations of it's citizens (McClain 2017; Palliser 2014). Ultimately, a shift in focus on centralizing trade and power around London, as well as a broader European economic recession due to a series of bullion shortages in the 15th century, diminished the identity of York as a dominant centre of commerce (Palliser 2014). During it's peak medieval York was inhabited by a series of diverse cultural groups that could be described as Anglian, Northumbrian, Scandinavian, Saxon, Norman and, ultimately English. The occupants of York built domestic tenement dwellings, workshops and storefronts for small-scale industries relating to food production and handcrafts which would be preserved in the form of archaeological sites like Coppergate (R. A. Hall 2014; R. A. Hall and Hunter-Mann 2002). Though identities shifted over time, the social fabric of York as a cosmopolitan urban centre of religious, political, and social power remained strong, with Coppergate acting as a particularly rich type site (R. A. Hall 2014; R. A. Hall and Hunter-Mann 2002).

Materials

The Coppergate site has a variably reported total fish bone assemblage of between 20,000 and 32,000 fish bones, depending on which publication or report is referenced. This large discrepancy is based on a significant decrease in recorded bones that could be re-identified and verified upon a second review of fish bone material at the site, which will be briefly detailed here. The original fish bone identifications (Table 6) were conducted by Dr. Andrew K.G. Jones in the late 1980s, and the surviving recording sheets indicate a fish bone count of 32,015. Later, in 2008 Dr. Jen Harland re-assessed the extant Coppergate assemblage of fish bones and was able to verify the presence and identifications of 22,886 total fish bones. These numbers were later revised further to a total fish bone assemblage of 20,463 bones, with 5685 unidentified fish elements and a NISP of 14,778 (J. F. Harland, Jones,

and Orton 2016).

	AKGJ Original Records (1988)	**Harland Updated Records (2008)**	**Harland et al. (2016)**	**LMQ Thesis Review**
Total Recorded Fish Elements	32015	22886	20463	NA
Fish NISP	9858	14835	14778	NA
Unidentified Fish	22157	8051	5685	NA
Salmo sp.	394	67	115	256

TABLE 2.6: Coppergate Fish Species Data Discrepancies

Taxon	mid-late 800s/early 900s	c. 930/35 to c. 955/6	c. 955/6	c. 955/6 to early/mid-1000s	mid-later 1000s	mid-1000s to mid-1100s	mid-1000s to early 1200s	mid-1100s to 1200	1200 to late-1200s	1275 to mid-1300s	1300 to late 1300s	1360-1500	Other	Total
Ray family					2	3	4		1					10
Thornback ray					1				3	1				5
Eel	265	767	327	406	479	148	132	7	189	11	13	11	176	2931
Herring family		2	1									23		26
Atlantic herring	145	1982	834	1961	1550	438	393	34	683	97	93	253	366	8829
Shads	2		1	2	3	3	2						1	14
Allis Shad						1								1
Twaite Shad						1								1
Pilchard		1												1
Carp family	83	483	106	115	67	24	13		13	4		5	21	934
Gudgeon		4												4
Dace		5	3											8
Roach		12	3	2	2	1		1						21
Roach?		1												1
Rudd		2												2
Chub		2			1									3
Tench		2		1										3
Tench?		1												1
Pike	8	90	53	37	32	10	11		24	1			9	275
Smelt	4	66	24	27	4	5	1		6	2		4	8	151
Salmon and trout family	21	24	23	14	11	10	2		4			1	5	115
Cod family	1	2	2	3	22	6	3		6	2	1	4	5	57
Cod		24	3	68	220	72	31	7	81	22	9	46	27	610
Whiting			2	1	2	3			6	8	13	26	9	70
Pollack									1					1
Saithe						1				3				4
Haddock				1	4	98	25	15	197	25	4	47	60	476
Burbot	2	5	4	2	9				3	1				26
Burbot?									2					2
Tusk										1				1
Ling						2		1	3			2	1	9
Perch	1	18	6	8			2		4	1	1	1	1	43
Atlantic horse mackerel/scad					2		1						2	5
Atlantic horse mackerel		3	1	1	2	3			1			1	2	14
Turbot family						1								1
Halibut family	7	13	5	6	11	9	5	1	24	7		9	5	102
Plaice				1		2			7		1		1	12
Halibut					1									1
Flounder						1			2				1	4
Total Identified	539	3509	1398	2656	2423	839	621	66	1259	186	135	433	700	14764
Unidentified	189	933	395	818	761	677	196	44	789	158	136	274	315	5685
GRAND TOTAL	728	4442	1793	3474	3184	1516	817	110	2048	344	271	707	1015	20449

TABLE 2.7: Coppergate recorded fish samples, reproduced in part from (J. F. Harland, Jones, and Orton 2016)

In addition to the NISP and unidentified fish bone data, there were also significant differences between the original records of recorded *Salmo* sp. elements. Jones originally recorded 394 bones belonging to his taxonomic groupings "Salmonidae", "Salmon", "Salmon/Trout", "Trout", "Salmon?" and "Trout?". Jen Harland was only

able to verify 67 of these original 393 identifications in 2008, but was able to revise this value to a *Salmo* sp. NISP of 116 as published in 2016 (J. F. Harland, Jones, and Orton 2016). The discrepancies in the *Salmo* sp. and overall fish NISPs are likely related to factors of collections management, preservation, identification, or a combination thereof. This may including collection curation and preservation over time, confidence of individual faunal analysts in identifying *Salmo* sp. fishes, and varying access to the archaeological material over the years. To this effect, Harland noted in a personal communication that Jones appeared to not only be more confident in identifying elements to species, but also more confident in identifying some commonly-unidentified elements (fin rays, spines, etc.) Because of these present data discrepancies, I decided to fully review the existing fish remains to look for any and all identifiable *Salmo sp.* bones. My review was conducted in October-December of 2020, and resulted in a recorded *Salmo* sp. NISP of 256, with 27 of these elements not previously identified by either Harland or Jones.

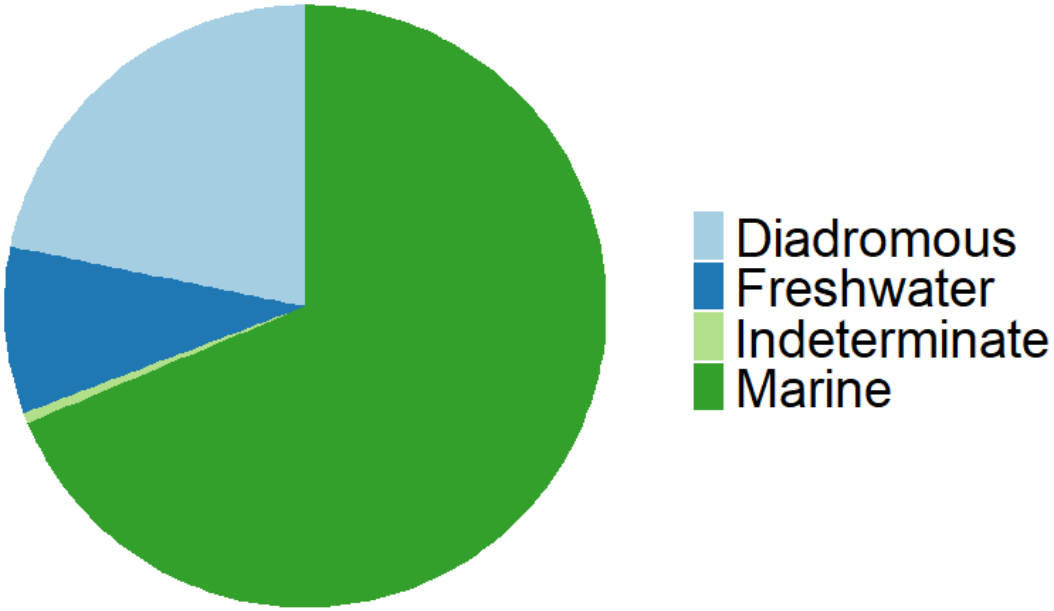


FIGURE 2.4: Proportions of marine, freshwater, diadromous, and indeterminate fish bones identified at 16-22 Coppergate

Based on the confirmed NISP of 14764, Figure 4 above shows the percentages of Marine (n=68.7%), Fresh-

water (n=9.0%), Diadromous (n=21.8%) and Indeterminate (n=0.5%) fish elements identified at the Coppergate site. A selection (n=81) of bones from this assemblage was subsampled in order to perform bulk stable isotope analysis and zooarchaeology by mass spectrometry analysis. The final assemblage of Coppergate samples with available biomolecular results contains 81 bones– 55 samples with bone ZooMs and bulk SI data which remained after applying quality control methods, 21 samples with only bulk stable isotopes results, and 5 with only ZooMS data. Two samples did not produce enough collagen for bulk stable isotope analysis, and were not further sampled for ZooMS analysis as they were from comparative taxa. The final Coppergate biomolecular dataset contains 59 *Salmo* sp. elements with available biomolecular results (Table 8), from 17 distinct temporal contexts across the site (Table 9). The majority (n=50) of the *Salmo* sp. sample from Coppergate are vertebral elements, with a fairly even split between caudal (n=23) and precaudal vertebrae (n=25) and two indeterminate vertebral centrum fragments. The remainder (n=11) is comprised of an articular, one dentary, one unidentified cranial bone, two ceratohyals, three ribs, and three indeterminate elements. The comparative taxa assemblage collected with these *Salmo* sp. samples was made up of 20 bones from four taxonomic families– Anguillidae (n=7), Esocidae (n=3), Gadidae (n=7), Cyprinidae (n=1), as well as two bones, a dentary and a rib, which were had originally been identified as *Salmo* sp. but were actually from a pike (*Esox lucius*) and a cod (*Gadus morhua*), respectively.

Family	Element	NISP
Anguillidae		
	dentary	2
	vertebra	5
Cyprinidae		
	pharyngeal	1
Esocidae		
	caudal vertebra	1
	dentary	1
	hyomandibular	1
	vertebra	1
Gadidae		
	articular	3
	hyomandibular	3
	postcleithrum	1
	precaudal vertebra	1
Salmonidae		
	articular	3
	caudal vertebra	23
	ceratohyal	2
	cranial bone	1
	dentary	1
	indeterminate	3
	precaudal vertebra	25
	rib	3
	vertebral fragment	2
TOTAL		81

TABLE 2.8: Element breakdown from 16-22 Coppergate Biomolecular Sample

Lumped Phasing	Original Start/End Dates of Included Contexts (CE)	Biomolecular Sample NISP
400-850 CE	400-850	1
850-950 CE	850-950; 850-956; 875-935; 930-956	22
950-1050 CE	955-56; 955-1050	23
1050-1200 CE	1050-1100; 1100-1140	8
1200-1350 CE	1200-1240; 1200-1280; 1200-1350; 1275-1350	12
Early Mixed Medieval	1040-1160; 1040-1220; 1040-1280; 1040-1480	12
Late Mixed Medieval	1230-1720; 1360-1500; 1370-1720	2
Unknown	Unknown	1
TOTAL		81

TABLE 2.9: 16-22 Coppergate Phase Groupings

The freshwater fish bone subsample consists of pike (*Esox lucius* (n = 4) and a Cyprinid (n=1), the migratory subsample consists of eel *Anguilla anguilla* (n = 7), and the marine fish bone subsample (n=8) consists entirely of gadids, with 2 haddock (*Melanogrammus aeglefinus*) bones, 5 cod (*Gadus morhua*) bones, and 1 unspecified Gadidae bone sampled. All cod elements selected for bulk stable isotope analysis from all sites were cranial, to limit the chance of individuals being sampled which were not from local North Sea waters. Haddock remains, both cranial and postcranial, from Coppergate are thought to reflect local fisheries (J. F. Harland, Jones, and Orton 2016), and therefore both types of element were selected for bulk SI analysis to be used as local marine proxies.

2.3.3 ASR 9 Posthuset - Ribe, Denmark - 700-1200 CE

Phasing and Background

Archaeological investigations to uncover the location of *Gamle Ribe* ("Old Ribe"), which was attested to in historical records as early as 1736 (Feveile 2006), began in the 1950s, and the location of the oldest portion of the settlement was first discovered in 1971 (Bencard, Jørgensen, and Madsen 1981; Feveile 2006). Between 1973-75, 1986, and 1990-1991 there were three major excavation campaigns focused on the 8th-9th century marketplace and settlement. The marketplace developed out of a brief earlier phase of agrarian activity and settlement, and was ultimately planned and constructed in the first decade of the 8th-century (Feveile 2006). It was first established around the year 700 CE as a loose association of domestic dwellings and small craft workshops, with the earliest evidence for craft activities at dated to c. 705 CE, (Feveile 2006). The settlement was rapidly consolidated into a permanent marketplace, or *emporium*, and it is proposed that by 710CE the market had been divided systematically into plots laid out along a main road, which would remain in operation at least into the middle of the 9th-century (Bencard, Jørgensen, and Madsen 1981; Croix 2015; Feveile 2006). Interspersed throughout the marketplace and domestic units were numerous waste pits and middens, several of which were included in the excavation designated as ASR 9 "Posthuset", with phases that date to between 700-1200 CE.

Numismatic and dendrochronological investigations of the Posthuset site have contributed greatly to the exceptionally well dated sequence of the wider Ribe emporium complex. The early Ribe emporium was part of a wider Northern European network of emporia that arose out of the same post-Roman power vacuum seen in English sites like Coppergate, and represent the beginnings of medieval urbanisation across the region (Croix 2015; Feveile and S. Jensen 2000; Sovso 2020). The site spans the Danish "Late Iron Age", a period of transition

from what is locally termed the "Germanic Iron Age" to the "Viking Age", dated in Denmark to the early 5th-11th centuries, and is a prime example of how the means and methods of trade and manufacture were shifting during the period (Näsman 1989). The 8th century saw an overall increase in long distance trade and local production of both everyday and luxury items, something for which there is ample evidence at the ASR 9 Posthuset site (Ashby, Coutu, and Sindbæk 2015; Baug et al. 2019; Feveile 2006; Näsman 1989). Items for local sale and long distance trade were produced within dedicated workshops for glassmaking, boneworking, smithing, and numerous other skilled artisanal crafts (Feveile 2006). Pottery originally produced in England, France, Germany, Belgiuma and Holland has been found in the late 9th century deposits on the site, connecting Ribe to contemporary 7th-9th century sites like Lundenwic, Valkenburg, Dorestad, Emden, and Kaupang (Croix 2015; Feveile 2008; Sovso 2020). Additionally, an exceptional number of *sceatta* coins, likely from Northern Frisia, have been found in across both 8th-9th century deposits, contributing to the evidence for both precise dating and well-connected regional trade networks (Feveile 2008).

The origin of the political and economic power behind the observed changes in trade and production strategy across Northwestern Europe, and specifically the marketplace at Ribe, is much-debated. It has been suggested that the marketplace may have been built on the orders of a local *stormand* (autocrat) looking to increase their power, or even Ongendus– reported to be King of the Danes by Willibrord circa 710 CE, the same time as the founding of the Ribe market (Feveile 2006; Talbot 1981). An alternative, but equally as likely interpretation, is that the Ribe marketplace was the result of Frisian merchants from Dorestad seeking to establish a northern trade stronghold in order to bypass early settlements near Hedeby/Haithabu (Feveile 2006). Regardless of the motivation behind it's founding, the Ribe marketplace was ideally placed on the western shore of southern Jutland, less than 10km from the mouth of the Ribe Å with direct access to the North Sea. Craft production, domestic space use, and planning evidence from the marketplace excavations indicate year-round occupation and industry, constituting an established town environment rather than a seasonal trade centre. (Croix 2015; Sovso 2020). There may have been fluctuations in both residents and activity– fish bone remains indicate a seasonallocal fishing economy , with heavy emphasis on summer fishing for horse mackerel, flatfish, sea trout and salmon (Enghoff 2006). Interestingly, an unusual amount of thin-lipped grey mullet (*Liza ramada*) remains may indicate long-distance trade not only for artisan crafts at the marketplace, but fish as well (Enghoff 2006). It's clear to see why the Ribe marketplace and early town has been described as "the most important trading centre of South Scandinavia" during the time period, with it's inhabitants benefiting greatly from the robust trade opportunities available to them (Feveile 2006; Näsman 1989).

Materials

The ASR 9 Posthuset site from Ribe had the second-largest overall *Salmo* sp. assemblage included in this thesis research, with 200 recorded *Salmo* sp. bones (Table 10). All fish bone material (n=3319) from all contexts of this site were reviewed during an in-person visit to the Zoological Museum at the University of Copenhagen in November of 2021. Previous identifications were made by Dr. Inge Bødker Enghoff, and were reported as part of Claus Feveile's 2006 summary publication of excavations at Ribe (Enghoff 2006; Feveile 2006). The fish bone assemblage from the ASR 9 Posthuset site has a NISP of 3163, with 156 unidentified elements. The Ribe fish material constitutes one of the most diverse subfossil assemblages in Denmark, with a total of 16 species represented (Enghoff 2006). For the most part all fish bone was recovered from water sieved contexts, using between 2-4mm mesh sieves, and only occasional hand collection recorded. Enghoff notes that the Ribe assemblage is "extremely well preserved", and concludes that most species represented can theoretically be caught either from the Ribe Å (Ribe River), the Wadden Sea, or further out into the North Sea.

Species Group		**Germanic Iron Age**				**Viking Age**		**Middle Age**	
Common Name	*Phase B*	*Phase C*	*Phase D*	*Phase E*	*Phase F*	*Phase G*	*Phase H-I*	*Phase J*	*TOTAL*
	705-725	**725-760**	**760-780**	**780-790**	**790-800**	**800-820**	**820-850**	**12th-13th**	
Marine Species	**CE**	**CE**	**CE**	**CE**	**CE**	**CE**	**CE**	**Century**	
Smallspotted catshark	-	-	-	-	-	-	-	1	1
Cod	-	9	7	4	4	-	164	48	236
Haddock	-	1	-	-	18	-	103	90	212
Ling	-	-	-	-	-	-	14	1	15
Unspec. Gadids	1	39	7	11	1	-	36	36	131
Atlantic horse mackerel	-	-	2	2	-	-	1	-	5
Thinlip grey mullet	2	112	9	16	5	-	-	-	144
Turbot/Brill	1	-	-	-	-	-	-	-	1
Dab	-	1	-	-	-	-	-	-	1
Flounder	-	2	-	-	-	-	-	-	2
Plaice/ Flounder/Dab	43	829	149	515	385	8	50	5	1984
Common Sole	-	-	-	1	-	-	-	-	1
Migratory Species									
Salmon/trout	12	113	23	28	13	3	7	-	199
Whitefish	-	15	1	1	2	-	-	-	19
Eel	-	29	-	15	7	-	-	-	51
Freshwater Species									
Pike	-	20	8	6	9	3	4	-	50
Common bream	-	1	-	-	-	-	-	-	1
Unspec. Cyprinids	2	55	1	10	18	1	2	-	89
Perch	-	4	-	1	15	-	1	-	21
Total identified	*61*	*1230*	*207*	*610*	*477*	*15*	*382*	*181*	*3163*
Total unidentified	*10*	*73*	*3*	*4*	*23*	-	*36*	*7*	*156*
GRAND TOTAL									**3319**

TABLE 2.10: Taxonomic breakdown of fish recovered from the ASR 9 Posthuset excavation, after (Enghoff 2006)

All *Salmo* sp. elements from ASR 9 Posthuset are vertebrae, and are recorded as *Salmo* sp. Enghoff remarks within the text of her report that this is a conscious decision– that it is "not possible to determine which of the two species [salmon or trout] are present..." (Enghoff, 2006). The earlier phases of the site date from the German Iron Age (705-790 CE), and are dominated by various flatfish species, followed by the thinlip grey mullet, and *Salmo* sp. groups. This site is unique among the sampled sites due to it's large presence of thinlip mullet (*Liza ramada*) elements– with a NISP of nearly 150 specimens of these fish, which are primarily found in southern Atlantic and Mediterranean waters. Enghoff interprets the large presence of *Salmo* sp., shallow-sea foraging flatfish, and seasonally migrating *Liza ramada* at the site as evidence for seasonality of the marketplace during it's first 100 years of operation (Enghoff, 2006). She indicates that this fish bone evidence likely means the periods of high activity occurred during the early summer-autumn months (Enghoff, 2006). The Viking Period phases (790-850 CE) show an almost even split between various gadids and flatfishes, and a drastically reduced *Salmo sp.* assemblage. This shows the early beginnings of supplemental fishing for deep water marine species, which would eventually tie into the Northern European Fish Event Horizon (Barrett et al., 2004) later in the 10th century. Finally, the short Middle Age phase (12th-13th Centuries CE) show no *Salmo* sp. identifications, and is completely dominated by various Gadidae species. A total of 83 fish bones were sampled from this site, and a total of 75 bones yielded enough collagen for biomolecular analysis (Table 11). 16 samples were analysed using both bulk stable isotope and ZooMS analysis, 30 samples only have bulk stable isotope results, and the remaining 29 samples only have ZooMS results. The 8 samples which did not yield enough collagen for bulk stable isotope analysis were primarily comparative taxa that were not selected for further ZooMS analysis. Unlike all other biomolecular samples included in this thesis, the bones from ASR 9 were cut and sampled on location in Copenhagen, at the request of the zooarchaeological collections manager.

Taxa	**Element**	**NISP**
Anguilla anguilla	caudal vertebra	1
Cyprinidae	caudal vertebrae	7
	first vertebra	1
	pharyngeal	1
	ultimate vertebra	1
Esox lucius	precaudal vertebra	2
Melanogrammus aeglefinus	caudal vertebrae	2
Liza ramada	caudal vertebrae	8
Perca fluviatilis	caudal vertebra	1
Pleuronectidae	caudal vertebra	5
Salmo sp.	caudal vertebrae	20
	precaudal vertebrae	20
	vertebral fragments	6
TOTAL		**75**

TABLE 2.11: Fish bone elements sampled for biomolecular analysis from ASR 9 Posthuset

2.3.4 ASR 13 Lindegården - Ribe, Denmark - 1200-1300 CE

Phasing and Background

On the opposite side of the Ribe Å from the ASR 9 Posthuset site's 8th-10th century marketplace lies the modern day centre of Ribe, where the main settlement relocated in the 11th century (Feveile 2006; Sovso and T. B. Jensen 2016). Excavations between 2008-2012 focused on an area of land directly adjacent to the Ribe *Domkirke* (Cathedral), and which was suspected to be the location of a medieval cemetery (Sovso and T. B. Jensen 2016). Excavations revealed approximately 4m of cultural material, dating from 850-1850 CE. The suspected cemetery was identified, and site phasing indicates that it was abandoned around 1050-1060 CE and, eventually, a series of timbered buildings were erected that were associated with the early church that likely stood in the same location as the modern day Domkirke (Sovso and T. B. Jensen 2016). This early church is often interpreted as either the initial church, or a later replacement, purportedly built by Saint Ansgar, a Franciscan missionary partially responsible for the Christianisation of Jutland in 860 CE (Feveile 2006; Näsman 1989; Robinson 1921). The successful conversion of several Danish kings and their alliance with Frankish rulers to the south increased the strength of a central Danish authority in the late 10th-early 11th century (Feveile 2006; Hybel and Poulsen 2007; Robinson 1921). This, along with centralization of powers in England and continental Europe who were able to resist Viking raiding, resulted in the establishment of a complex network of petty kingdoms throughout Denmark (Hybel and Poulsen 2007). As the 11th century progressed the ties between the Church and royal power grew, and by the mid-12th century a united Danish kingdom was formed under Valdemar I in 1157 CE (Hybel and Poulsen 2007). While the town of Ribe remained an important ecclesiastical centre throughout this period, it's importance as a key trading and manufacturing emporium was diminished after the closure of the marketplace from ASR 9 and relocation of the town across the river.

Materials

All fish bone material from the site was recovered from a ditch feature K476, which was likely a midden associated with the early cloisters of the *Domkirke*. A total of 245 fish bones were recovered from this context, and, while some preliminary sorting had taken place after excavations, they had not been formally recorded prior to my visit to the archaeological collections of the Sydvestjyske Museer in November 2021. Nearly all of the remains (Table 12), which were hand collected during the initial excavations, were Gadidae elements of some kind, with the notable exceptions being a single anal pterygiophore of a Pleuronectid, and 2 *Salmo* sp. vertebrae. The two *Salmo* sp. vertebrae were removed with the permission of the collections manager, and both sampled for bulk stable isotope and ZooMS analysis, in addition to two haddock samples– a caudal vertebra and a cleithrum (the cleithrum did not yield enough collagen for bulk stable isotope analysis).

Taxa	Element	Count
Gadidae	caudal vertebrae	41
	precaudal vertebrae	158
	articular	1
	cleithrum	16
	first vertebrae	16
	maxilla	1
	opercular	1
	preopercular	1
	quadrate	1
	unidentified cranial	6
Pleuronectidae	anal pterygiophore	1
Salmo sp.	caudal vertebra	1
	precaudal vertebra	1
TOTAL		**245**

TABLE 2.12: Fish bone elements recorded from the ASR 13 Lindegården site

2.3.5 ASR 2090 von Støckens Plads - Ribe, Denmark - 1000-1200 CE

Phasing

Located around the corner from the ASR 13 Lindegården site is another cluster of medieval cesspits that was designated as ASR 2090 and was located underneath the modern day street of von Støckens Plads (Slippe, Sogn, and Sovso 2006).The mitigation excavation of ASR 2090 was triggered by planned roadworks that would impact known layers of medieval cultural material (Slippe, Sogn, and Sovso 2006). A comparatively small site, ASR 2090 represents what was determined to be the oldest planned road in "new" Ribe– the settlement after it was moved across the river from the earlier marketplace found at ASR 9 Posthuset (Slippe, Sogn, and Sovso 2006; Sovso and T. B. Jensen 2016). The road was originally constructed as a "bone road" made from compressed kitchen refuse and assorted bone material sometime between 1050-1100CE, and was later covered over with woven wattle mats (Slippe, Sogn, and Sovso 2006).

Materials

The majority of fish bone material (n=212) (Table 13) recorded from this site were found in waste pits (K169/170/171) located adjacent to the road, while the remainder (n= 40) were found within the bone road layer itself (Slippe, Sogn, and Sovso 2006), and all fish bones date to approximately 1050-1150 CE. The fish bones were sorted during the post-excavation processing of site materials and prelminary identifications were indicated on notes within each find bag. A total of four *Salmo* sp. bones were identified within the fish bone assemblage from ASR 2090, and all four were sampled for bulk stable isotope and ZooMS analysis, in addition to 4 haddock and 3 cyprinid bones– all but one (a haddock cleithrum) yielded enough collagen for analysis bulk stable isotope analysis.

Taxa	Element	Count
Cyprinidae	caudal vertebrae	3
	preopercular	1
	subopercular	1
Gadidae	articular	5
	caudal vertebrae	40
	ceratohyal/epihyal	1
	cleithra	10
	dentary	7
	first vertebrae	9
	hyomandibular	5
	indeterminate	2
	maxillae	3
	neurocrania	3
	opercular	1
	otolith	2
	posttemporal	7
	precaudal vertebrae	75
	subopercular	1
	supracleithra	7
	unidentified cranial	10
	vomer	2
Pleuronectidae	anal pterygiophore	1
Salmo sp.	caudal vertebrae	4
Sparidae	caudal vertebra	1
Unidentified	cranial elements	22
	ribs/rays	25
	vertebrae	4
TOTAL		**254**

TABLE 2.13: Fish bone elements recorded from ASR 2090 von Støckens Plads site

2.3.6 Earl's Bu - Orphir, Scotland - 881-1164 CE

Phasing and Background

Located approximately 14 kilometres southwest of Kirkwall, the largest town in the Orkney archipelago, the site of Earl's Bu at Orphir has a complex settlement history spanning the Norse occupation of these northern islands of Scotland. The past and present structures at the site include a Norse mill, several Norse domestic and agricultural structures, the remains of a 12th-century round *kirk* (church), a small graveyard, and a modern farm (J. Harland 2006). The site was first investigated by antiquarians in the mid-18th and 19th centuries, and later again in the 1930s and 40s– with little official recording done of the excavations completed during any of these periods (J. Harland 2006). Academic excavations led by Colleen Batey and the University of Durham began in 1979,

and continued off and on until 1993, with large amounts of environmental material recovered, including one of the largest assemblages of fish bones from any Scottish medieval site, with a total fish NISP of 18957 (Barrett, Beukens, et al. 2000; J. Harland 2006).

The Norse period of occupation in the Orkney archipelago began in the early 9th-century CE, and the islands were reportedly annexed and placed under Norwegian rule by Harald Fairhair in the late 9th-century (Anderson 1873; Barrett, Beukens, et al. 2000; J. Harland 2006). One of the most crucial historical sources about the Norse period in Orkney is the 12th-century Orkneyinga Saga, which chronicles the history of both the Orkney and Shetland island groups, and their political interactions with Norway and Scotland. Earl's Bu is specifically mentioned in the Orkneyinga Saga, as an estate called *Orfjara*, consisting of the *bu*, or large farm, with its associated church (Anderson 1873; J. Harland 2006). Originally built by Earl Paul Haakonsson, Orfjara was reportedly the site of several political meetings and feasts during the early-mid 12th century (Anderson 1873; J. Harland 2006). Chapters 55 and 66 of the Orkneyinga Saga describe the layout of the farmstead, church, and, most importantly, the drinking-hall where at least one large Christmas feast was held in 1135 CE (Anderson 1873). The first evidence for Norse occupation at Earl's Bu are early midden deposits from c. 881CE, likely associated with early iterations of the Earl's hall, or *skáli*, and other associated buildings (Batey 2023; Mainland and Batey 2018). These middens, and associated structures, were subsequently overlain by a later 10th-11th century complex which included the Earl's hall, a horizontal water mill (with associated head race, tail race, and underhouse), and one of extant features of the site, the round church, or *kirk* (Batey 2023; J. Harland 2006; Historic Environment Scotland 2020; Historic Scotland 2014; Mainland and Batey 2018). This church is the only existing Scottish example of a round church, and was most likely built by Earl Haakon Paulsson and designed to resemble the Church of the Holy Sepulchre he visited on Crusade in 1099 (J. Harland 2006; Historic Environment Scotland 2020). Orkney followed similar patterns of Christianization and colonisation as other Norse holdings in the British Isles, and was a key stopping point between the Kingdom of Norway proper and its lands further afield in Ireland, the Faroes and Iceland. The stone-lined horizontal mill is also one of the earliest examples of it's kind outside of Scandinavia, and it's size and complexity provide direct evidence for local and regional control of agricultural and environmental resources by the ruling Earls (Batey 2023).

Direct Norse control of the Orkney Islands continued well into the 1200s, really only experiencing a weakening of power with the murder of Earl Jon Haraldsson in 1231 CE (Anderson 1873). Archaeological sites across the Orkney and Shetland archipelagos provide direct evidence for long-distance trade across the Norse kingdom during the 9th-13th centuries, with strong ties to Norway, Ireland, mainland Scotland as well as other North Sea locales (Barrett, Beukens, et al. 2000; J. Harland 2006). In fact, it's estimated that a sail powered boat with a good wind could make the trip from Norway to Shetland in approximately 24 hours, allowing for quick and efficient trade of commodities (Crawford 2013).

Materials

The fish bone assemblage from Earl's Bu was initially analysed as part of two separate doctoral research projects; first by James Barrett shortly after excavation, and then later completed by Jennifer Harland (Barrett 1995; J. Harland 2006). The initial site phasing was clarified within Harland's doctoral research, which locates the majority of the fish bones– and all *Salmo* sp. remains– within Phases M, P, T, V, X (Table 14). These phases date between 881 - 1164 CE, which covers the early-middle Norse period on Orkney and includes material from both before and after the construction of the feasting hall structure, farm, and mill buildings associated with the occupation of the site by Earl Paul Haakonsson, who ruled as joint Earl of Orkney from 1122-1137 CE (Anderson 1873; J. Harland 2006).

Phase	Dating (CE)	Feature Description
M	881-1050 (C14 Dated)	Viking-period middens located south and east of the mill
P	1032-1155	Redeposited midden, burnt mound, and natural clay materials used as structural infill behind walls of collapsed underhouse and tail race as part of new mill structures.
T	946-1024	Midden housed within collapsed underhouse
V	997-1164	Following site levelling, midden and other rubbish material used to fill in remains of underhouse
X	941-1155	Midden deposits dumped uniformly over the site, spread over the now flat area. Some were disturbed during later modern activity

TABLE 2.14: Site Phasing for Contexts with *Salmo* sp. remains from Earl's Bu (after Harland, 2006; Batey et al., ND)

A total of 58 bones from the Earl's Bu site were sampled for biomolecular analysis, with 42 of those yielding enough collagen for bulk stable isotope analysis, and 15 with only ZooMS analysis applied. Of the 57 fish bones with biomolecular analysis results (Table 15), 32 were either *Salmo* sp. or suspected *Salmo* sp. The comparative assemblage was unique amongst the other sites targeted for bulk stable isotope analysis, as there was a complete absence of identified pike bones from the site and no cyprinid bones large enough to use. This left eel bones as the only potential freshwater comparative species, however eel bones do not always reliably display the low $\delta^{13}C$ values expected for freshwater taxa (Robson et al. 2012) (see Chapter 9).

Taxa	Element	Count
Anguillidae	caudal vertebrae	2
	dentary	1
Gadidae	caudal vertebrae	3
	cleithrum	3
	dentary	3
	maxilla	2
	parasphenoid	3
	precaudal vertebrae	5
Pleuronectidae	precaudal vertebrae	1
Rajidae	buckler spine	1
Salmo sp.	caudal vertebrae	17
	first vertebrae	3
	operculum	1
	precaudal vertebrae	2
	vertebral centra fragment	9
Salmo sp.?	caudal vertebra	1
	cranial bone	1
	vertebral centra fragment	8
TOTAL		**57**

TABLE 2.15: Fish bone elements sampled from Earl's Bu for biomolecular analysis

2.3.7 Tjitsma Foarryp - Wijnaldum, Netherlands - 400-950 CE

Phasing and Background

Though it is more-or-less contemporary with the material from the Johan van Oldenbarneveltlaan and Oegsgeest sites discussed below, the assemblage from the Tjitsma Foarryp site is fairly different in character, as it was recovered during an excavation centered around an early *terp*, or constructed dwelling mound in a marshland area located in the modern day northern Dutch province of Friesland (Besteman and Nieuwhof 1999). The mound and it's surrounding area was excavated from 1991-1993, and several periods of habitation from approximately 175-950 CE were uncovered, all taking place prior to a known 12th-century period of embankment/land reclamation in the area (Besteman and Nieuwhof 1999). The early occupation periods include a late Roman phase from approximately 175-350CE and a Migration phase from approximately 425-550 CE, with indications that the settlement was briefly abandoned during the post-Roman period (Besteman and Nieuwhof 1999). It appears that the *terp* was resettled in the Migration period by Germanic tribes, either the descendants of the ancient Frisians (*Frisii*) first mentioned by Pliny the Elder, or an unrelated people who were eventually named after the Frisians by the later Frankish invaders (Elder 2019; IJssennagger 2017). Whether there was any cultural continuity from the ancient *Frisii* to the 7th and 8th-century Frisians who had prolonged conflicts and interactions with the invading Franks is still debated, but their influence in the area is clear. While the Tjitsma Foarryp site is located on the western edge of Friesland, the historical extent of Frisian territories in the Netherlands, sometimes referred to as *Magna Frisia*, stretched along the North Sea coast from the mouth of the River Eems at Eemshaven, south to

the mouth of the Old Rhine at Katwijk at the end of the 4th century, and later encompassing all of South Holland, Zeeland, Utrecht and parts of North Brabant (IJssennagger 2017; Vandermuelen 1998). By the 7-8th centuries Frisian traders were demonstrating their involvement in Early Medieval trade through the establishment and/or later control of small port towns, coastal colonies, and, eventually, trading emporia like Dorestad and possibly even Ribe (see Section 3.3.1 above) (Feveile 2006; IJssennagger 2017; Vandermuelen 1998). Frisian and Frankish struggles for control of Dorestad and other southern trading centres continued through the 7th-9th centuries with first the Merovingians, and, subsequently the Carolingians, entering into conflicts with Frisian kings (Vandermuelen 1998). The Frisians resisted Christianization for longer than many other northern European groups, and it wasn't until Charlemagne's rule that the Frisians were fully conquered and incorporated into the Holy Roman Empire in 785 CE (Vandermuelen 1998). Still, there were regional differences in occupation and control of areas, and the Tjitsma Foarryp site clearly demonstrates this– though it is further north than some other Frisian strongholds, the official interpretations of the site phasing describe the following occupation periods: Migration (425-550 CE) to Merovingian (550-750 CE), Carolingian (750-850 CE) and, finally, Ottonian (850-950 CE) (Prummel, K. Esser, and Zeiler 2013). Given it's far northern location it's likely that the earliness of the described Merovingian period at Tjitsma Foarryp is due to increased contact, through both trade and conflict, between the Frisians and Franks rather than being an exceptionally early example of full colonization by the Franks. This *terp* site was a domestic settlement with no high status buildings, and the majority of contexts were wet sieved using 4mm mesh, which led to a large amount of fish bones being recovered (Besteman and Nieuwhof 1999; Prummel, K. Esser, and Zeiler 2013). This notably large fish assemblage indicates the importance of fishing at the site, with it's access to the ecologically rich Wadden Sea intertidal region of the wider North Sea making the site a key provisioning location that likely participated in the wider Frisian and Frankish trade networks (Prummel, K. Esser, and Zeiler 2013).

Materials

At least 20 fish taxa were identified at the site, with the vast majority being flatfish (NISP of 3500), but there were also significant amounts of freshwater, catadromous, anadromous, and marine species present at the site as well (Prummel, K. Esser, and Zeiler 2013). A large *Salmo* sp. NISP of 42 elements was recorded, with the majority (n=23) coming from the Frisian "migration" period as well as a significant amount (n=16) from Merovingian, and Carolingian contexts (Prummel, K. Esser, and Zeiler 2013). During my assessment of the fish bone material from this site during July of 2021, I was able to find 38 of the recorded *Salmo* sp. bones, and chose 11 samples for further biomolecular analysis. Five of those samples did not yield enough collagen for bulk stable isotope analysis and/or did not have conclusive ZooMS identifications. The remaining six are made up of one with both ZooMS and SI results, two with only SI results, and three with only ZooMS results.

2.3.8 Johan van Oldenbarneveltlaan 91-95 - 's-Gravenhage, Netherlands - 450-700 CE

Phasing and Background

In 1983 a survey excavation ahead of planned demolition on Johan van Oldenbarneveltlaan street in Den Haag located an Early Medieval settlement and triggered full excavations, which began in 1984 (Magendans and Waasdorp 1989). The resulting project exposed the first example of an early Merovingian settlement to be systematically excavated in Den Haag, located within a well-defined context isolated from contamination from the surrounding 20th-century buildings (Magendans and Waasdorp 1989). While the population of what is now referred to as the province of Zuid-Holland was approximately 10,000 people in the 2nd century CE, there was an observ-

able contraction of both population and economic output due to the overall instability of the post-Roman era during the 3rd and 4th centuries CE (Bavel 2010; Magendans and Waasdorp 1989). Despite these declines in population and economic productivity, this settlement is indicative of renewed 5th-century concentrations of habitations and the development of early trading centres, and was ideally located between the Old Rhine (*Oude Rijn*) and Old Meuse (*Oude Maas)* rivers, with access to the North Sea (Bavel 2010; Magendans and Waasdorp 1989). This location allowed the occupants either direct or trade access to freshwater, estuarine, marine resources (Magendans and Waasdorp 1989). The craft workshops and domestic spaces that make up the Johan van Oldenbarneveltlaan site was likely first a Frisian outpost, which would later come under Frankish control as the Merovingians, and, later, Carolingians pushed further into Frisian territory; expanding their borders as far north as the Old Rhine in the beginning of the 6th century, only to lose ground to the Frisians again by the end of the same century (Magendans and Waasdorp 1989). Despite the fluctuating boundaries of control in the region, it's clear that there were both Frisian and Frankish influences at the site, and it's inhabitants were likely part of the same Early Medieval pan-North Sea trading networks as the Dutch sites at Tjitsma-Foarryp, Nieuw Rhijngeest-zuid, and Plantage Leiderdorp and which likely extended as far as York and Ribe (Ayers 2016; Bruin, Bakels, and Theuws 2021; Dijkstra, Verhoeven, and Straten 2016; Feveile 2006; R. A. Hall 2014; Magendans and Waasdorp 1989).

Materials

A comparatively large assemblage of fish (n=547) were recovered from the site as the excavation progressed slowly enough to allow for thorough sieving of material using 1cm sieves. Though the majority of fish remains were cod, a marine spcies, there was also a notably large amount of sturgeon remains (n=120), perhaps indcating a heavy reliance on riverine fishing (Magendans and Waasdorp 1989). A total of 8 *Salmo* sp. bones were identified from the site, and permission was given to sample two of them for ZooMS analysis– one precaudal and one caudal vertebra.

Family	**NISP**
Cod	373
Sturgeon	120
Flatfish	29
Salmo sp.	8
Haddock	6
Halibut	3
Gurnard	2
Ray	2
Dogfish	2
Pike	1
Mullet	1

TABLE 2.16: Fish bone NISP reported for the Johan van Oldenbarneveltlaan site, after Magendans and Waasdorp 1989.

2.3.9 Nieuw Rhijngeest-zuid 2009/2010 2014 - Oegstgeest, Netherlands - 400-800 CE

Phasing and Background

Multiple series of excavations were conducted on an area of archaeological significance in the Dutch town of Oegstgeest, which was first discovered during planned construction by an existing motorway in 1990. Trial excavations were dug on the identified site in 2004-2005, and full scale excavations were conducted by Leiden University from 2009-2014 (Bruin, Bakels, and Theuws 2021). The excavations uncovered a rich variety of dwellings, waste pits, wells, and flood management structures from an Early Medieval settlement that was dated to between 400-800 CE, with it's most active periods from 550-725 CE (Bruin, Bakels, and Theuws 2021). At least 26 Early Medieval houses were found, with 73 associated outbuildings and over 100 wells, many with wooden linings, distributed across the breadth of the settlement (Bruin, Bakels, and Theuws 2021). This impressive collection of structures indicates that the site supported a robust farming, fishing and trading community within the influence of both Frisian and Merovingian dynastic kings, and again participating in the same regional network as the contemporary settlement at Johan van Oldenbarneveltlaan 91-95 (Bavel 2010; Bruin, Bakels, and Theuws 2021; Magendans and Waasdorp 1989). There is ample evidence for increasingly active trade networks from the middle Rhine area through these Zuid-Holland trading outposts as the Merovingian period progressed through the 6th-8th centuries(Bruin, Bakels, and Theuws 2021). The formation of an aristocratic class within the early Frankish empire, as well as the ever-increasing power of ecclesiastical institutions, allowed for the creation of large surplus-producing estates that could ship commodities, like wine, from the interior of the modern-day Netherlands towards trading centres across the North Sea, like York (Bruin, Bakels, and Theuws 2021). Detailed accounts of wine trade exist, with an exchange of Anglo-Saxon *sceattas* for Frankish wine, and it's likely that at least some marine resources were also traded along the same routes (Bruin, Bakels, and Theuws 2021). There is convincing evidence for the production of fishing net weights and wooden artifacts at the Oegstgeest outpost that may have been part of fish traps or weirs destined for the nearby Rhine, which would indicate the involvement of this site and it's inhabitants in these trade networks (Bruin, Bakels, and Theuws 2021).

Materials

Though there was a large amount of *Salmo* sp. bones recovered from the 2009-2010 excavations (fish NISP = 1281, *Salmo* sp. NISP = 19), access to all of these remains were not possible during the sampling visit in July of 2021. Furthermore, though the 2014 excavation season yielded a fish NISP of 5286 and an exceptional *Salmo* sp. NISP of 111, only 22 bones were able to be accessed and identified upon a second review, which limited the biomolecular sample from the site considerably. The fish bones from the 2014 season were recovered from three pit features and a well, and a total of 39 fish bones (Table 16) were sampled, including 24 *Salmo* sp. bones and 20 from comparative taxa. While taphonomic preservation at the site was good, it appears that collagen preservation was less well established, with only 6 comparative specimens and 4 *Salmo* sp. specimens yielding enough collagen for bulk stable isotope analysis. An additional 12 *Salmo* sp. samples were also subjected to ZooMS analysis and all confirmed to be *Salmo salar* specimens.

Taxa	Element	NISP
Anguilla anguilla	caudal vertebra	1
Alosa fallax	caudal vertebra	1
Coregonus sp.	caudal vertebra	1
Abramis brama	hyomandibular	1
Perca fluviatilis	caudal vertebra	1
	precaudal vertebra	1
Salmo sp.	caudal vertebra	1
	precaudal vertebrae	3
	vertebral fragment	12
TOTAL		**21**

TABLE 2.17: Dutch fish bone elements with available biomolecular analysis results from Nieuw Rhijngeest-zuid 2014

2.3.10 Plantage - Leiderdorp, Netherlands - 650-850 CE

Phasing and Background

Archaeological excavations were carried out in 2013, ahead of planned construction at the Plantage site in Leiderdorp–a suburb of Leiden and location of several earlier investigations into the medieval character of the area (Dijkstra, Verhoeven, and Straten 2016). Excavations were led by the University of Amsterdam, and revealed rich deposits of ceramics, animal remains, and metal objects from the Merovingian, Carolingian and other later medieval contexts (Dijkstra, Verhoeven, and Straten 2016). The Merovingian period is traditionally dated from circa 481 CE, beginning with the reign of Clovis I, whose rule united the divided Frankish tribes into one discrete entity for the first time (Wood 2014). The Frankish empire expanded throughout the 5th-7th centuries, with sustained conflict with the Frisian kingdoms over trading centres (see Sections 3.7-3.9), and it's second dynasty, the Carolingians, was established in 751 CE with overthrow of the last Merovingian King of the Franks, Childeric III (McKitterick 1983; Wood 2014). The aristocratic and economic organization of this Frankish dynasty was typified by a system of feudal *demesne*, or manorial estates within the central Austrasian homeland of the Carolingians (McKitterick 1983; Riché 1993). The trading centres like those seen at Nieuw Rhijngeest-zuid and Dorestad, as well as affiliated outpost sites like Johan van Oldenbarneveltlaan and even Tjitsma-Foarryp, have been interpreted as Frisian, and later Frankish, alternatives to these established manorial systems (Kemme 2021). Thus, the role of the Plantage site was likely as a settlement affiliated with both Frisian and Frankish traders and goods produced in the large urban center of Dorestad, or perhaps even Nieuw Rhijngeest-zuid, making it another key part of the large Early Medieval North Sea trade network that focused on textiles, metal, ceramics, and, of course, fish (Ayers 2016; Dijkstra, Verhoeven, and Straten 2016). Evidence for local fishing is seen at the Plantage site, with at least one fishing hook, several net weights and bobbins, and three partially complete fish traps recovered from the excavations (Dijkstra, Verhoeven, and Straten 2016).

Materials

A total of ten *Salmo* sp. bones were identified within the site NISP of 1807 fish bones with a further 927 unidentified fish bones recovered from the site (B. Beerenhout 2016). Fish remains were primarily recovered from trench

and well contexts, and were collected through a combination of hand collection and wet sieving (B. Beerenhout 2016). Six *Salmo* sp. bones were made available for biomolecular analysis, from two separate contexts– three from a Merovingian trench dated to between 650-675 CE, and three from a Carolingian gully context dated to between 800-850 CE (B. Beerenhout 2016; Dijkstra, Verhoeven, and Straten 2016). The Carolingian samples and one of the Merovingian ones did not yield enough collagen for bulk stable isotope analysis, and had inconclusive ZooMS results, but the remaining two samples (lmq_NL_salmo_037 and lmq_NL_salmo_039) have available bulk stable isotope data and ZooMS identifications.

Taxon	Merovingian (S1040)	Merovingian (S3699)	Late Merovingian (S3293)	Late Merovingian (S3576)	Early Carolingian (S3281)	Early Carolingian (S3389)	Early Carolingian (S3573)	Early Carolingian (S3575)	Carolingian (S3061)	Carolingian S3356	Carolingian (S5174)
Abramis brama	31		9			2		1	4	6	18
Abramis björkna											1
Abramis sp.	2		1							1	
Anguilla anguilla	2		1			4			50	22	27
Clupeidae			1								
Clupea harengus									3		
Coregonus oxyrinchus										1	
Cyprinidae	53	1	11			26	2		44	165	98
Dasyatis pastinaca									1		
Esox lucius	10		4			2			9	7	13
Gadus morhua	1								14	1	9
Gadidae									1		1
Gasterosteus aculeatus											1
Gymnocephalus cernuus									3		
Melanogrammus aeglefinus									3		5
Merlangius merlangus									1		1
Osmerus eperlanus									1		
Perca fluviatilis	115	1	13		1	38	7		110	154	157
Pleuronectidae	90	1	1			18	1	1	99	30	261
Platichthys flesus	8								4		3
Pleuronectus platessa									2		2
Rutilus rutilus	4								2		
Rutilus erythrophthalmus	2								1		
Salmo salar									4		1
Siluris glanis									1		
Unknown	91	0	29	1	0	75	13	0	262	250	206
TOTAL	409	3	70	1	1	165	23	2	619	637	804

TABLE 2.18: Reported fish bone remains from Plantage - Leiderdorp

2.3.11 Huis Malburg - Kerk-Avezaath, Netherlands - 900-1050 CE

Phasing and Background

The Huis Malburg site is located within the modern day Dutch village of Kerk-Avezaath, and was excavated between 1997-1998, and had six distinct phases of occupation ranging from the Merovingian (450-725 CE) to Early Modern (1500-19000 CE) period (E. Esser 2000). While the site spans an approximately 1450 year period, the majority of fish bone (n=551) remains were recovered from the Ottonian and High Medieval periods, with the sole *Salmo* sp. bone from the site coming from the Ottonian phase, dating to between 900-1050 CE. This Ottonian period post-dates the 843 CE treaty of Verdun, which signalled the formal end of the united Carolingian Empire. The modern-day village of Kerk-Avezaath was included within the region known as Lotharingia under Lothar I, and later included within the kingdom of East Francia under Otto I and his Ottonian dynastic successors (MacLean 2013; Riché 1993; Rietbergen 2006). This period in the eastern Netherlands and modern-day Germany was characterized by the spread of small vassal duchies within the spreading Holy Roman Empire, with a fair amount of disagreement as to whether these duchies constituted any kind of true ethnic or cultural community, or were simply administrative units within the Empire (MacLean 2013). This 10-11th century period of fluctuating power and control did eventually result in a stabilized hierarchy, with a "feudal revolution" of sorts characterized in some areas by the "privatisation of judicial institutions, the intensification of local lordship and the domination of the peasantry through coercion and violence" (MacLean 2013). The role of the church within these systems was ever increasing, and the Huis Malburg site itself appears to have been a primarily agricultural settlement that was gifted, along with control of the Kerk-Avezaath parish, to the Abbey of Thorn by the Bishop of Utrecht around the year 1000 CE (E. Esser 2000). The economic value of the land and labor of the people living within the area of the Huis Malburg site was essential to the prosperity of the Limburg Benedictine order which managed them from afar, bur it is unclear what, if any, role organized commercial fishing activities played in this local feudal system (E. Esser 2000).

Materials

The only identified *Salmo* sp. bone from this site was uncovered in the Ottonian Period (Phase 3; 900-1050 CE), within a small fish bone assemblage of 189 individual specimens from one pit and one riverine ditch feature. The majority of fish bones recovered from the Huis Malburg site were freshwater, but there was a small presence of migratory and marine fish as well, indicating that the settlement was not entirely closed off to fish trade from other areas (E. Esser 2000). The *Salmo* sp. bone (Figure 5), a complete precaudal vertebra, was identified as belonging to an Atlantic salmon via ZooMS analysis.



FIGURE 2.5: Sample NL_Salmo_060 from the Huis Malburg site, a *Salmo salar* precaudal vertebra.

2.3.12 Huize van den Kasteele - Zutphen, Netherlands - 1000-1100 CE

Phasing and Background

Both the Huize van den Kasteel and Stadhuis (see Section 3.13) sites from Zutphen were excavated as part of a series of excavations at the palatial complex located at the site of the modern day city hall in Zutphen. These excavations took place from 1993-1999, and the resulting study of fish bone material from both sites was part of a "quick scan" assessment undertaken by archaeozoologist Bob Beerenhout, to cover a small, but representative, sample of both the hand collected and 2mm sieved material recovered from the sites (Bob Beerenhout 2011). Like the location of Huis Malburg (Section 3.11), the city of Zutphen was first part of the post-Treaty of Verdun kingdom of Lotharingia, and later incorporated into the holdings of the Germanic Ottonian dynastic kings and under the direct control of dynastic Counts of Zutphen and, later, Guelders (MacLean 2013; Nijsten 2004; Rietbergen 2006). The Huize van den Kasteel site was primarily associated with the palatial complex of the Counts of Zutphen, and had three contexts with fish remains– a late 10th-century fireplace pit, and two separate waste pits dated to between 1000-1100 CE (Bob Beerenhout 2011).

Materials

Of the NISP of 691 fish bones recovered from the Huize van den Kasteel fireplace and waste pits, only one bone, a ceratohyal (Figure 6) was identified during the initial "quick scan" as belonging to the genus *Salmo*. Upon review in July of 2021 I determined it was most likely not a *Salmo* sp. bone, and collagen peptide barcode analysis resulted in a ZooMS ID of *Esox lucius* or Northern Pike.



FIGURE 2.6: Sample lmq_NL_Salmo_112 from the Huize van den Kasteele site, an *Esox lucius* ceratohyal.

Taxon	VNR 81	VNR 51
Abramis brama	43	8
Acipenser sturio	0	4
Anguilla anguilla	11	6
Clupea harengus	2	2
Cyprinidae	41	137
Esox lucius	20	18
Leuciscus idus	2	1
Perca fluviatilis	4	13
Rutilus rutilus	2	0
Salmo salar	0	1
Undetermined	141	235
TOTAL	**266**	**425**

TABLE 2.19: Fish bone material recorded from contexts VNR 81 and VNR 51 from the Huize van den Kasteele site (after Beerenhout, 2011)

2.3.13 Stadhuis - Zutphen, Netherlands 1125-1175 CE

Phasing and Background

Excavated in tandem with the previously covered Huize van den Kasteele site, the Staduis site also focused on structures associated with the palatial residence, but from time period after the dynastic Counts of Gelderland had acquired the County of Zutphen via marriage in circa 1120 CE (Bob Beerenhout 2011; Nijsten 2004). During the 12-13th centuries a series of catastrophic floods, climatic fluctuations, long-term erosion, and failure of previously built barriers led to the creation of the Zuiderzee, a shallow salt water bay connected to the North Sea (Bavel 2010). This brackish environment persisted until it was eventually cut off in the 20th century by the construction of the Afsluitdijk, creating the modern day IJsselmeer, IJmeere and Markermeer freshwater lakes (Bavel 2010). During the occupation of the palatial complex at Zutphen, then, there was direct connection to these highly productive shallow bays, and the North Sea they emptied into, via the IJssel river (Bob Beerenhout 2011). In light of this, the relative lack of high status and taxable fish remains, referred to as *vroonvis* by the 15th century (Jager 1445) seen at this palatial complex is interesting given the contemporary availability of migratory fish in the region, as well as directly attested control of high value fish, like salmon, by the Counts of both Zutphen and Gelders (Bob Beerenhout 2011). Six representative bulk soil samples were taken from a suspected food waste pit found adjacent to the kitchen of the complex and included in the "quick scan" conducted by Beerenhout, and a total NISP of 1590 fish bones were recovered (Bob Beerenhout 2011).

Materials

The single recorded *Salmo* sp. bone, a caudal vertebra, was identified from the Stadhuis site's kitchen waste layers, and it was subsequently sampled for biomolecular analysis. The specimen was identified using ZooMS

as an Atantic salmon, and therefore constitutes the only positively identified *Salmo* sp. bone found within the palatial complex that included both the Huize van den Kasteele and Stadhuis sites.

2.3.14 Minderbroedersklooster - 's-Hertogenbosch, Netherlands - 1175-1500 CE

Phasing and Background

The first Franciscan friary in the Netherlands was established in 's-Hertogenbosch shortly after St. Francis of Assisi's death, and the Franciscans eventually built several monastic complexes within the town including what would later be known as the Minderbroedersklooster site (Genabeek 2016). While the first church and it's associated buildings were consecrated in the mid-13th century, there was an expansion of monastic buildings in the end of the 14th-beginning of the 15th century that resulted in the construction of several kitchens, cellars, guest accommodations, and outbuildings (Genabeek 2016). These buildings were uncovered during excavations held between 1997-1999, designated with the site code HTMK, which was prompted by the planned demotion of 20th-century buildings (Genabeek 2016). Several phases of occupation were recorded during these excavations, including an early ducal residence dated to between 1150-1250 CE, which was supplanted by the Minderbroedersklooster occupation from 1250 CE onward (Genabeek 2016). The pre-monastic ducal residence was the manor house of Hertog Hendrik van Brabant, for whom the town of s-Hertogenbosch was named, and it can be assumed that food waste from that period was from the Duke and affiliated occupants (Genabeek 2016). While under both ducal and monastic control this site was ideally situated within the centrally located Duchy of Brabant, which enjoyed a "golden age" in the 13th-14th centuries (Rietbergen 2006). This was a "highly urbanised" region, with commercial, political, and military centres that facilitated access to North Sea ports like Bruges and Antwerp (Caluwe 2003). These excellent trade connections and increased prosperity are evident in the material culture and fish remains recovered from the Minderbroedersklooster site's ducal and monastic periods, as well as historic attempts to sack the growing town by the rivals of the Duke of Brabant in the early 13th century (Genabeek 2016).

Materials

A total of 5,642 fish remains were recovered from all phases of the Minderbroedersklooster site, with 2,224 of those recorded fish remains coming from three contexts of interest; the early ducal court period, and two pit features associated with the later monastery period. Table 17 below displays these three contexts with their reported fish NISP and *Salmo* sp. NISP, an updated *Salmo* sp. NISP recorded in July of 2021, and the final numbers of biomolecular samples obtained from the site.

Context	Dating	Total Fish NISP (Reported)	Total *Salmo* sp. NISP (Reported)	LMQ Recorded *Salmo* sp. NISP	Total Sampled Fish Bones	Total Sampled *Salmo* sp. Bones
Phase 1: Ducal court	1150-1250 CE	267	3	9	31	9
Phase 4: Monastery Pit 1	1350-1450 CE	1957	9	3	3	3
Phase 4: Monastery Pit 2	1400-1500 CE	2271	6	11	25	10
TOTAL		**4495**	**18**	**23**	**59**	**22**

TABLE 2.20: Minderbroedersklooster Contexts of Interest and Associated Sample Numbers

Table 18 lists all taxa sampled from the site, both *Salmo* sp. and comparative marine, migratory and freshwater fishes. The preservation of *Salmo* sp. bones from this site was exceptionally poor when compared to the other fish taxa, and though 23 samples were subjected to collagen extraction for bulk stable isotope analysis, only 8 yielded enough collagen to test. One of these was actually a Northern pike dentary misidentified as a *Salmo* sp. bone, but the remaining seven yielded acceptable bulk isotope data. The *Salmo* sp. samples were primarily vertebral elements, many of them fragmentary, and all resulted in ZooMS identifications. The comparative sample was comprised of migratory *Coregonus sp.*, freshwater cyprinids and pike, and marine gadids and haddock.

Taxa	Element	Count
Coregonus sp.	caudal vertebrae	6
Cyprinidae	pharyngeal	2
	serrated spine	3
Esox lucius	precaudal vertebrae	11
Melanogrammus aeglefinus	opercular	1
Gadidae	caudal vertebrae	10
	premaxilla	1
Salmo sp.	caudal vertebrae	7
	dentary	1
	precaudal vertebrae	5
	vertebral fragments	8
TOTAL		**55**

TABLE 2.21: Fish bone elements sampled for biomolecular analysis from Minderbroedersklooster

2.3.15 Kasteel Voorst - Zwolle, Netherlands - 1280-1362 CE

Phasing and Background

Kasteel Voorst is a small castle site that was occupied by the Van Voorst tot Voorst family during the 12th-14th centuries and is located in the modern day Dutch city of Zwolle, in Overijssel province (Hove 2005). While the Stadhuis site from Zutphen (Section 3.13) is dated to the very early expansion of control in the East Netherlands

by Counts of Guelders, at the time of occupation at Kasteel Voorst the County of Guelders constituted the largest secular power in the Lower Rhine region (Nijsten 2004). The Waal, Maas, Lek, and IJssel rivers were all either directly controlled by the Counts of Guelders, or managed by their vassal nobles, including the Van Voorst tot Voorst family (Nijsten 2004). With Zwolle lying directly on the banks of the IJssel river, and even closer than Zutphen to the contemporary brackish Zuiderzee, it was likely an ideal location for migratory and freshwater fishing. The castle structures themselves went through several periods of razing, demolition, and rebuilding due to ongoing religio-political conflicts in the area, with the final structure being razed and demolished in 1362 CE by the Bishop Jan van Arkel and troops from the cities of Zwolle, Deventer and Kampen (Hove 2005). The fish remains from this site were mostly from a well context dated to between 1280-1362 CE, with a NISP of 311 bones and scales from various taxa (IJzereef 1983).

Materials

The Kasteel Voorst assemblage was mostly freshwater fish, with very few marine taxa represented, and the initial analysis proposes that the majority of fish were caught locally, and perhaps even from the identified moat feature of the castle (Hove 2005). Site records indicate that there were 4 *Salmo* sp. bones identified (IJzereef 1983), however only two bones were recovered during a storage depot visit, both cranial bones. Only one of the bones yielded enough collagen for bulk stable isotope analysis, and, due to suspected environmental contaminants, clear ZooMS identifications of the bones were not possible. The bulk carbon results of the Kasteel Voorst sample (lmq_nl_salmo_047) indicated that it was a freshwater fish, which may mean this element (Figure 7) belongs to a freshwater Brown trout rather than an anadromous Atlantic salmon, as originally identified.

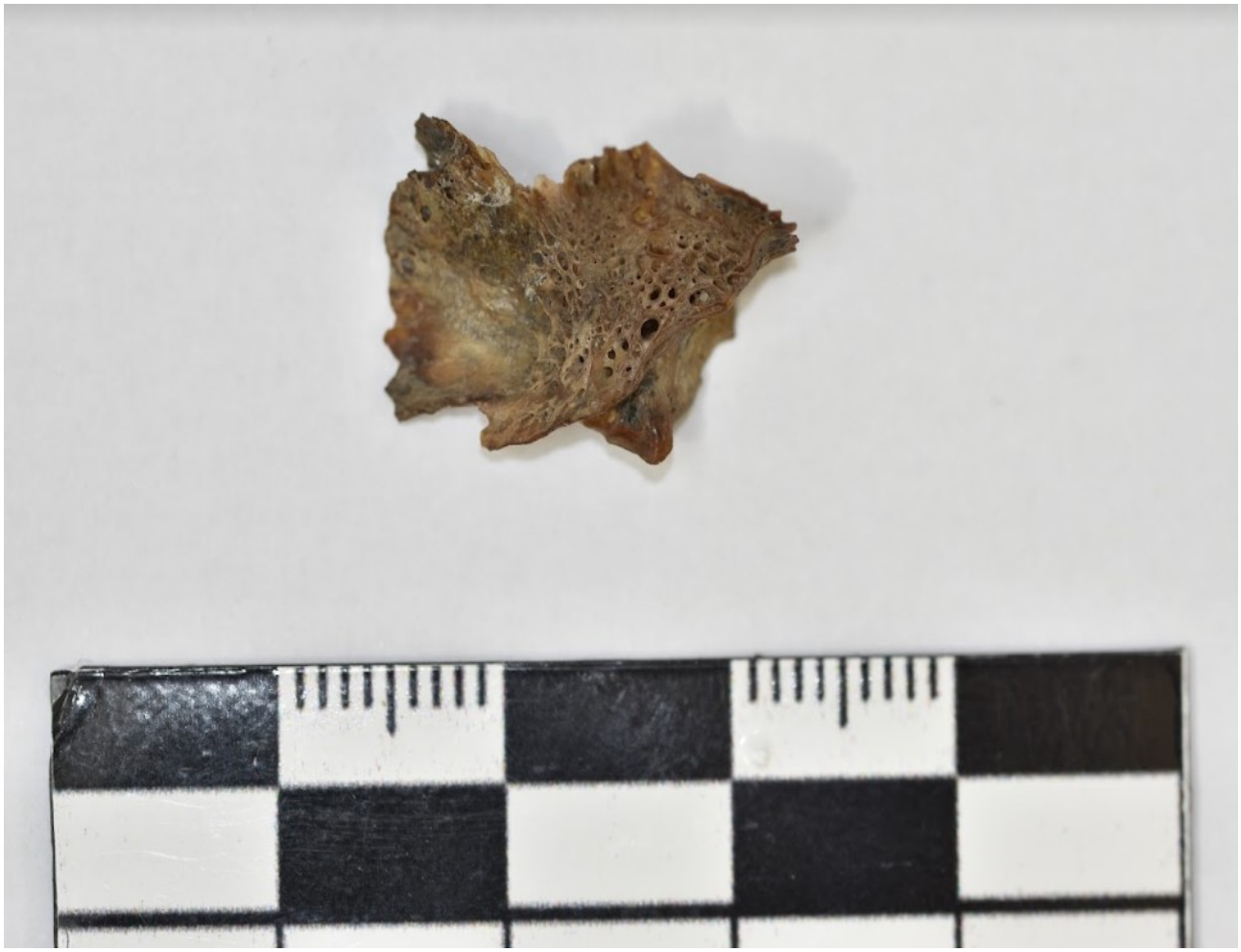


FIGURE 2.7: Sample lmq_NL_salmo_047 from the Kasteel Voorst site, identified by original researchers as a *Salmo* sp. basioccipital fragment.

2.3.16 Heveskesklooster (Johannitercommanderij Oosterwierum) 1300-1500 CE

Phasing, Background and Materials

Very little has been written about the Heveskesklooster site, which was uncovered as part of wider excavations on the Oosterwierum terp located near the previous village of Heveskes, now part of the larger municipality of Eemsdelta. Only a single bone was made available for study from this site, and collections managers at the Noordelijk Archeologisch Depot were unable to offer any further provenience information beyond the site code and general date range due to poor records availability. It appears that some of the original reports relating to the 1970s-80s excavations focused on the ecclesiastial order house may have been lost, and the brief history discussed here is from a reconstructed report shared by Dutch archaeologist J.W. Boersma with a local Groningen amateur historian and subsequently uploaded online (Boersma 1988). The historic structure, part of the Order of St. John, or *Johaniter Orde*, was a commanderij (monastic grange) founded by 1319 CE at the latest, which by that point was under the administrative management of the German Holy Roman County of Steinfurt and referred to as the *Johannitercommanderij Oosterwierum* (Boersma 1988). The Order of St. John, formally known as the "Bailiwick of Brandenburg of the Chivalric Order of Saint John of the Hospital at Jerusalem" is the oldest surviving

chivalric order, likely founded in Jerusalem in 1099, and by the 14th-century was a well-established military order focused on the protection of pilgrims to the Holy Land (Hoegen Dijkhof 2006). The agricultural products of the *commanderij* would have supported the military order's actions both within Europe and in the Holy Land, and historical records indicate that the order house was a fairly large and prosperous estate (Boersma 1988). The last known visitation report, from 1540 CE, discussed various instances of unrest in the region, likely related to pre-Reformation religious and political tensions, and reports that the *commanderij* was sacked by local residents several times in the early 16th-century(Boersma 1988). Fish are listed among the products of the *commanderij*, though no specifics are given about species. Atlantic salmon must certainly have been among the fish that passed through the *commanderij*, as evidenced by the precaudal vertebra included in this study. Though only a single sample, it still provides both ZooMS and bulk stable isotope data, as well as a lifetime length estimate of roughly 100cm for the fish.

2.3.17 Oude en nieuwe Gasthuis - Delft, Netherlands - 1400-1450 CE

Phasing and Background

The Oude en Nieuwe Gasthuis sites located in Delft were the physical manifestations of a hospital organization that was founded in the mid-13th century, and is generally considered to be a precursor to the modern day Reiner de Graaf Hospital (E. Esser 1992; Reinier de Graaf Gasthuis 2022). A Papal bull dated to 1252 CE confirms the existence of a hospital at Delft, and the complex of buildings collectively known as the "Oude en Nieuwe Gasthuis", or Old and New Infirmary, and remained in operation even after a 1536 CE fire destroyed many of the associated buildings, only truly ceasing operation within the city of Delft in 1968 (Onisto, Maat, and Bult 1998). While the contemporary early 15th-century monastery at Minderbroedersklooster (Section 3.14) was under Franciscan control, the hospital at Oude en Nieuwe Gasthuis was, until at least 1450 CE, affiliated with the Norbertine Koningsveld Priory located just outside Delft (Westen, Groen, and Maat 2013). Delft itself was a growing regional marketplace in the then-Duchy of Holland, which would eventually come under Burgundian control. As the 14th and 15th-centuries progressed the majority of the Netherlands, along with the remainder of the Low Countries, were united, either directly or indirectly, under the control of the Dukes of Burgundy (Rietbergen 2006). Though they were an extension of the French royal House of Valois, the 14th-century dukes, beginning with Phillip the Bold (1363-1404), were often operating largely independently from the influence of both the Kingdom of France and the Holy Roman Empire (Rietbergen 2006; Schepper 1994). Irrespective of the political environment surrounding the Oude en Nieuwe Gasthuis, the hospital was operated first by religious lay brothers and sisters, and later by the municipality of Delft itself (Onisto, Maat, and Bult 1998). It catered to the sick and disabled, acted as temporary shelter for vagrants, and later housed paying lodgers from the town's aging population (Onisto, Maat, and Bult 1998). The only available report of faunal and botanical remains from this site comes from Dr. Kinie Esser's 1992 MA thesis, which involved a preliminary assessment of the materials from several cesspit features associated with the hospital's inhabitants during the 15th-17th centuries (E. Esser 1992). Fish remains were recovered from two contexts; a cesspit (context V169) and a beer cellar (context V360) that had been filled with mixed hospital waste sometime between 1400-1450 CE (E. Esser 1992).

Materials

The total fish NISP from the site was 690, with only one *Salmo* sp. bone (lmq_NL_salmo_001) reported– interestingly, Esser identified this bone (see Figure 8) as belonging to a sea trout (E. Esser 1992). While ZooMS results show that she was correct that the species was *Salmo trutta*, the bulk carbon results from this sample indicate

it followed a primarily freshwater foraging ecology, and is therefore most likely a Brown trout. Upon reviewing several large bags of undetermined Gadidae vertebrae from the site, three additional potential *Salmo* sp. vertebral elements were identified and sampled for biomolecular analysis– two were determined to be from Atlantic salmon(*Salmo salar*) and one (Figure 9) was confirmed to be from a cod (*Gadus morhua*).



FIGURE 2.8: Sample NL_Salmo_001 from the Oude en nieuwe Gasthuis site, a *Salmo trutta* axis vertebra.



FIGURE 2.9: Sample NL_Salmo_004 from the Oude en nieuwe Gasthuis site, a *Gadus morhua* vertebral fragment.

2.3.18 In den Struys - Veere, Netherlands - 1425-1500 CE

Phasing and Background

The In den Struys site consists of a single cesspit feature uncovered during a 1994 excavation in the basement of one of the so-called "Scottish Houses" in the modern-day municipality of Veere, Zeeland (Laarman and Lauwerier 1996). A small town founded in the late-13th century, Veere was a trading depot centered around it's harbor, with important merchant houses lining the quay from approximately 1350 CE onward (Laarman and Lauwerier 1996; Stenvert et al. 2003). Veere, and the rest of Zeeland, had come under Burgundian control during the time of Philip the Good, and by the early 16th-century the province was not only economically successful but also undergoing a major shift in administration (Schepper 1994). Zeeland, like the other wealthy mercantile Burgundian provinces of Holland, Brabant and Flanders, was seeing a centralization of power in the hands of magistrates and other appointed officials, rather than hereditary elites (Schepper 1994). By the mid-16th century, Veere had become a key trading outpost for emigrating Scottish merchants looking to expand their influence across the North Sea. These Scottish traders eventually took over houses built by earlier merchant citizens, including those located at 25-27 Kaai– the addresses associated with the In den Struys cesspit (Laarman and Lauwerier 1996). Kaai 27 was the original house structure associated with the 15th-century cesspit, but was only connected to the

neighboring building around the year 1539 CE, making it likely that the inhabitants were not the later Scottish traders but Dutch ones from Veere (Stenvert et al. 2003). The cesspit was the only feature excavated at the house, but it contained a very rich assemblage of ceramics, glass, household items and food remains which indicated the presence of a wealthy merchant family (Laarman and Lauwerier 1996).

Materials

A total of 2797 fish bones were recovered from the cesspit using both sieving and hand collection, and six bones were identified as *Salmo* sp. remains by initial analysts (Laarman and Lauwerier 1996). Four of those six *Salmo* sp. bones were sampled for both bulk stable isotope and ZooMS analysis. One of these samples, lmq_NL_salmo_020, was found in a labeled bag from original zooarchaeological analysis, but turned out to be a misidentified flatfish cranial element.

2.4 General Site Summary

The 17 archaeological sites included in this study provide an excellent opportunity to investigate *Salmo* sp. fish exploitation by people living through a roughly 1000-year period of economic and political development, urbanisation, and environmental change. The North Sea region was the site of many concurrent and successive periods of cultural change, necessitating the inclusion of archaeological sites under the control of powerful groups including those from Norse/Scandinavian (Ribe ASR 9; Ribe ASR 13; Ribe ASR 2090; Earl's Bu; Coppergate), Anglian/Saxon/Germanic (Coppergate; Huis Malburg; Huize van den Kasteele; Stadhuis-Zutphen; Kasteel Voorst; Heveskesklooster), Frankish (Johan van Oldenbarneveltlaan; Nieuww Rijngeest-zuid; Plantage-Leiderdorp; Tjitsma Foarryp - Wijnaldum; Huis Malburg; Huize van den Kasteele; Minderbroederskloster), Frisian (Ribe ASR 9; Johan van Oldenbarneveltlaan; Nieuww Rijngeest-zuid; Plantage-Leiderdorp; Tjitsma Foarryp - Wijnaldum), and Burgundian/Habsburg (Minderbroederskloster; In den Struys; Oude en nieuwe Gasthuis) origins. The 17 sites include a wide variety of site contexts, ranging from urban to rural, in order to provide as clear a picture as possible of *Salmo* sp. usage by humans with different levels of social status, economic power, and trade access. The inclusion of large proto-urban and urban marketplaces located in the modern settlements of Ribe, York, den Haag, and Oegsgeest, provide an opportunity to understand the role of *Salmo* sp. fishes within culturally diverse and complex periods of settlement and industrial activity in Denmark, England and the Netherlands. Sites from high status (Earl's Bu, Stadhuis-Zutphen, Huize van den Kasteele, and Kasteel Voorst) and ecclesiastical (Heveskesklooster, Oude en nieuwe Gasthuis, and Minderbroederskloster) contexts provide insight into the characterisation of salmon as "prestige" fish. By including sites with both very large (e.g. Coppergate, n=256; Ribe ASR 9, n=100) and very small (e.g. Heveskesklooster, Huis Malburg, and Huize van den Kasteele, all n=1) this study makes the best of an unusually limited regional NISP for *Salmo* sp. fishes (see Chapter 8), and allows us to investigate presence/absence in more detail. The diversity of site location, sample size, cultural and social characteristics, and chronology found within this study assemblage offers a unique opportunity to investigate the role of fish like Atlantic salmon, brown trout, and sea trout in the archaeological and historical record of the North Sea basin.

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Chapter 3

Methods

3.1 Introduction

This chapter will examine analytical methods utilized throughout the course of this project, with the aim of introducing the techniques applied to materials acquired for the thesis. As the sole archaeological materials were fish bones, the chapter begins by discussing the difficulties inherent in accurately identifying archaeological Atlantic salmon bones. Sources and contextual information for the osteological samples used in this thesis are also described, as well as the recording methods used to note metric and taphonomic data. Biomolecular methods, including zooarchaeology by mass spectrometry (ZooMS) and bulk stable isotope analysis, are also described. The qualitative and quantitative methods applied to analysis of documentary and literary sources, as well as various artistic representations of salmon and salmon-like fish, are outlined and discussed. Finally, the statistical analytical methods, and subsequent open data products, are discussed.

The sampling process began with identification of likely sites to include for biomolecular analysis, and progressed through several stages. Sites with large assemblages of salmonid bones (n>20) were compiled into a spreadsheet with related site information and collections stewards and analysts responsible for the remains were contacted to begin the process of requesting loans for further analysis. Materials were collected from storage locations and brought to the University of York's BioArCh laboratory. All samples with more than 20mg of usable bone went through a collagen extraction process and, if the collagen yield was high enough, were analysed for bulk carbon and nitrogen isotope values. Remaining collagen was used to confirm species identification using ZooMS analysis. All samples with less than 20mg of bone had collagen extracted only for ZooMS analysis. All samples were photographed and cleaned prior to beginning the demineralization process, using one of two methods. Larger, more robust samples were cleaned using a Vaniman Master Problast 3 micro-abrasive blasting unit, using aluminum oxide blast media. All samples too fragile or small to sandblast were water sonicated to remove dirt and debris, and then dried before moving on to further laboratory protocols.

3.2 Osteology

Building the collection of faunal material used for this thesis involved a major review of available fish bone data from the North Sea Basin area, which focused on identifying archaeological sites with *Salmo* sp. remains(Chapter 7). This review covered 146 archaeological sites and identified a total of 2515 salmonid remains from Scotland, England, France, Belgium, the Netherlands, Germany, Denmark and Norway. The vast majority of these sites contained 10 salmonid bones or fewer, so sites with larger assemblages were targeted for extensive bulk stable isotope analysis combined with ZooMS, and smaller sites were only targeted for ZooMS. Site selection was dependent on material availability, coordination with managing institutions, and fluctuating COVID-19 travel and work restrictions. In the end 20 archaeological sites were chosen for study– one each from England and Scotland, three from Denmark, and the remaining 15 from the Netherlands. The six sites with large assemblages chosen for an intersite comparative isotopic study were Coppergate, Earl's Bu, Ribe Posthuset, Nieuw Rhijngeest-zuid Oegsgeest, Minderbroedersklooster Den Bosch, and Tjitsma Foarryp Wijnaldum. The zooarchaeological assemblage for this thesis consisted of two major categories; 1) *Salmo* sp. bones and 2) freshwater, marine and migratory fish species local to the sites included in the study (Chapter 2). This section on osteology will focus on species identification procedures (in the case of *Salmo* sp. remains), and general recording and quantification of fish remains, including brief comments on pathology and butchery.

3.2.1 Taxonomic Identification

All identification of skeletal elements for this project was conducted according to commonly employed methods of zooarchaeological study, utilizing comparative specimens, literature references, and digitized resources to make genus or species level determinations (see Figs. 1 and 2). Comparative reference skeletons from the Terry O'Connor Zooarchaeology Laboratory housed in the University of York's BioArCh Centre were primarily used for direct morphological comparison. The fish collection is moderately comprehensive, with multiple high quality complete skeletons available for most commercially exploited marine and freshwater fish from the UK. Some reference skeletons were not as complete, were older, or were otherwise of lesser quality, and online resources like the University of Nottingham Archaeological Fish Resource (Sykes and Saddler 2017) and the Idaho Virtual Museum Osteology collection (Betts et al. 2011; Holmer et al. 2014) were used to fill in these gaps. In addition to these resources, the fish reference collection at the Rijksdienst voor het Cultureel Erfgoed (RCE) in Amersfoort, the Laboratory for Archaeozoology at the University of Leiden, and the Zooarchaeology Laboratory at the Groningen Institute of Archaeology at the University of Groningen were also consulted during sampling trips. The majority of fish bones analysed for this thesis, other than the two salmonid species of interest, included gadids (cod, haddock, saithe, etc), cyprinids (bream, chub, dace, carp), pike, and eel.

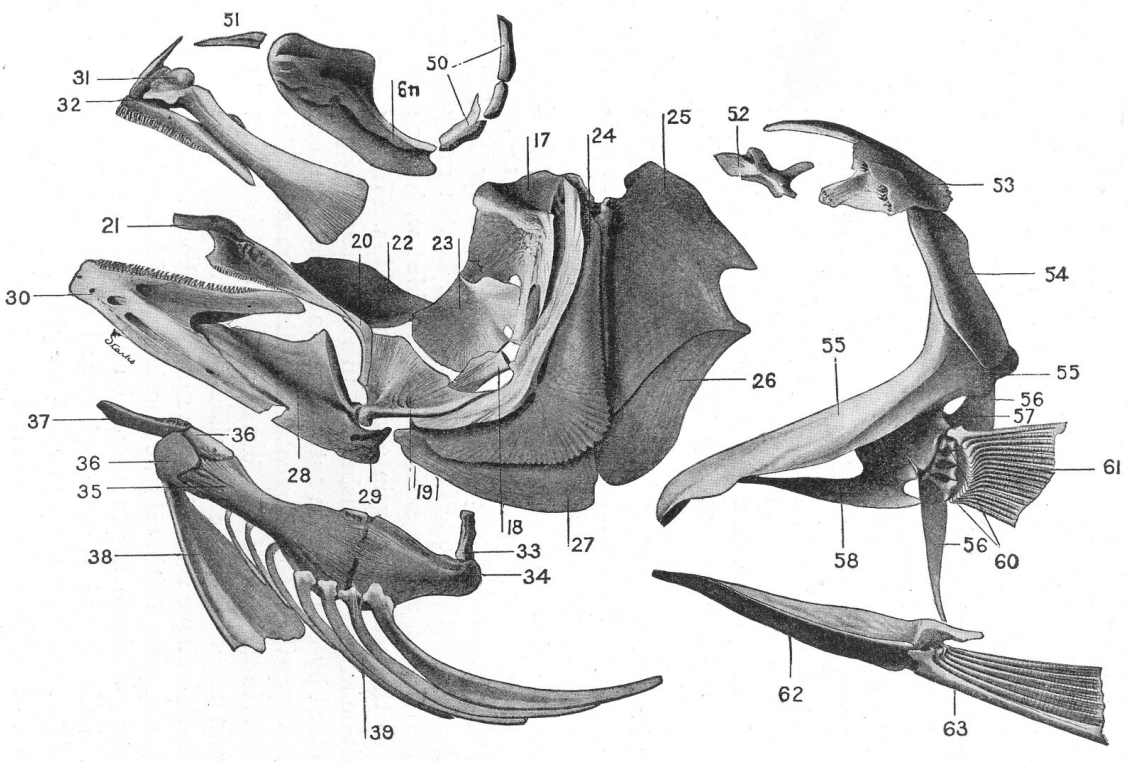


FIGURE 3.1: Labeled I=illustration of the skull and pectoral girdle of a striped sea bass (*Morone saxatalis): 17 Hyomandibular; 18 Symplectic; 19 Quadrate; 20 Pterygoid; 21 Palatine; 22 Endopterygoid (mesopterygoid); 23 Metapterygoid; 24 Preopercule; 25 Opercle; 26 Subopercle; 27 Interopercle; 28 Articular; 29 Angular; 30 Dentary; 31 Maxilla; 32 Premaxilla; 33 Interhyal; 34 Epihyal; 35 Ceratohyal; 36 Basihyal; 37 Glossohyal; 38 Urohyal; 39 Branchiostegals; 49 Preorbital; 50 Suborbital; 51 Nasal; 52 Supratemporal; 53 Post-temporal; 54 Supracleithrum; 55 Cleithrum; 56 Postcleithrum; 57 Hypercoracoid; 58 Hypocoracoid; 60 Actinosts; 61 Pectoral fin; 62 Pelvic girdle; 63 Pelvic (ventral) fin. Reproduced from Jordan (1905), courtesy of the Australian Museum and Mark McGrouther.*

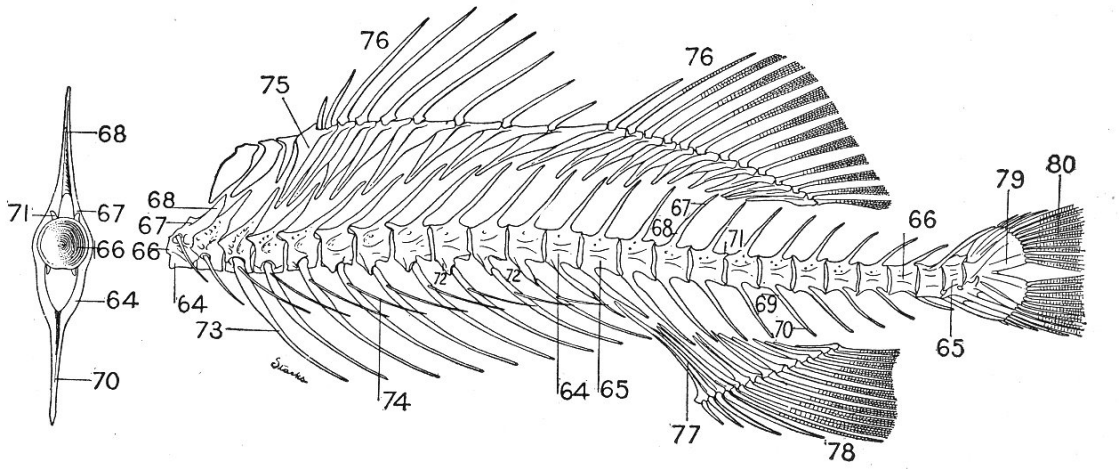


FIGURE 3.2: Labeled I=illustration of the vertebral column and fins of a striped sea bass (*Morone saxatalis): 64 Abdominal vertebrae; 65 Caudal vertebrae; 66 Centrum; 67 Neurapophysis; 68 Neural spine; 69 Haemapophysis; 70 Haemal spine; 71 Zygapophysis; 72 Parapophysis; 73 Ribs; 74 Epipleurals; 75 Interneural; 76 Dorsal fin; 77 Interhaemal; 78 Anal fin; 79 Hypural; 80 Caudal fin. Reproduced from Jordan (1905), courtesy of the Australian Museum and Mark McGrouther.*

Differentiation between Atlantic salmon (*Salmo salar* and brown/sea trout (*Salmo trutta*) was a major facet of the initial research design for this thesis, which originally involved an extensive geometric morphometric study of differences in shape and form of vertebrae from Atlantic salmon and brown/sea trout. Due to the ongoing COVID-19 pandemic and difficulties sourcing skeletal elements from modern wild salmon and trout, this portion of the thesis did not go forward. While farmed Atlantic salmon and brown/sea trout are readily available in the commercial market, farmed individuals are unsuitable for geometric morphometrics studies. Farmed salmon and trout are highly susceptible to skeletal deformities, especially in early stages of vertebral growth, due to a combination of industry-standard vaccine protocols, unvaried diet, and poor environmental conditions (Berg et al. 2012; Holm et al. 2020; Peruzzi et al. 2018; Silverstone and Hammell 2002; Ytteborg et al. 2010).

However, some insight into differentiation between different *Salmo* species has been gained during the research process. There is some commentary in the available literature discussing specific differences between skeletal elements of Atlantic salmon and freshwater brown trout. Some of the most commonly mentioned skeletal elements that show clear differences are the dentary, premaxilla, maxilla, supraethmoid, vomer, and atlas vertebra (Kacem and Meunier 2009; Norden 1961; Tchernavin 1938; Watt, Pierce, and Boyle 1997). The case of the ethmoid, dentary, maxilla and premaxilla is more dependent on sex and age, and so are not able to be used 100% of the time to distinguish between salmon and trout. The development of the "kype" (Fig. 3) or hooked beak is a characteristic of male anadromous *Salmo sp.* individuals, including anadromous Atlantic salmon and, occasionally, Sea trout (*Salmo trutta morpha trutta*). This kype is generally assumed to be a secondary sexual characteristic which may attract female salmon during spawning, and may aid in defense from attacks made by other male salmon (Tchernavin 1938; P Eckhard Witten and Brian K Hall 2003, 2002). While the most prominent osteological changes seen in kype development involve the dentary, or lower jaw, of the fish, significant changes also occur within the supraethmoid, premaxilla and maxilla (Kacem and Meunier 2009; Tchernavin 1938; P. Eckhard Witten, Rosenthal, and Brian K. Hall 2004).

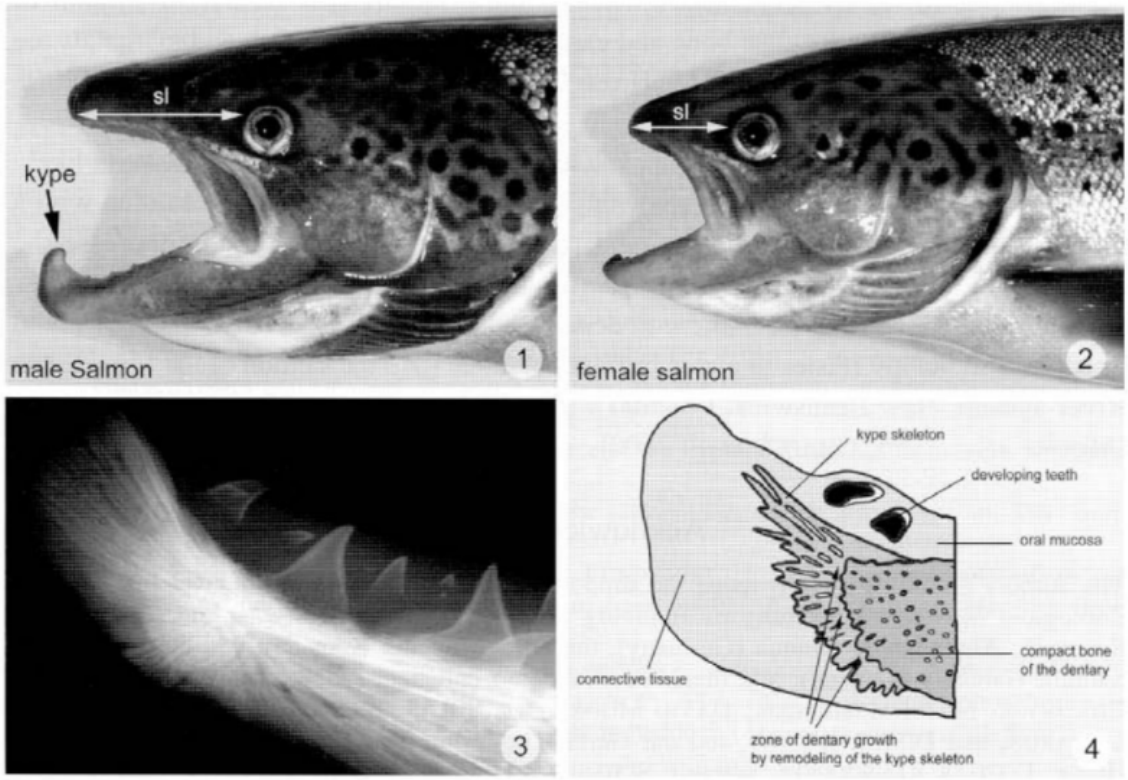


FIGURE 3.3: Reproduction of Figures 1-4 from Witten et al. (2003) showing the following: 1. Head of sexually mature male Atlantic salmon showing male sex-related traits, the prolonged snout length (sl) and the kype. 2. Head of sexually mature female Atlantic salmon. 3. Radiograph of the lower jaw tips from a sexually mature male Atlantic salmon showing the kype supported by skeletal needles extending apically and ventrally. 4. Diagrammatic representation of the tissues that constitute the kype in male salmon.

The supraethmoid, is an anterior cranial bone which generally articulates at various points with the vomer, frontal, parasphenoid and premaxilla bones. In the *Salmo sp.* fishes the supraethmoid is roughly wing shaped, and key differences between the ethmoid of the salmon and trout are mostly due to sexually dimorphic changes which occur as a result of spawning. Trout have the possibility of developing a hypethmoid portion of the main ethmoid bone, which is not reported in salmon and may be used to differentiate between the two, but is highly dependent on the individual fish. The largest differences are seen between the shape of the supraethmoid, which is the ossified region covering the ethmoid cartilage that makes up most of the ethmoid complex (Norden 1961; Tchernavin 1938). In their basic non-breeding form the male and female salmon have a supraethmoid with a maximum width at the posterior end, and which narrows anteriorly (Norden 1961; Tchernavin 1938). Trout show a slight difference in overall supraethmoid shape between males and females, with males displaying a slightly rhomboid shape, but both sexes retain a more consistent width along the total length, relative to that seen in the salmon (Norden 1961; Tchernavin 1938). Breeding male salmon show a marked widening of the anterior portion of the supraethmoid (due to the formation of the kype), making them appear much similar in shape to both male and female trout (Tchernavin 1938). In short, the supraethmoid may be used to differentiate between breeding male and female salmon, and all trout of both sexes. Presence of a hypethmoid would indicate the species is *Salmo trutta*, as these are not reported in *Salmo salar* (Norden 1961).

The maxilla is an anterior cranial bone which articulates with the premaxilla and palatine bones. The maxillae

of brown trout contain between 15-22 teeth during its entire adult life, always fully ossified with the maxillary bone itself (Norden 1961). Salmon, however, lose their ossified maxillary teeth while they are in their ocean form, after the smolting process. They do possess some small teeth in the maxillary area, but these attach directly to the skin (Norden 1961) and would generally not be preserved archaeologically. Therefore the presence of ossified teeth on the maxilla may be used to differentiate between post-smolt salmon and adult trout.

The premaxilla is an anterior cranial bone which articulates with the maxilla, supraethmoid, and vomer and contains between 8-12 conical teeth (Norden 1961). There is a clear morphological difference reported between the premaxillae of adult salmon and adult trout, relating to the ratio of height to length. In salmon the value for premaxillae height is equal to half of the premaxillae total length (measurements after Morales Muniz and Rosenlund (1979)), whereas the height of trout premaxillae are roughly 70% the length (Watt, Pierce, and Boyle 1997). In trout there is also a convex thickening or bulge reported on the medial aspect of the bone, just above the row of teeth (Watt, Pierce, and Boyle 1997). Though male salmon go through significant changes in size of the premaxillae during the formation of the kype, including losing and reforming multiple teeth (Tchernavin 1938), the ratio of 1/2 height to total length stays consistent, and the medial bulge is still distinct only to trout, allowing for diagnostic identification criteria.

The dentary is an anterior cranial bone which articulates with the angular and maxilla, and is the largest bone within the lower jaw of salmonid fishes (Norden 1961). It undergoes the most significant morphological changes during kype formation, and retains distinct morphological differences in anadromous *Salmo sp.* fishes even after the breeding season (Tchernavin 1938; P. Eckhard Witten and Brian K Hall 2002). The characteristic hook shape of the mature adult male salmon is extremely distinctive, and may survive to show in the archaeological record. The formation of the kype involves reabsorption of mineral material from other cranial bones as well as scales, and the hooked projection is made up of a mesh-like area of spongiose bone, which are made up of "skeletal needles" which thicken and ossify to form a cap over the original dentary (P. Eckhard Witten and Brian K Hall 2002). Though initially an open matrix, as the breeding season progresses the kype changes into compact bone, and both the underlying dentary structure and the newly formed osseous material of the kype increase in overall size and length (P. Eckhard Witten and Brian K Hall 2002). The post-spawning salmon, or *kelts*, do show some reduction in size of the kype and dentary, with tooth loss and demineralization of the bone material evident, but male kelts are reported to retain a morphologically distinct dentary form (P. Eckhard Witten and Brian K Hall 2002). This does allow the dentary to be used to differentiate between salmon and trout, but only in regards to male adult salmon and kelts.

The vomer is an anterior cranial bone which articulates with the parasphenoid, and is the most consistently distinctive cranial element that can be used to differentiate between Atlantic salmon and brown trout (Kirczuk and Domagała 2011; Locke 1929; Norden 1961; Tchernavin 1938). The vomer of the Atlantic salmon displays only a single row of teeth along its central shaft and head, forming a "T" shape, and may even lose teeth during spawning due to bone reabsorption for kype formation and egg development (Kirczuk and Domagała 2011; Tchernavin 1938). Conversely, all adult brown trout show two rows of well-rooted vomerine teeth, alternating in a zig-zag fashion, on both the central shaft and the head (Kirczuk and Domagała 2011; Locke 1929). The head of the vomer is differently shaped in both species, with the Atlantic salmon having a roughly pentagonal shape and the brown trout having a clear triangular vomerine head (Kirczuk and Domagała 2011; Tchernavin 1938).

The atlas, or first vertebra, of both salmon and trout is easily distinguished from the precaudal and caudal vertebra that make up the remainder of a salmonid vertebral column. An comprehensive study of the visible and metric differences between Atlantic salmon and brown trout was published in 1989 by zoologists Feltham and Marquiss (Feltham and Marquiss 1989). The authors identified three physical characteristics of the atlas

vertebra which can be used in some cases to distinguish between salmon and trout; vertebral height and waist, pore shape, and process shape (Feltham and Marquiss 1989). Table 1 details the observed differences described by Feltham and Marquiss, and which they showed can be used to correctly classify species with 79-81% certainty (Feltham and Marquiss 1989). In addition to these visual characteristics, Feltham and Marquiss also tested the reliability of a regression analysis which plotted first vertebra width against total fish length, which they found able to classify species with 90% certainty.

Visual characteristics	***Salmo salar***	***Salmo trutta***
Overall height and shape	Generally "squat" appearance, short relative to vertebral width, lack of a defined "waist"	Defined "waist", taller height relative to vertebral width
Pore shape	Generally slit-like or narrowly ovate	Ovate or round pores
Process shape	Distinctly ear-shaped protrusion, and generally rounded processes	Angular or flattened processes, no ear-like protrusion from the body of the vertebra

TABLE 3.1: First Vertebra Descriptions outlined in 1989

3.2.2 Recording and Quantification

In order to most accurately assess the archaeological material reviewed for this thesis a system of recording and quantification was developed based on commonly used zooarchaeological methods. Only fish bones from undisturbed archaeological contexts which could be securely dated were included in the database of fish bones recorded for this thesis. Data on individual skeletal elements were collected and recorded in a Google Sheets spreadsheet database, which allowed for easy export into CSV format to be analysed using the R statistical programming language. In addition to basic site information about phasing, collection methods and and dating, a variety of osteometric and descriptive information about the bones were recorded within this database. Measurements were based on those standardized by Morales and Roselund (1979), and generally recorded length, width and height of various portions of individual elements. As the vast majority of recorded *Salmo* sp. elements were vertebrae or vertebral fragments, the most commonly recorded measurements were:

- M1 = greatest dorso-ventral height of centrum,
- M2 = greatest medio-lateral breadth of centrum,
- M3 = greatest lateral height of hemal and neural spines, and
- M4 = greatest cranio-caudal length of the centrum

For the most part only elements which could be reliably identified were included in this dataset, which means that the most important quantification of these bones is NISP, or number of identified specimens. When assessing entire faunal assemblages, which may include tens of thousands of mammal, bird and fish bones and fragments, NISP can be a problematic quantification of the number of animals present on a site. The issue of interdependence involves the uncertainty of whether, for example, a group of 20 salmon vertebrae belong to a single salmon, or to anywhere from 2-20 different fish (Grayson 1984; Lyman 1994). This specific issue is somewhat mitigated in the case of this assemblage by differences in estimated total length, which were calculated

using regression formulas (Watt, Pierce, and Boyle 1997). Calculating total length estimates also allows for some estimate of the minimum number of individuals (MNI) within the sub-assemblage, but this is obviously not representative of the MNI of the particular species on each site. The very nature of this dataset, which has, for most sites, been subsampled from the existing fish remains, means that all quantifications of NISP and MNI are accurate only for the dataset itself, not the sites which these bones come from.

3.2.3 Taphonomy

Taphonomic factors recorded for this project included fragmentation and condition, burning, digestion markers, gnawing, unusual staining, and butchery. Digestion markers included both acid etching and chewing compression, which was recorded separately from gnawing marks made by rodents or carnivores. Normal staining, such as browning and other discoloration which is expected from deposition in humic soils (Dupras and Schultz 2013), was not generally noted, but any staining from metals like copper or iron was recorded separately. All bones with evident butchery showed one or two types of cutmarks; 1) surface modifications made by a knife or other sharp cutting implement, or 2) clean splits or otherwise nearly-complete separations of bone. Finally, burning was recorded using three general categories– charred, burnt, or fully calcined.

These categories are simplified versions of noted taphonomic changes observed in experimental studies conducted on animal bone (R. A. Nicholson 1992; Steffen and Mackie 2005). As observed by Nicholson 1992, fish bone generally has between 3-4 macroscopically visible types of taphonomic change when burned at temperatures from 200°C to 900°C. The lowest temperature changes involve surface cracking, progressing to peeling "bubbly" char layers, and finally a complete absence of the dark char layer with a smooth chalky surface (R. A. Nicholson 1992). In the context of this project the phrase "charred" refers to the first low-temperature burn stage, with surface cracking and the beginnings of discolouration. The phrase "burnt" refers to the mid-range temperature burn stage with a visible "peeling bubbly char" layer. Finally, "calcined" refers to the <800C burn stage with smooth, chalky, and generally white/light grey color (R. A. Nicholson 1992).

The majority of charred, burnt or fully calcined bone seen during reviews of archaeological material for this study were not intentionally sampled for biomolecular analysis for several reasons. First, one of the characteristic diagenetic features of burnt bone is the removal of water, collagen, and other organic components (Gallo et al. 2021; Stiner et al. 1995). Burning also results in alterations and recrystallization of the remaining bioapatite structure, leaving burned bone far more fragile than fresh (Gallo et al. 2021; Stiner et al. 1995). This means burned bone not only contains less collagen overall, but is also far more susceptible to complete demineralization when exposed to the dilute hydrochloric acid used for bulk stable isotope analysis.

3.3 Zooarchaeology by Mass Spectrometry (ZooMS)

The main purpose of Zooarchaeology by Mass Spectrometry (ZooMS) analysis is to identify animal remains to genus or species level using collagen peptide sequencing techniques. Developed in 2009, ZooMS analysis utilizes the unique sequence of amino acid peptide markers found in bone collagen to distinguish between the bones of animal species commonly found on archaeological sites (Buckley 2018; Buckley, Collins, et al. 2009; Collins et al. 2010). ZooMS has a distinct advantage over other biomolecular species identification methods like ancient DNA analysis, as it uses a comparatively stable protein (collagen) which is found in all faunal bone samples (Buckley 2018; Buckley, Collins, et al. 2009; Collins et al. 2010). The first discussion of ZooMS use for archaeological fish remains was published in 2009, and since that point ZooMs markers, or molecular barcodes, for fish species

identifications have been published in a variety of sources (Collins et al. 2010; Harvey, Daugnora, and Buckley 2018; Kristine K. Richter et al. 2011; Kristine Korzow Richter et al. 2022). ZooMS markers for both Atlantic salmon and brown trout were first published in 2011 (Kristine K. Richter et al. 2011), and later updated in 2018 (Harvey, Daugnora, and Buckley 2018) and 2022 (Buckley, Harvey, et al. 2022). All samples selected only for ZooMS species identification were prepared and processed according to the University of York's BioArCh Laboratory Standard Operating Procedure for Species Identification by ZooMS (Doc. 42).

3.3.1 Demineralisation

For 45.1% of the total ZooMS sample (n=88) the individual specimens began as bone chips weighing between 10-30mg, and were placed in 250μL of 0.6M HCl at 4$\circ$C until demineralised. Samples were then centrifuged, HCl removed, and 250μL 0.1M NaOH solution was used to wash the specimen and remove any remaining humic acids. Specimens were then rinsed three times in 200μL of 50mM ammonium bicarbonate (NH_4HCO_3) pH 8.0 (AmBic solution).

3.3.2 Gelatinisation

After three washes, 100μL of AmBic was added to each Eppendorf tube containing the demineralized bone chips. These were then incubated at 65°C for approximately 1 hour, in order to gelatinise the collagen within the demineralised sample.

3.3.3 Digestion

After gelatinisation was complete, 50μL of the supernatant was extracted and 1μL of trypsin solution added to the 50μL sample and left to incubate overnight at 37°C. The trypsin digestion step is essential to unravel the gelatinised collagen samples to a point where the collagen peptides can be sequenced and "read" using the established species markers. Trypsin digestion was stopped using 1μL 5% of trifluoroacetic acid (TFA) solution.

The remaining 54.9% of the ZooMS sample (n=107) consisted of collagen specimens which were previously extracted for bulk stable isotope analysis (see following section). This freeze dried collagen was rehydrated with 50μL of AmBic and then had 1μL of trypsin added to digest overnight as described above. The protocol for both demineralized bone and freeze dried collagen samples was the same from the trypsin digestion step onward.

3.3.4 Extraction

Digested peptides were extracted using a C18S ZipTip, which involves the use of a washing and conditioning solution to prepare the tips. The washing solution is made up of 0.01% TFA in ultrapure water, while the conditioning solution is made up of 0.01% TFA, in a 50:50 Acetonitrile and ultrapure water solution. Each ZipTip was conditioned twice, washed twice, then the 50μL sample was drawn over the filter at least 10 times. The empty ZipTip with collagen peptides held on it's filter was then washed twice more, and 50μL of conditioning solution was drawn up and transferred to a new Eppendorf tube. The resulting collagen extract was drawn over the ZipTip filter at least 10 times before being expelled fully into the new Eppendorf.

3.3.5 Spotting

These filtered collagen samples were then spotted onto a 384 ground steel well plate to be used in a Bruker Ultraflextreme MALDI-TOF mass spectrometer. Each sample was spotted in triplicate, and calibrant spots were added to allow the MALDI-TOF to calibrate it's laser for each row of samples. Both sample and calibrant spots were mixed with a matrix solution, in order to aid the laser in ionizing samples.

3.3.6 MALDI-TOF Analysis

Analysis of samples using the MALDI-TOF mass spectrometer consisted of loading the desired well plate into the machine, and using the accompanying Bruker software to first calibrate the laser using one or more of the calibration spots. Once calibration was confirmed, the run was begun, and the resulting mass spectra data was exported as .txt files and saved to a local drive.

3.3.7 Spectra Analysis

The .txt files, in triplicate for each sample, were then combined with descriptive data from plate maps made at time of spotting using a short program written in the Python programming language so that each file was renamed with its correct sample name. The samples were then averaged, and a list of present peaks and their associated peptide positions generated for each averaged sample, with peak picking based on intensity and using a signal-to-noise threshold of 2. Each sample was manually checked for marker peaks, species assigned accordingly, and any unclear samples were viewed using the mMass spectra viewer software.

3.4 Bulk Stable Isotope Analysis

The purpose of bulk stable isotope analysis is multifold in this thesis study, with a variety of environmental, geographic and dietary information which can be obtained from evaluating the ratio of certain stable isotopes found within fish bone (see Chapters 4 and 5). The two stable isotopes primarily discussed in this thesis are ^{13}C (Carbon-13) and ^{15}N (Nitrogen-15), which are naturally occurring stable isotopes in all animal bone collagen. The calculated values of ^{13}C and ^{15}N are represented as a "ratio-of-ratios" (Fry, 2006: 24), using δ ‰ notation and the following equation.

$$\delta(‰ = (RSample/RStandard - 1)x1000$$

This equation expresses the ratio of two separate ratios; 1) the RSample, which is the ratio of heavy to light isotopes in the sample analyzed and 2) the RStandard, which is the ratio of heavy to light isotopes in a laboratory standard used for comparison (Fry 2006; Michener and Lajtha 2007). The ratio of these two ratios is expressed in percentage per-mille (‰), and represented as a δ value– e.g. a δ^{13}C value when dealing with carbon stable isotopes.

3.4.1 Delipidification

Work in the field of food chemistry and isotope ecology has shown that fish collagen has markedly different isotopic characteristics when compared to mammal collagen (Szpak 2011).Fish collagen tends to exhibit more variable chemical compositions than that found in mammals, mainly due to differences in fish bone chemistry

and structure that allows for an increase in carbon contamination from sources like humic acids and lipids (Guiry, Szpak, and Richards 2016; Szpak 2011). To mitigate some of these challenges a lipid extraction protocol was applied to 323 samples; the remaining 59 were processed prior to making the decision to de-fat the majority of remains. This decision was based on results reported in a 2016 study, which concluded that the most efficient method of removing 13C-deplete lipids from fish bone was to use a 2:1 dichloromethane (DCM) solution and that removing lipids significantly improved isotopic measurements (Guiry, Szpak, and Richards 2016). The lipid extraction protocol used was based on that described in Colonese et al. (2015), where bone samples were placed in glass tubes containing 8ml of DCM solution and then sonicated at 30kHz for 15 minute cycles. After each 15 minute cycle the samples were removed from the sonicator, the DCM solution decanted with glass pasteur pipettes and DCM solution refreshed before being placed back into the sonicator. This process was repeated a minimum of three times, until the DCM solution remained clear and showed no evidence of lipids remaining. At this stage the samples were rinsed to neutral pH in ultrapure water, and then the normal demineralization protocol was followed.

3.4.2 Demineralisation

After defatting they were placed in glass tubes containing 8ml of 0.4M HCl– 0.4M HCl was used rather than the standard 0.6M HCl solution due to the fragile nature of the fish bone samples. The samples were then agitated on a roller-rocker tube rack at between -2 and 10°C, and checked for adequate demineralization first at 24 hours, and then every 12 hours until demineralization was complete. Once demineralized the samples were flexible and often depleted in natural coloring, sometimes appearing as a collagen pseudomorph that took the shape of the original bone.

3.4.3 Gelatinisation

The demineralized samples were rinsed to neutrality with ultrapure water, and then placed in 8ml of pH3 HCl solution. The samples were placed in a heater block set at 80°C to gelatinise for between 24-48 hours, and removed from heat when agitation produced a uniform froth.

3.4.4 Freeze Drying

After gelatinisation the samples were cooled to room temperature, filtered using an EEZE™ filter to remove remaining mineral debris, frozen at -20°C for 48 hours, and then transferred to a Lablyo bench-top freeze-drier. After 48 hours the freeze-dried samples were removed and eventually weighed out into tin capsules for mass spectrometry. Each sample was run in duplicate, in a sample of approximately 0.5mg. All stable carbon and nitrogen isotopic values reported in this thesis were determined using a Sercon 20-22 continuous flow isotope ratio mass spectrometer (IRMS) coupled to a Sercon GSL elemental analyzer at the University of York's BioArCh laboratory.

3.5 Documentary and Representational Analysis

In order to properly contextualize the zooarchaeological and biomolecular data collected and analyzed as part of this these, reviews of related medieval documentary and artistic records were also undertaken. Reviews of documentary and literary works were approached using semi-structured document analysis methods, where quan-

titative variables like cost and amount were recorded along with qualitative variables like variations in recorded words (Blandford 2014; Bowen 2009). Time was a major limiting factor in how exhaustive the documentary and representational analysis could be, as was the availability of transcribed medieval records. Documents consulted for this series of qualitative and quantitative review were exclusively published in either English translation, Old English or Latin, and, where necessary, additional translation from Latin and Old English was performed. Four series of documentary publications were consulted, which included seven total volumes of text (Table 2), all of which were from English contexts spanning the 13th-16th centuries. All seven texts were available in digitized formats online, and all are examples of medieval manuscripts which were transcribed in printed form during the late 19th to early 20th centuries. Additionally, all of these texts were available in a "searchable" format, meaning that the text was either digitally typeset, or had been scanned and converted using optical character recognition. These factors mean that the texts included in this thesis are not a fully representative dataset of all medieval English municipal and ecclesiastical publications in existence, but merely the most accessible. This dichotomy of comprehensiveness vs. accessibility is similar to those faced when reviewing published zooarchaeological data, or even interpreting archaeological materials in general– it is the very nature of the field that we will only be able to review what has survived in the most accessible formats. That being said, the seven texts included in a dataset explored in Chapter 6 represent an interesting variety of customs, tax, purchase, receipts, and gift records from High-Late Medieval periods. These texts include two volumes of records of the Corporation of Leicester, three volumes of account rolls from Durham Priory, a volume of "usages", or customs, of the City of Winchester, and a volume focused on early English customs systems which covers tax and customs records from cities and towns including London, Southampton, Lynn and Torksey– all cities and towns within the catchment of the North Sea and English Channel (Bateson 1899, 1901; Fowler 1898, 1899, 1901; Gras 1918; Toulmin Smith 1870).

Text Name	Recorded Dates	Publication Date	Translator/Editor
Corporation of Leicester Records 1103-1327	1264-1321	1899	Mary Bateson
Corporation of Leicester Records 1327-1509	1335-1371	1899	Mary Bateson
English gilds: þe olde vsages of þe cite of Wynchestre	1350	1870	Joshua Toulmin Smith
Extracts from the account rolls of the Abbey of Durham, Vol. 1	1308-1449	1898	J.T. Fowler
Extracts from the account rolls of the Abbey of Durham, Vol. 2	1299-1340	1899	J.T. Fowler
Extracts from the account rolls of the Abbey of Durham, Vol. 3	1409-1524	1901	J.T. Fowler
The early English customs system; a documentary study of the institutional and economical history of the customs from the thirteenth to the sixteenth century	1228-1467	1918	Norman Scott Brien Gras

TABLE 3.2: English documentary records reviewed for the thesis

Prior to a review of texts, a list of potential search words was compiled, which included various conjugations and forms of the Latin roots *salmō* and *trutta*, as well as the Old High German *lahs*, Old English *leax*, and Old Norse *lax*. As most of the records were in Latin, or translated from Latin, the most relevant search term was "salm", which allowed simple text searches to pick up singular forms like *salmonis* and *salmone*, plural forms like *salmonibus*, and abbreviated forms like "*salmon.*". A total of 150 entries were added to the preliminary documentary review dataset, which includes references to salmon, and other fish, being bought, sold, and gifted by individuals and institutions. There are also several references to specific customs duties and fees related to salmon, such as the 14th-century "salmon-fee" from the Corporation of Leicester (Bateson 1899, 1901). In the case of records that refer to salmon and other fish with associated costs or values, the price at the time was recorded as well as a rough conversion to pounds sterling (GBP) as of July 2023. This conversion was done in two parts, the first utilising the National Archives online currency converter, which provides conversions from the pre-decimalisation values of pounds, shillings and pence from 1270-2017 CE (Archives 2017). The second step of the conversion was to use the Bank of England's official inflation calculator (England 2023) to convert the 2017 GBP to 2023 GBP, providing a very rough estimate of modern day value of the medieval shipments, gifts, and sales. These estimates allowed for direct comparison of the value of different preparations of salmon over

time and between ecclesiastical and municipal records (see Chapter 6, Section 3.1).

In addition to this more in-depth documentary review, a very brief review of both literary sources and visual representations of salmon and brown/sea trout was included. The literary sources included 32 texts dated to between c. 990-1663 CE, ranging from French, English, and German cookbooks, Dutch and English treatises on fishing, and isolated stanzas of Norse poetry. The date range of this review extends well into the "Early Modern" period, and the decision was made to include later publications to diversify the sources included. These sources, as with the documentary records, were easily accessible, searchable, and, often, available in translation. The texts were searched for references to salmon, trout, and sea trout, and notable instances are discussed in Section 3.2 of Chapter 6. The visual representations of salmon included what may be variously defined as "symbolic" or "artistic" depictions of salmon and salmon-like fish, and was focused primarily on Pictish monumental stele, bestiary illustrations, and medieval heraldry.

3.6 Data Analysis and Visualization Methods

Database management and manipulation was completed using a combination of Google Sheets, Microsoft Excel and the R statistical programming language. Data was initially recorded in spreadsheet format with variables such as site names, dating and phasing information, morphological identifications, and measurements input on a sample-by-sample basis. Each sampling instance/trip was originally recorded separately, and the datasets were later merged into a master spreadsheet-based database which contains unique identifiers, site information, morphological identifications, and biomolecular data information. Data exploration and statistical analysis was completed using a combination of manual data cleaning, as well as manual and programmatic filtering based both on quantitative values and qualitative criteria. As the data involved in this study was semi-structured and initially compiled and analyzed in piecemeal steps, statistical methods like PCA analysis were not appropriate for initial filtering. General statistical analysis and data visualization in R was performed using the Tidyverse environment and base R methods, using packages like dplyr and ggplot2, and was conducted using the RStudio platform (R Core Team 2020; RStudio Team 2020; Wickham, Chang, et al. 2023; Wickham, Francois, et al. 2023). A full list of packages used for this project and all code produced can be found in Appendix E. The majority of programming packages used were aimed at performing basic statistical functions and visualizing the datasets presented in this thesis, but one package, "rKIN", played a major analytical and interpretative part in the production of Chapter 9. This chapter is focused on the analysis and interpretation of a large isotopic dataset, with particular focus on the regional differences apparent between archaeological salmon and trout populations, as well as isotopic niche size and overlap estimates for archaeological salmon, trout, Northern pike and haddock. The rKIN package was initially developed for use with ecological datasets, in order to implement and compare three commonly used methods of calculating isotope niche spaces (Albeke 2017; Eckrich et al. 2020; J. R. Robinson 2022). Isotope niche spaces are intended to be an estimate of lifetime ecological niches, isotopically representing both resource and bioclimactic factors that contribute to the ecological niche of a given animal (Newsome et al. 2007; J. R. Robinson 2022). The use of rKIN for analysis of archaeological material is a relatively recent development, and has previously been limited to studies of bulk stable isotope data of humans and human-ancestors (Hermes et al. 2018; J. R. Robinson 2022, 2023).

Multiple methods of estimating isotopic niche spaces from bulk stable isotope data have been proposed, all of which have their own benefits and barriers to usage. Convex hull/polygon calculations use the total area of a convex hull to estimate the total extent of trophic diversity seen within a population, or even across an entire food web, but can be highly susceptible to intra-species variations (Layman et al. 2007; N. Robinson et al. 2021).

Standard ellipse area calculations accounts for some of the intra-specific variation that can skew convex hull analysis, but doesn't give a clear view of potential overlap between groups (Jackson et al. 2011; J. R. Robinson 2022). In order to provide the most comprehensive view of both istope niche widths and potentional ecological niche overlaps, kernel utilization density calculations were proposed by Eckrich et al. (2020) to work in conjunction with convex hull and standard ellipse area methods. The resulting rKIN package produces five sets of data; minimum convex polygon (hull) estimates, bivariate normal ellipse estimates, bivariate normal kernel utilization density estimates, isotope niche widths, and pairwise overlap calculations (Albeke 2017; Eckrich et al. 2020; J. R. Robinson 2022). The overlaps calculated help identify areas of potential overlap in ecological niches for different taxa and different populations of the same tax (J. R. Robinson 2022). The rKIN package provides visualizations of these data using the standard isotope bi-plot combined with the calculated ellipses, kernels, and polygons at 50%, 75% and 95% confidence interval levels (Albeke 2017; Eckrich et al. 2020). Bulk stable isotope data for four species was formatted for use with the rKIN package to allow for comparison between known marine species haddock, known freshwater species pike, and the two *Salmo* sp. groups. Additionally, regional comparisons between archaeological samples identified as *Salmo salar* and *Salmo trutta* were made to understand more about both the isotope niche space of these populations, and the North Sea trade in *Salmo* sp. fishes.

3.7 Open Science Methods

This PhD research project was part of the SeaChanges Innovative Training Network funded as part of a Marie Skłodowska-Curie Action grant agreement under the eighth Framework Programme for Research and Technological Development, (Horizon 2020), and is subsequently governed by the open science objectives of the European Commission (MSCA-NET 2023). These objectives centre around the generation of open access and FAIR (Findable, Accessible, Interoperable, and Re-usable) data (Wilkinson et al. 2016), and removing barriers for sharing research outputs that result from work funded by European Commission initiatives like MSCA grants (MSCA-NET 2023). Projects, like the SeaChanges ITN, which are funded by MSCA grants are specifically required to comply with mandatory open science practices, and encouraged to creatively share research outputs wherever possible (MSCA-NET 2023). The SeaChanges ITN, for example, not only provided workshops on open data and open science practices as part of doctoral training, but also operated a social media account on Twitter/X to disseminate research information in short form, and a long form blog and website. Calls for open science and open data practices began in earnest during the late 2000's, with discussions about it's place in archaeological research following shortly after and continuing to today (Costa et al. 2013; Marwick et al. 2017; Murray-Rust 2008; C. Nicholson et al. 2023; Royal Society (Great Britain). 2012; Wilkinson et al. 2016).

With the aim of both complying with MSCA requirements for open data sharing and contributing to ongoing efforts to standardize open science practices, all data produced as part of this PhD work will be published in multiple formats. The primary output is, of course, the thesis itself, which will be deposited in the White Rose eTheses Online repository– a shared repository of scholarly work produced by students and researchers from the Universities of Leeds, Sheffield and York. Additionally, any peer-reviewed papers produced from this research will be published Open Access, as required by the MSCA grant agreement. Working beyond the requirements, all bulk stable isotope data will, with the permission of the original sample stewards, be deposited in the IsoArcH initiative's open isotope database (Plomp et al. 2022). Publications, including this thesis, will have full bulk stable isotope and biomolecular data associated with the articles as supplemental materials. Finally, throughout the course of this thesis I have compiled a master rMarkdown document with all code written for analysis and data visualization. This rMarkdown document (Appendix E) will be published, with the associated isotope, ZooMS,

and zooarchaeological datasets, on my personal, publicly-available, GitHub repository. This will enable anyone to download the data and rMarkdown file, and run all code for the project on their own to reproduce the PhD research in it's entirety and investigate other avenues of analysis as desired. This contributes to the goals of computational reproducibilty outlined by Marwick (2019), and make the data generated during this project findable, accessible, and reusable– three quarters of the way to being FAIR.

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Chapter 4

Review of Biomolecular Analyses

4.1 Introduction

This chapter will present a comprehensive review of the biomolecular analytical methods applied to the thesis material, namely bulk stable isotope (SI) and zooarchaeology by mass spectrometry (ZooMS) analysis. While the laboratory methods for each analysis have been presented in Chapter 3, this chapter primarily deals with the underlying theory of bulk SI and ZooMS analyses in archaeology and ecology. The first section focuses on bulk SI analysis and isotope chemistry in animal remains. In addition to a review of the theoretical background, this chapter reviews specific case studies of archaeological applications of ZooMS and SI, with a particular focus on marine and freshwater fish.

4.2 Bulk Stable Isotope Analysis

Applications of bulk stable isotope analysis in ecology and archaeology first emerged in the 1960s, with particular focus on analysis of oxygen, hydrogen, carbon, and nitrogen isotope ratios in shell, animal tissue, and insect chitin e.g. (Michael J DeNiro 1985; Michael J. DeNiro and Epstein 1978; Fritz and Poplawski 1974; Merwe 1982; Minson, Ludlow, and Troughton 1975; Park and Epstein 1961; Schoeninger and Michael J DeNiro 1984; Smith and Epstein 1970). The extraction of collagen from muscle, bone and other animal tissue was soon established as the most representative method for modelling animal diet using bulk stable isotope analysis (Bender, Baerreis, and Steventon 1981; Michael J. DeNiro and Epstein 1978). The benefit of focusing on stable isotopes like carbon, nitrogen and oxygen is that they cycle closely with organic matter within a given environment, allowing for the estimation of food web characteristics e.g. (Fritz and Poplawski 1974; Fry 2006; Minson, Ludlow, and Troughton 1975; Park and Epstein 1961; Smith and Epstein 1970). This section will cover the theoretical background of isotope chemistry and associated laboratory methods, as well as it's applications in archaeology and ecology. Specific case studies in ichthyoarchaeology will round out the discussion of bulk SI analysis in this chapter.

4.2.1 Theoretical Background

Isotope Chemistry

An isotope is a form of a given chemical element that contains the same base number of protons as all other forms of the element, but differs in the number of neutrons. This results in the isotope being either heavier (more neutrons than standard) or lighter (less than standard). While radioisotopes are cosmogenically formed and eventually will decay over time, stable isotopes are energetically stable (Sulzman 2007) and will remain viable for study over long periods of time. This, combined with the process of isotope deposition in the tissue of living organisms, forms the basis of ecological and archaeological usage of stable isotope analysis. While muscle, chitin, keratin and other animal tissues are commonly used in bulk stable isotope (SI) analysis, the primary material used in archaeology is collagen derived from bone material (Pilaar Birch 2013). The metabolic processes that form bone involve the uptake and deposition of chemical compounds from the organism's environment (Hedges, Stevens, and M. Richards 2004). This creates an isotopic record within the structure of the bone, which can be accessed by extracting collagen– a protein which accounts for roughly 20% by weight of bone material (Hedges, Stevens, and M. Richards 2004).

Several mechanisms contribute to the fractionation, or partitioning of heavier and light isotopes of an element– equilibrium reactions, nuclear spin, and kinetic isotope reactions (Michener and Lajtha 2007). For bulk SI analysis the mechanism that most impacts results are kinetic effects, described in terms of a kinetic fractionation

factor, which is as follows:

$$\alpha = \frac{dX_{h,p}/X_{h,s}}{dX_{l,p}/X_{l,p}} \tag{4.1}$$

In the above equation, X_{h} refers to the heavy isotope of the element in question, X_{l} the light isotope, s the substrate, and p the product (Fogel and Cifuentes 1993). Depletion of heavier isotopes are indicated by negative isotope fractionation values, and enrichment of heavier isotopes are indicated by positive isotope fractionation values (Fogel and Cifuentes 1993). These kinetic isotope reactions are those found in biological processes, such as digestion and bone formation, which result in the fractionation of isotopes according to a variety of factors– e.g. individual reaction rates, concentrations of products and reactants in the reaction, environmental conditions, and even species (Kendall and Caldwell 1999). These reactions are generally unidirectional, resulting in the concentration of light isotopes in the product of a reaction, which, in the case of animal tissue formation, would be the collagen, chitin, or muscle proteins that can later be extracted (Kendall and Caldwell 1999) and analysed using mass spectrometry. Fractionation in animal tissue, like collagen, can also result from the inheritance of different isotope values found in soluble proteins, carbohydrates, and fats consumed by the organism as part of its diet (Michael J. DeNiro and Epstein 1978; Merwe 1982). The "balance sheet" (Merwe 1982) of enrichment and depletion of a given element over the lifetime results in calculable ‰ increases and decreases as you move from analysing primary producers at the bottom of the food chain upwards through various levels of consumers (Michael J. DeNiro and Epstein 1978; Merwe 1982).

The results of the analysis of a given animal tissue (in the case of this thesis, bone collagen) are reported using the δ notation, e.g. δ^{13}C or δ^{15}N, and in terms of values ‰, which gives rise to the so-called "ratio-of-ratios" expressed by the following equation:

$$\delta = (R_{SAMPLE}/R_{STANDARD} - 1) * 1000 \tag{4.2}$$

This is because the δ ratio expands the absolute differences in isotope compositions in a given sample into much larger numbers that typically fall in a theoretical range of -100‰ to +100‰, giving an approximation of the heavy isotopes in a sample (Fry 2006). Practically, the ‰ range seen in bulk stable isotope analysis of archaeological bone material falls within a much smaller range– typically between 0 and 20‰ for δ^{15}N, and -30 to 0‰ for δ^{13}C values in animals. The obtained δ values can be used to accurately represent the heavy isotopes as the relationship between δ values and isotope content is linear (Fry 2006). Bulk SI values are generally reported in terms of enrichment and depletion in relation to the standards used, with, for example, a value of zero reflecting no difference from the given standard, and a δ value of -13.56‰ reflecting a sample that is depleted in relation to the standard (Fry 2006).

Associated Laboratory Methods

While the laboratory procedures followed for the extraction of collagen from archaeological bone material used in this thesis are briefly described in Chapter 3, this section aims to break down the theory behind the established protocols as well as the analytical processes used on the extracted collagen. The collagen extraction method used at the University of York's BioArCh laboratory is largely based on pre-treatment methods for AMS radiocarbon dating developed at the Oxford Radio Accelerator Unit (Brock, Thomas Higham, et al. 2010; Brock, Tom Higham, and Ramsey 2013). This extraction protocol was developed using methods first proposed by Longin (1971), and refined by Ambrose (1990). This process involves acidification of bone material in order to remove carbonates,

phosphates, and fulvic acids, followed by solubilization with weak (pH3) acid, and filtration to remove any remaining contaminants (Ambrose 1990). The filtration step at BioArCh is conducted using an Ezee-Filter™, after Brock et al. (2013).

All samples for this thesis were analysed with a Sercon 20-22 continuous flow isotope ratio mass spectrometer, coupled to a Sercon GSL elemental analyser (EA-IRMS). Continuous flow IRMS instruments allow a researcher to introduce multiple component samples and obtain isotope information for both individual elements and compounds within the sample (Michener and Lajtha 2007). The IRMS separates charged atoms or molecules of a given sample on the basis of their mass-to-charge ratio (*m/z*) (Michener and Lajtha 2007). Lyphilised samples are first combusted and then carried through a helium stream to a chromatographic column, where CO_2 (for carbon isotope analysis) or N_2 (for nitrogen isotope analysis) from the combustion is separated from other waste gases (Michener and Lajtha 2007; Tea et al. 2021). Electrons are then released under high vacuum from an ion source (usually tungsten, rhenium or thoriated iridium), accelerated, and allowed to impact the sample CO_2 or N_2 gas to form positively charged particles (Michener and Lajtha 2007). The resulting ion beam is accelerated through a flight tube, where it is bent by a magnetic field set up perpendicular to the flight path and the lighter isotopes within the beam bend more than the heavier ones (Michener and Lajtha 2007). Ions of identical mass are grouped and forced through an aperture, and the beams are captured by specialized Faraday cups in the ion detector apparatus (Michener and Lajtha 2007). The Faraday cups are grounded by a high ohmic resistor, and the ion beam current flowing through results in a measurable voltage that is used as the mass spectrometer output (Michener and Lajtha 2007). This voltage output has its relative signal strength converted to a mass ratio (45/44 for CO_2 and 29/28 for N_2), which is converted into an isotope ratio ($^{13}C/^{12}C$ and $^{14}N/^{15}N$ (Michener and Lajtha 2007; Tea et al. 2021). The process is repeated from the start with known isotope standards, and final results are reported as the δ value of each element analysed in parts-per-thousand (‰) for the original sample compared to the known standard– the aforementioned ratio of ratios. (Michener and Lajtha 2007; Tea et al. 2021).

Once the $\delta^{15}N$ and $\delta^{13}C$ values were obtained for fish bone samples from this thesis research assemblage, the dataset required cleaning according to quality control standards established to ensure that the values used for interpretation were as accurate as possible. Contaminants within a collagen sample can influence the eventual δ values obtained via EA-IRMS analysis, so various methods of post-extraction quality control methods to exclude potentially contaminted samples have been proposed throughout the years (Michael J DeNiro 1985; E. J. Guiry and Szpak 2021; Klinken 1999; Szpak 2011). Most impactful quality control takes place during the extraction process itself, with some protocols using sodium hydroxide (NaOH) to remove base-soluble contaminants such as humic acids, and others focusing on lipid extraction using either chloroform/methanol ($CHCl_3$/MeOH 2:1) or dichloromethane/methanol (CH_2Cl_2/MeOH 2:1) solutions (Ambrose 1990; Cequier-Sánchez et al. 2008; E. J. Guiry, Szpak, and M. P. Richards 2016). Lipid extraction using a CH_2Cl_2/MeOH 2:1 solution was performed on all salmonid samples for this thesis prior to the acidification step in order to mitigate lipid effects on $\delta^{15}N$ and $\delta^{13}C$ values (E. J. Guiry, Szpak, and M. P. Richards 2016). To further control for possible contaminants, samples with carbon-to-nitrogen ratios (C:N) outside of a certain range were excluded. This method of quality control is based on initial observations by DeNiro 1985, which showed that unexpected alterations in $^{13}C/^{12}C$ and $^{15}N/^{14}N$ isotope ratios were more often observed in collagen samples with C:N ratios outside the range 2.9-3.6 (Michael J DeNiro 1985). This range was determined through the comparison of prehistoric and modern mammals, and is the standard exclusion range used in most bulk stable isotope analysis papers today (Michael J DeNiro 1985). However, there are noted issues with applying this relatively wide exclusion range to fish bone remains from archaeological sites.

The first proposal to narrow the range of acceptable C:N ratios is found in Van Klinken (1999), where a new

range of 3.1-3.5 was proposed as more precise alternative to DeNiro's range (Klinken 1999). This new range was not widely adopted, however, and was also only applied to collagen extracts from mammal bone, an oversight directly addressed by Guiry and Szpak (2021). They report variations in quality control criteria which change across both class and environmental categories, resulting in different acceptable ranges for fish, mammals, birds, and those individuals living in different climate conditions (E. J. Guiry and Szpak 2021). The C:N ratios for fish from cold water and warm water environments fall on opposite ends of a relatively narrow range, with cold water species like cod (and, by extension, anadromous *Salmo* sp. fish) having C:N ratios that generally fall between a 3.00-3.20 range, and warm water species falling between 3.20-3.30 (E. J. Guiry and Szpak 2021). Guiry and Szpak report that C:N values greater than 3.33 for cold water fish may show δ^{13}C shifts of -0.5‰, and even as much as -1.85‰ (E. J. Guiry and Szpak 2021). Given the fact that the majority of fish included in this study are cold water fish species like cod, haddock, Atlantic salmon, and sea trout, the decision was made to exclude all fish samples outside of the C:N range of 3.0-3.33 when variations in δ^{13}C formed a major focus of the research questions– for example, in Chapter 9's study of regional isotopic variations of *Salmo* sp. fishes. For studies focused on δ^{15}N values, as in Chapter 8's study of isotopic differentiation of *Salmo* sp. ecotypes, Guiry and Szpak suggest that the allowable range can include higher values (up to the DeNiro limit of 3.6), as they presence of humic contaminants only minimally effects δ^{15}N (E. J. Guiry and Szpak 2021). For the database of δ values used for this PhD thesis, this resulted in two different C:N QC range criteria being applied to create two subsets of a (see Table 1 below).

Data Subset	**C:N Range**	**Samples**	**Description**
Master δ^{13}C	3.00-3.33	190	All samples, both comparative species and *Salmo* sp. fish. Forms the basis of Chapter 8 - Intersite Isotope Analysis
Salmo sp. δ^{15}N	3.00-3.60	98	All *Salmo* sp. samples used to investigate biomolecular ecotype differentiation methods in Chapter 7; an additional six *Salmo* sp. samples, ranging from 3.38-3.50, were added.

TABLE 4.1: Subsets of Bulk Stable Isotope Values Used in this Thesis Research

4.2.2 Use in Archaeology and Ecology

The δ values obtained from bulk stable isotope analysis can be translated into meaningful interpretations of archaeological and ecological situations, including diet, environmental conditions, and migratory pathways e.g. (Michael J DeNiro 1985; Michael J. DeNiro and Epstein 1978; Eriksson 2013; McMahon, Hamady, and Thorrold 2013; Merwe 1982; Pilaar Birch 2013; Schoeninger and Michael J DeNiro 1984; Trueman and St John Glew 2019). A more detailed discussion of fish isotope ecology can be found in Chapter 5, but the primary applications of bulk stable isotope analysis in ecological research are focused on tracking trophic position, migration and home environments, anthropogenic environmental change, and animal life history (Fry 2006). The most commonly used isotopes in ecology are light stable isotopes of hydrogen, carbon, nitrogen, oxygen and sulfur (H,C,N,O,S) (Fry 2006). Hydrogen and oxygen generally involve hydrological cycling, and therefore can provide information about drinking water sources, water temperature and salinity (Fry 2006). Similarly, sulfur remains quite closely associated with water sources as it is tied to sediment accumulation and runoff, and is used to determine terrestrial input of water sources in ichthyoarchaeological contexts (Fry 2006). The two elements used for interpretation in this PhD research are carbon and nitrogen, and the isotope values obtained for carbon and nitrogen reflect

distributions in the biosphere, providing information on diet and trophic level, marine or terrestrial origin, and environmental pollutants (Fry 2006). The information derived from these stable isotope compositions in modern or historical ecological samples can also be obtained from archaeological materials, with a few key differences.

The major difference between archaeological and ecological samples is often lack of information about a study organism's lifetime characteristics, such as weight, age, and origin, among others. This is due mostly to the taphonomic processes involved in the eventual deposition of a given archaeological sample of bone, shell, otoliths etc. All archaeological material is selected by humans for a variety of reasons, both known and unknown, and each step along the way to its deposition removes more information. For example, from the moment of catch in a fish's home environment, transport to a domestic context, cooking, consumption, and discard of carcass material all result in the loss of information about fish size, age, species, capture season, and catch environment. However, when combined with morphological identification and collagen peptide analysis, as in this thesis, the bulk stable isotope analysis of archaeological material is a powerful interpretive tool. The main sources of variation in bulk stable isotope values found in recovered material and their broad applications to archaeological interpretation are detailed below in Table 2 below (after Eriksson, 2013).

Element	**Target material**	**Main source of variation**	**Archaeological appplications**
Carbon (δ^{13}C)	Collagen or bioapatite	Marine and terrestrial environments, plants. Can indicate freshwater/marine environment, salinity, aridity, canopy.	Diet, mobility, food preference
Nitrogen (δ^{15}N)	Collagen	Trophic level, anthropogenic industrial waste. Can indicate nutritional stress and aridity.	Diet, mobility breastfeeding patterns, food preference, physiology
Oxygen (δ^{18}O)	Collagen or bioapatite	Climate. Can indicate water origin, latitude, elevation, coast/inland location, humidity, precipitation, temperature.	Climate, mobility, seasonality, habitat, breastfeeding patterns.
Suphur (δ^{34}S)	Collagen	Geological origin	Mobility, origin

TABLE 4.2: Light stable isotopes used in archaeology after 2013

4.2.3 Stable Isotopes in Ichthyoarchaeology

Just as with archaeology in general, the applications of bulk stable isotope analysis within the specific subfield of ichthyoarchaeology are varied and broad. Aquatic ecosystems support various complex ecological networks, with the possibility of human-species interaction not just limited to fish species, but also marine mammals like cetaceans and pinnipeds, and reptiles like sea turtles (Schoeninger and Michael J DeNiro 1984). However, as this thesis is focused on the exploitation of *Salmo* sp. fishes like Atlantic salmon, brown trout and sea trout, the most helpful research to draw upon is that involving other fishes. One of the most important characteristics of archaeological fish that bulk stable isotope analysis can reveal is living environment, whether that is freshwater streams, the open ocean, estuarine inlets, or a combination of multiple aquatic environments. Overall, it has generally been accepted that high δ^{13}C and high δ^{15}N indicate lifetime feeding in a marine environment, while

low δ^{13}C and high δ^{15}N would indicate feeding in a freshwater environment. At a theoretical level, δ^{13}C values in fish of approximately -15‰ and above could be considered "high", while values under that point could be classified as "low"– however, in reality, what constitutes a high or low is not as clearly defined. The basal food webs which support freshwater and estuarine populations of fish have demonstrated wider ranges of isotopic compositions than were thought to be "normal" (E. Guiry 2019). This can mean that the normal mean range of δ^{13}C values for fish of the same species, and even those with similar feeding strategies, can vary greatly across their total geographic range. For a demonstration of this observed variation in *Salmo* sp. fishes, see Fig. 4 in Chapter 5 and Figs. 16-17 in Chapter 9 of this thesis.

Ichythyoarchaeological isotope studies have focused on the migratory nature of anadromous fish, diachronic changes in human fishing activity, inter- and intra-species variation in stable isotope values, regional trade, and anthropogenic effects on fish species (J. Barrett et al. 2008; J. H. Barrett, D. Orton, et al. 2011; Fuller et al. 2012; E. J. Guiry, Kennedy, et al. 2021; E. J. Guiry, Needs-Howarth, et al. 2016; E. J. Guiry, Szpak, and M. P. Richards 2016; Häberle, Fuller, et al. 2016; Häberle and Hüster Plogmann 2019; Häberle, Nehlich, et al. 2016; Miller, Capriles, and Hastorf 2010; D. C. Orton et al. 2011; Tsutaya et al. 2022). Some of these studies will be reviewed more thoroughly below, while attention is first paid to a relatively recent review of archaeological fish bulk stable isotope contributions to knowledge of North Sea fisheries, both past and present.

Barrett (2019) offers an especially good assessment of the past and potential future applications of bulk stable isotope analysis to fish remains, identifying a gap in current scholarship where the chemical analysis of archaeological aquatic material can pick up where historical sources may become unclear. The review highlights the usefulness of this material in understanding long-term changes in not only aquatic environment, but also fish biogeography– especially with regard to overfishing, habitat loss, and prehistoric climate change. Barrett is careful to point out that archaeological fish bones are not an exact proxy for past populations, but still assert that archaeological evidence for changes in fish biogeography over time may provide insight into how modern anthropogenic climate change could affect the current range of economically important species. Bulk, compound specific, and sequential stable isotope analyses are especially useful in monitoring past water salinity, temperature, nutrient sources, and trophic level changes in individual fish (J. H. Barrett 2019). Bulk nitrogen and carbon analysis in particular have been especially important for establishing isotopic signature continuity in major bodies of water like the North Sea. Barrett specifically calls for continued use of isotope analysis to investigate exploitation intensity, size changes, and trophic level shifts– all in the pursuit of understanding commodification and globalisation through aquatic archaeological material (J. H. Barrett 2019).

Fish-specific isotopic studies in archaeology have increased dramatically in the last fifteen years, with some of the foundational work for archaeolgical sites surrounding the northern seas conducted on Atlantic cod (*Gadus morhua*) (J. Barrett et al. 2008; J. H. Barrett, D. Orton, et al. 2011; D. C. Orton et al. 2011). Several studies by Barrett, Orton, and other collaborators provide a structural and theoretical model for species-level isotopic study of archaeological fish remains during the broadly Medieval Period (J. Barrett et al. 2008; J. H. Barrett, D. Orton, et al. 2011; D. C. Orton et al. 2011). The aim of these studies was primarily the use of δ^{15}N and δ^{13}C isotope ratios to track increasing demand for Atlantic cod through time and across the Atlantic Ocean, as well as specifically in the North, Norwegian, and Baltic Seas (J. Barrett et al. 2008; J. H. Barrett, D. Orton, et al. 2011; D. C. Orton et al. 2011). Through the mapping of δ^{15}N and δ^{13}C isotope ratios from archaeological cod bones, the researchers were able to conclusively infer catch origin from inter-regional variability observed in the samples included in the studies (J. Barrett et al. 2008). In the original 2008 pilot study of these archaeological cod bones, a linear discriminant function analysis was applied to reclassify samples into isotopic groups, which the researchers hypothesized would show isotopic groups that could be compared with control samples to determine fish origin (J. Barrett

et al. 2008). After the success of this pilot study, further investigation into archaeological fish bones from the Northeast Atlantic, Arctic Norway, Eastern Baltic, North Sea, Kattegat/Western Baltic, and Newfoundland regions was conducted (J. H. Barrett, D. Orton, et al. 2011; D. C. Orton et al. 2011).

As the use of bulk δ^{15}N and δ^{13}C isotope values to determine catch origin had been established in the earlier pilot study, the 2011 Barrett et al. and Orton et al. papers were both concerned with exploring the driving factors behind the expansion of medieval sea fishing (J. H. Barrett, D. Orton, et al. 2011; D. C. Orton et al. 2011). Two driving factors behind the expansion– observed and described in Barrett et al. (2004) among others– are explored, supply-led and demand-led expansion (J. H. Barrett, D. Orton, et al. 2011). In order to determine the driver (or drivers) of change behind this marine 'fish event horizon' (FEH) (J. H. Barrett, Locker, and Roberts 2004), Barret et al. looked at variability in fish size, location, and time period, in addition to statistically examining changes in isotopic characteristics over time (J. H. Barrett, D. Orton, et al. 2011). They concluded that the changes observed were primarily demand driven, showing clear changes in proportions of long-distance traded cod remains recovered from locations in the southern North Sea (E. J. Guiry, Kennedy, et al. 2021; Häberle, Fuller, et al. 2016; Häberle, Nehlich, et al. 2016; Miller, Capriles, and Hastorf 2010; D. C. Orton et al. 2011; Tsutaya et al. 2022) While Barrett et al. explored changes over time from the advent of the FEH, Orton et al.'s research provides an interesting contrast in the Baltic (D. C. Orton et al. 2011). The Baltic sites explored in this paper display a similar monopoly of imported cod, primarily from the Norwegian Arctic, during the 12th-14th centuries (D. C. Orton et al. 2011). However, the authors do observe that proportions of locally-derived cod remains increase at late-Medieval Period Baltic sites, suggesting a strong local fishery developing in the 14th-16th centuries (D. C. Orton et al. 2011).

While the Barrett et al. and Orton et al. papers focused on a single species as an indicator of widespread trade and exploitation change, a more comprehensive view of region-specific isotope characteristics can be found in Fuller et al. (2012). This pilot study provides a broad overview of the isotopic characteristics of freshwater, marine, and brackish fish species from Belgian archaeological sites spanning the 3rd-18th centuries CE ((Fuller et al. 2012)). Though the researchers sampled over 150 individual fish bones for bulk carbon and nitrogen isotope analysis, only 40% yielded adequate collagen—likely a product of taphonomic processes increasing post-deposition bone diagenesis (Fuller et al. 2012). However, despite this barrier, the Fuller et al. paper offers especially useful observations about the former biogeography of Belgium and the inter-and-intra-species variation in bulk stable isotope ratios seen in fish. The samples of fish species included migratory species like eel, smelt and sturgeon; freshwater species like roach, carp, and pike; and marine species like haddock, whiting, and plaice (Fuller et al. 2012). Fuller et al. observed that the catadromous eels and freshwater pike both displayed a highly varied range of δ^{15}N isotope values, reflecting both species tendencies to feed at several different trophic levels (Fuller et al. 2012). In contrast, the δ^{15}N values of anadromous sturgeon and marine haddock remained tightly clustered in a narrow range, reflecting their respective specialized diets (Fuller et al. 2012). Fuller et al. argue that these observations about trophic level patterns in the sampled fish species show how fish can be a complicating factor in the reconstruction of past human diet using bulk stable isotope analysis (Fuller et al. 2012). Though the small overall sample size barred Fuller et al. from examining diachronic and age/size related trends in the fish samples, the study provides an excellent framework for structuring the multi-species, inter-site analysis of bulk stable isotopes found in Chapter 9. Fuller et al. conclude that isotopic investigations of archaeological fish bones will be especially helpful in determining catch origins, identifying trade, understanding the role of proto-aquaculture, and observing shifts in consumption patterns (Fuller et al. 2012). Additionally, several species which are no longer present in the Schedlt and Meuse river systems were included in this pilot study, providing a model for interpreting the isotopic characteristics of extirpated salmonids from various North Sea river basins that are contained

within this thesis.

Though Fuller et al. (2012) were unable to fully address diachronic changes in human fishing activity in their pilot study, others have since done so with varying levels of in-depth study (E. J. Guiry, Kennedy, et al. 2021; Häberle, Fuller, et al. 2016; Häberle, Nehlich, et al. 2016; Miller, Capriles, and Hastorf 2010; D. C. Orton et al. 2011; Tsutaya et al. 2022). Two recent publications, from Guiry et al. (2021) and Tsutaya et al. (2022), neatly demonstrate the importance of this particular study approach. Though these studies are focused on two very different environments and time periods— 1720-1910CE Louisiana and 4th-century BCE to 950CE Hokkaido, respectively—they both successfully use diachronic changes in bulk stable isotope ratios and size estimation to infer past changes in human fishing (E. J. Guiry, Kennedy, et al. 2021; Tsutaya et al. 2022). Guiry et al. focus on changes in sheepshead (*Archosargus probatocephalus*) estimated body length seen from pre-contact Early Woodland Period archaeological sites through the early 20th-century, as well as changes in δ^{13}C composition (E. J. Guiry, Kennedy, et al. 2021). The osteometric study shows a decreasing average length from the EWP to 1830s/40s, a slight increase in average length in the 1840s-1860s, and a return to consistently decreasing standard lengths post-1870 (E. J. Guiry, Kennedy, et al. 2021). Meanwhile, there is a complementary and parallel trend in isotope ratio composition, with elevations in both δ^{13}C and δ^{15}N values indicating a "broadening isotopic niche" for sheepshead in this area of coastal Louisiana (E. J. Guiry, Kennedy, et al. 2021). A particularly interesting conclusion from this study involves the proposed cause of the unusually elevated δ^{13}C values in the later periods of exploitation—Guiry et al. interpret this as being indicative of sheepshead expanding their habitat to seagrass meadows and barrier islands as a result of human fishing pressure in their previous habitats, and provide evidence for human expansion of fishing grounds in response (E. J. Guiry, Kennedy, et al. 2021).

Tsutaya et al. takes a broader look at human fishing patterns through time at the study site of Hamanaka 2 located in Hokkaido 2022. The study site and periods not only encompass several distinct cultural occupation periods from 400BCE - 950CE, with differences in fishing technology observable from the archaeological record, but also several worldwide climatic events, such as the Medieval Warm Period and Little Ice Age (Tsutaya et al. 2022). Due to a robust sample of 285 fish bones from 12 taxa over four distinct cultural periods, Tsutaya et al. were able to provide a multi-species view of change over time in environment and exploitation patterns at the site (Tsutaya et al. 2022). Using a combined approach of statistical tests, the researchers were able to demonstrate significant diachronic differences in δ^{13}C values of rockfish, and δ^{15}N values of cod and herring (Tsutaya et al. 2022). Combing the isotope data with osteometric values, the authors suggest that, for cod, larger individuals were primarily caught during the earlier Epi-Jomon period (450 BCE-650CE) with an observed 1.3‰ decrease in δ^{15}N values by the Final Okhotsk period (850-1200 CE) (Tsutaya et al. 2022). Similar decreases in size were inferred from size and isotopic data for herring and rockfish, leading the authors to consider not only the increase in fishing pressure from immigrant fishers from the northeastern of Hokkaido, as suggested by human aDNA and archaeological evidence, but also climatic pressures on fish (Tsutaya et al. 2022). Cooling periods affecting Hokkaido are evident from pollen records starting around 400CE, coinciding with both the transition from the Epi-Jomon cultural period to the Okhotsk cultural period and the decrease in fish size and δ^{15}N values seen in the ichthyarchaeological record (Tsutaya et al. 2022). The authors conclude that changes in fishing technology, increased fishing pressure over time, and cooling events all likely impacted the eventual archaeological assemblage of fish bones recovered from Hamanaka 2, showing the importance of a combined archaeological and ecological approach when interpreting such data (Tsutaya et al. 2022).

Returning briefly to single-species studies of isotope variation in the ichthyoarchaeological record, a particulary important source of not only methodological references but direct isotope ratio value comparison is Guiry et al.'s 2016 study of non-migratory Atlantic salmon from Lake Ontario (E. J. Guiry, Needs-Howarth, et al. 2016).

The major premise of this isotopic study of pre-contact and historical archaeological salmon from Ontario and Quebec was to provide baseline data on the local populations and determine whether the fish, extinct in the region since 1900 CE, were historically anadromous or potamodrous (E. J. Guiry, Needs-Howarth, et al. 2016). The intent in doing so was twofold– both solving a historical debate and providing key environmental data for modern species reintroduction efforts in Lake Ontario and the St. Lawrence River (E. J. Guiry, Needs-Howarth, et al. 2016). The researchers obtained δ^{13}C, δ^{15}N, and δ^{34}S ratio values for 74 archaeological and historical salmon bone and scale samples from Iroquoian and European sites, as well as Euro-Canadian museum collections (E. J. Guiry, Needs-Howarth, et al. 2016). The results of this study demonstrated that samples from the Western region of Lake Ontario all show a clear potamodromous signal (n=50, average δ^{13}C -20.0 +/- 0.4‰; average δ^{34}S= +8.7± 1.6‰), while those from the upper St. Lawrence River show a mix of potamodromous (n =7, average δ^{13}C = 22.2± 0.3‰; n= 2, average δ^{34}S = +3.6 ± 0.1‰) and anadromous n =8, average δ^{13}C = 15.7 ± 0.6‰; n = 5, average δ^{34}S = +15.1± 1.0‰) signals (See Section 3.2, Chapter 4). Guiry et al. conclude that these uniform stable carbon and sulphur isotope values indicate that Lake Ontario salmon were a behaviourally distinct ecotype than other Atlantic salmon, despite a lack of physical obstructions which would impede normal anadromous behavior (E. J. Guiry, Needs-Howarth, et al. 2016). The results presented in this paper provide an excellent comparative dataset for the study of anadromous North Sea salmon and sea trout contained in this thesis. Understanding the behavioral and isotopic characteristics of this distinct North American population will enrich interpretations of the European population dataset presented here, and allow for more detailed understanding of geographic variation in Atlantic salmon.

4.3 Zooarchaeology by Mass Spectrometry

The second biomolecular analysis approach employed in this thesis research is collagen peptide mass fingerprinting of archaeologically recovered bone material, known as zooarchaeology by mass spectrometry—ZooMS. First applied to archaeological material in 2009 (Michael Buckley, Collins, Thomas-Oates, and Wilson 2009), the method has already had an immense impact on how zooarchaeologists can approach the study of faunal remains. Especially useful for high-throughput screening of the small unidentified fragments often found *en masse* on archaeological sites, ZooMS is a method that greatly enhances our understanding of species diversity in faunal assemblages. In it's first decade or so of application, ZooMS has solidified its place as a key part of the biomolecular archaeological toolkit, but, as will be discussed below, much work still remains to standardize its application (Kristine Korzow Richter et al. 2022). Like bulk stable isotope analysis, ZooMS relies on the extraction of collagen from archaeological material such as bone and scales, and this section will first focus on the underlying theory and methodology of the analysis, then move on to discussing its applications in archaeological research, finishing with a short review of recent scholarship focused on ZooMS and archaeological fish remains.

4.3.1 Theory and Methods

While both bulk stable isotope analysis and ZooMS involve the extraction of preserved collagen from archaeological bone material, ZooMS relies more directly on the functional morphology of the collagen protein itself (Kristine Korzow Richter et al. 2022). Collagen technically refers to almost 30 different kinds of structural proteins, but the most abundant type, COL1 or Type 1 collagen, is what is analysed when applying ZooMS (Michael Buckley 2018; Michael Buckley, Collins, Thomas-Oates, and Wilson 2009; Collins et al. 2010; Kristine Korzow Richter et al. 2022). COL1 has a triple helical structure, with most organisms having two identical COL1α1 and

a single COL1α2 chain—teleost fish however, have a unique third COL1α3 chain (Kristine K. Richter et al. 2011; Kristine Korzow Richter et al. 2022). These COL1α chains are made up of peptide sequences centered around the amino acid glycine (Kristine Korzow Richter et al. 2022), and it is these peptides that are the basis of collagen peptide mass fingerprinting as a taxonomic identification method (Michael Buckley, Collins, Thomas-Oates, and Wilson 2009; Collins et al. 2010; Kristine K. Richter et al. 2011; Kristine Korzow Richter et al. 2022). The peptide mass fingerprinting technique was developed in the 1990s as a way to identify proteins by mass after digestion by enzymes using a matrix-assisted laser desorption/ionization (MALDI) method, coupled with a time-of-flight (TOF) analyzer (Michael Buckley, Collins, Thomas-Oates, and Wilson 2009; Henzel et al. 1993; James et al. 1993; Mann, Højrup, and Roepstorff 1993; Pappin, Hojrup, and Bleasby 1993; Kristine Korzow Richter et al. 2022; Yates et al. 1993).

The MALDI-TOF instrument is still the standard in ZooMS analysis today, and is used to analyse collagen peptides that are enzymatically digested after an extraction protocol similar to that used in bulk stable isotope analysis. Laboratory protocols are not standardized across the emerging discipline, but most follow the same basic procedure with bone samples being demineralized using a dilute hydrochloric acid solution, washed in an NaOH solution to remove potential humic acid contaminants, and then the resulting collagen gelatinized (Richter et al., 2022). Samples are then digested with trypsin, a naturally occurring enzyme which cleaves C-terminal peptide bonds in order to separate the peptide sequences that differ in their mass and length (Buckley et al., 2009; Richter et al., 2022). These differences in peptide mass and length vary according to taxa, sometimes down the species level, and thus can be used to identify unknown bone material (Buckley et al., 2009; Richter et al., 2022). The digested peptides are filtered, spotted onto a MALDI plate and crystallized with a matrix acid—most often αcyano-4-hydroxycinnamic acid— and the plate is loaded into the MALDI-TOF instrument for analysis (Buckley 2018; Richter et al., 2022). When the peptide and matrix samples are excited using a high intensity laser, the peptides ionize and are then directed into the time-of-flight tube by electromagnets to be separated by mass (Richter et al., 2022). The mass orders are recorded, and a spectrum is produced and calibrated so the time-of-flight value is converted into a mass-to-charge ratio, rendered as m/z (Richter et al., 2022).

The resulting spectra are used in both the development of known biomarkers for different taxa, as well as later analysis of unknown specimens. The basis of the biomarker development process is associating given m/z values with specific peptide sequences, and looking for unique occurrences of marker peaks in order to differentiate species. Marker peaks are generally identified using a combination of cluster analysis, protein identification software like Mascot or Byonic, and sequence alignment editors like BioEdit (Michael Buckley, Collins, and Thomas-Oates 2008; Dierickx et al. 2022; Kristine Korzow Richter et al. 2022). Most biomarkers are initially confirmed using genomic data or sequenced collagen (Michael Buckley, Collins, and Thomas-Oates 2008; Dierickx et al. 2022; Kristine Korzow Richter et al. 2022), and further confirmation of some biomarkers has been done using high-resolution liquid chromatography with tandem mass spectrometry (LC-MS/MS) with an ongoing push for this to become a standardized method (Kristine Korzow Richter et al. 2022). Once unique biomarkers for taxa identification are developed using reference specimens, they can then be used to assign taxonomic identifications to archaeological material. This process can be achieved several different ways, with the most basic approach involving a spectra viewer like MMass and direct manual comparison of known biomarkers to peak lists from each sample. Programmatic approaches to peak identification have been employed with varying degrees of success (see Chapter 3), but as of yet no fully automated method of ZooMS spectra identification exists (**hagan_SmooZy_2022**; Baker 2022; Michael Buckley, Collins, and Thomas-Oates 2008; Gu and Michael Buckley 2018; Kristine Korzow Richter et al. 2022).

4.3.2 Use in Archaeology

The identification of archaeological and historical material has been the subject of research since the very first publication on using collagen peptide mass fingerprinting for taxonomic identification (Michael Buckley, Collins, Thomas-Oates, and Wilson 2009). As described by Buckley et al. and others, COL1 is not only the dominant protein found in mineralized animal tissue, it is also cheaper to analyse than DNA, is not as susceptible to degradation and cross contamination, and can be extracted using minimally invasive techniques (Michael Buckley 2018; Michael Buckley, Collins, Thomas-Oates, and Wilson 2009; Collins et al. 2010; Kristine Korzow Richter et al. 2022). One of the most useful aspects of ZooMS identification markers is that they can be used for any archaeological or historical material that contains extractable COL1, which has resulted in applications of ZooMS to worked bone, parchment and vellum, glues and other composite artifacts (Ashby, Coutu, and Sindbæk 2015; Muñoz-Rodriguez et al. 2023; Kristine Korzow Richter et al. 2022; Von Holstein et al. 2014). Additionally, ZooMS has recently proved extremely helpful in identifying hominin remains within large assemblages of fragmentary bone material, like those found in palaeolithic cave sites like Denisova (Brown, Thomas Higham, et al. 2016; Brown, Massilani, et al. 2022). This is especially useful for examining movements of hominin species that are the subject of much bioanthropological debate, like *Homo neanderthalensis*, which may not yield sufficient DNA material due to preservation and age (Brown, Thomas Higham, et al. 2016; Brown, Massilani, et al. 2022; Brown, Wang, et al. 2021; Slimak et al. 2022).

The majority of early work on ZooMS focused primarily on large terrestrial mammals, which is a source of disciplinary bias that still exists today (Kristine Korzow Richter et al. 2022). Work focusing on the differentiation of sheep and goat collagen, animals which bones are notoriously difficult to identify to species, solidified ZooMS as a key tool in zooarchaeological research looking at domestication and animal husbandry (Mike Buckley, Whitcher Kansa, et al. 2010). Further work on key domestic and wild taxa from archaeological sites has resulted in increased ability to accurately assess taxonomic distribution of bovids like cattle and buffalo, as well as avian taxa like chickens, turkey, and ducks– all culturally and economically important important animals that are found across a vast geographic area (Bleasdale et al. 2021; Codlin, Douka, and Kristine K. Richter 2022; Janzen et al. 2021; Spengler et al. 2022). Similarly, the human exploitation of and/or interaction with wild cetaceans, turtles, bears, and microfauna like frogs, toads, black and brown rats, and shrews have been the focus of several recent studies (Michael Buckley, Virginia L Harvey, et al. 2020; Mike Buckley, Gu, et al. 2016; Virginia L Harvey et al. 2019; Virginia L. Harvey, LeFebvre, deFrance, et al. 2019; Hurk, Rielly, and Mike Buckley 2021; Mychajliw et al. 2020; Welker et al. 2015). One of the most recent, but arguably most important, taxonomic classes of animal to become the focus of much ongoing ZooMS study are fish, and the following section will detail the current state of ZooMS application to ichthyoarchaeological material and its importance to understanding past environments and human activity.

4.3.3 ZooMS in Ichthyoarchaeology

Fish bones are particularly well suited to taxonomic identification by collagen peptide mass fingerprinting due to their relatively small size and low rate of mineralization compared to mammal and even avian bones (Michael Buckley 2018; Kristine K. Richter et al. 2011; Kristine Korzow Richter et al. 2022). Because of the high rate of collagen sequence variation seen in the COL1α chains of fish, including the presence of a third chain for many taxa, there are proportionally more potential differences in collagen peptide masses (Michael Buckley 2018; Kristine Korzow Richter et al. 2022). With more potential differences, more taxonomically unique biomarkers may appear, allowing an increased likelihood of identification to genus and species level for fishes (Michael Buck-

ley 2018; Kristine K. Richter et al. 2011; Kristine Korzow Richter et al. 2022). While the first paper providing fish biomarkers was published in 2011 (Kristine K. Richter et al. 2011), it is only within the last 5 years that work on archaeological fish bones has exploded in popularity. Unique collagen peptide mass biomarkers for nearly 100 fish species have been published (Michael Buckley, Virginia L. Harvey, et al. 2022; Dierickx et al. 2022; Virginia L. Harvey, Daugnora, and Michael Buckley 2018; Virginia L. Harvey, LeFebvre, Sharpe, et al. 2022; Korzow Richter et al. 2020; Kristine K. Richter et al. 2011; Rick, Virginia L. Harvey, and Michael Buckley 2019). The markers for these species also allow significantly more higher-level taxonomic identifications to be made as they provide sets of peaks that appear to be common to certain genera and families. The following paragraphs will review several key publications on the use of large-scale fish collagen peptide mass fingerprinting, taxa identification for single orders or families, and examples of how ZooMS data can enhance archaeological investigations of human cultural, economic, and social interaction with fish.

The first publication focused specifically on using peptide mass fingerprinting of bone-derived collagen to differentiate between different taxa of fish was Richter et al. 2011, which presents the results of an experimental study using modern and archaeological fish bones. Fish bones from commonly landed species of the orders Clupeiformes, Salmoniformes, Gadiformes, and Perciformes were demineralized and their collagen extracted and analyzed using a MALDI-TOF instrument (Kristine K. Richter et al. 2011). The modern reference specimens used were processed in several different ways prior to demineralization, with some cooked (boiling and baking), others raw, and 3 cod specimens macerated using BioTex enzyme washing powder (Kristine K. Richter et al. 2011). These different methods were intended as an experiment to understand how bone collagen reacts to various common bone preparation techniques, and the researchers actually concluded that the use of washing powder like BioTex is inadvisable for specimens destined for ZooMS as it interferes with the resulting reference spectra (Kristine K. Richter et al. 2011). Statistical analysis using a partial least squares linear discriminant analysis model provided a set of consistent differences between the majority of the species studied, resulting in 89 biomarkers being identified across the 4 taxonomic orders (Kristine K. Richter et al. 2011). These biomarkers allow for identification of 8 species– herring, salmon, trout, cod, haddock, hake, bass, and lesser sand eel (Kristine K. Richter et al. 2011). Richter et al. finish by concluding that ZooMS analysis of archaeological fish remains is an ideal companion method for traditional archaeozoological analysis, and that the development of new taxonomic biomarkers for fish should be a priority (Kristine K. Richter et al. 2011).

While there have been a handful of studies since 2011 which provide new ZooMS markers for the identification of archaeological fish bone, it was not until 2022 that ZooMS was applied to particularly large samples of modern and archaeological fish bone (Michael Buckley, Virginia L. Harvey, et al. 2022; Virginia L. Harvey, LeFebvre, Sharpe, et al. 2022). Two studies, on European and circum-Caribbean fish taxa, have contributed biomarkers for the identification of 113 species belonging to at least 61 genera, 40 families, and 15 orders (Michael Buckley, Virginia L. Harvey, et al. 2022; Virginia L. Harvey, LeFebvre, Sharpe, et al. 2022). The Buckley et al. study used modern reference skeletons from 68 species to both develop new biomarkers for some species (like the common dentex, tub gurnard, and anglerfish) as well as refine existing biomarkers for species within the orders Gadiformes, Pleuronectiformes, and Cypriniformes (Michael Buckley, Virginia L. Harvey, et al. 2022). After presenting the results of their study of reference skeleton spectra, Buckley et al. applied this updated set of fish biomarkers to a sample of 77 fish bones recovered from the Late Medieval Newport shipwreck from the mouth of the River Usk in Wales (Michael Buckley, Virginia L. Harvey, et al. 2022). Their investigation of these fish remains found that the sampled assemblage was predominantly made up of ling, cod, and hake with over 70% of the sample able to be identified to species level (Michael Buckley, Virginia L. Harvey, et al. 2022). While there was a good deal of marker confirmation and refinement in the Buckley et al. paper, Harvey et al. presents a set of biomarkers that are nearly

all new and which may be seen as an attempt to rectify some of the European bias seen in fish ZooMS markers (Virginia L. Harvey, LeFebvre, Sharpe, et al. 2022; Kristine Korzow Richter et al. 2022). The dataset of biomarkers developed by Harvey et al. were applied to the largest assemblage of archaeological bone material to-date, with nearly 1000 morphologically identified fish bones analyzed, resulting in 720 identifications to family, genus or species level (Virginia L. Harvey, LeFebvre, Sharpe, et al. 2022).

While these large-scale approaches to development and application of ZooMS markers are useful in generating large volumes of new markers, smaller taxa-specific studies remain important to the expansion of ZooMS in ichthyoarchaeology. Three such studies have applied collagen peptide mass fingerprinting to modern and archaeological fish bone and introduced biomarkers for the identification of fish from the orders Pleuronectiformes, Istiophoriformes, and Salmoniformes (Dierickx et al. 2022; Korzow Richter et al. 2020; Rick, Virginia L. Harvey, and Michael Buckley 2019). Rick et al. investigated two families of billfish, Xiphiidae and Istiophoridae, from a relatively small geographic area in the Santa Barbara Channel located in California, USA (Rick, Virginia L. Harvey, and Michael Buckley 2019). This study used 17 modern references specimens to develop species identification markers, and applied the resulting markers to 30 unidentified fish bones suspected of belonging to a prehistoric Californian billfish fishery (Rick, Virginia L. Harvey, and Michael Buckley 2019). The Dierickx et al. study is again focused on multiple families, this time flatfish in the Citharidae, Soleidae, Scophthalmidae, Bothidae and Pleuronectidae families (Dierickx et al. 2022). Dierickx et al. were able to identify unique biomarkers for all 18 flatfish species analysed in the study, which included 12 species (e.g. plaice, flounder, common dab) which were commercially important in both the present and past (Dierickx et al. 2022). They, like all other studies discussed here, then applied these new markers to an archaeological dataset of flatfish bones (n=202) from medieval sites in England and France, which resulted in the identification of the vast majority as plaice and flounder, followed by smaller amounts of common dab and turbot (Dierickx et al. 2022). Finally, the Korzow-Richter et al. paper focused on a single genus of fish, Onchorhynchus, providing ZooMS biomarkers for five Pacific salmon species as well as rainbow trout (Korzow Richter et al. 2020). This study identified the resulting biomarkers using both modern reference skeletons and 28 DNA-identified bones from the Yup'ik site of Nunalleq, in Western Alaska, and confirmed the predominance of chum salmon, followed by sockeye, chinook, coho, and pink salmon (Korzow Richter et al. 2020).

The development of ZooMS biomarkers and application to ichthyoarchaeological remains is obviously an essential pursuit within the discipline of biomolecular archaeology, but it's use should be properly grounded in archaeological approaches in order to act as a complementary method—not a replacement for traditional zooarchaeology entirely (Kristine K. Richter et al. 2011; Kristine Korzow Richter et al. 2022). The previously discussed studies have all incorporated the analysis of ichthyoarchaeological material, with some even offering new interpretations of past human fishing activity (Dierickx et al. 2022; Virginia L. Harvey, LeFebvre, Sharpe, et al. 2022; Rick, Virginia L. Harvey, and Michael Buckley 2019). Broad scale application of ZooMS analysis to large samples of archaeological fish bone from a broad geographic area is a proven way to enhance our understanding of past biodiversity and biogeography, human exploitation patterns, and even cultural practices. The combined biomolecular approach presented in this thesis (see Chapter 8) is a logical next step, with in-depth analysis of a single taxon, like the Salmo genus, providing key data for investigating the history of *Salmo* sp. exploitation in the North Sea basin area.

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Chapter 5

Review of Salmon Ecology and Biology

5.1 Introduction

This chapter will detail the complex life cycle, physical characteristics, and ecological attributes of the Atlantic salmon (*Salmo salar*), with special focus on it's bone chemistry and isotopic features. This species is special among teleost fishes of Northwestern Europe, as it is one of only 9 anadromous species found in the North Sea Basin area (Puijenbroek et al. 2019). Anadromy is a migration strategy characterized by adult movement from salt water to fresh water, and involves specialized adaptations to allow fish born in freshwater environments to enter the ocean, grow and reside there for a period of time, and eventually return to freshwater. This chapter will go through the developmental steps that Atlantic salmon go through during their anadromous life cycle. It will also compare the bone chemistry and stable isotope characteristics found in all teleost fishes to unique variations seen in Atlantic salmon. Finally, it will examine the historical ecology of salmon, including their interactions with humans, known periods of population decline, and a brief summary of modern conservation status in the study area.

5.2 *Salmo* sp. Biology

5.2.1 Atlantic Salmon Biology and Life Cycle

Atlantic salmon undergo a series of eight distinct life stages throughout their development (Figure 1); eggs, alevins, fry, parr, smolts, post-smolts, returning adults, and breeding stage salmon (*grisle* or *kelts*). Salmon are oviparous fish which spawn and lay eggs in freshwater streams and rivers, generally favoring well-oxygenated and fast-flowing water with coarse gravelly substrate (Finstad, Armstrong, and NIslow 2010; McCormick et al. 1998). Eggs are left to incubate during the winter months in gravel streambeds, often in "redds"– nest-like depressions in the substrate formed by the laying adult female (Hansen and Quinn 1998; Thorstad et al. 2010). After hatching the fish are known as *alevins*, small larval hatchlings with the remaining egg yolk sac still physically attached in order to provide nutrients (Aas et al. 2010). Alevin, and later yolkless fry, stay close to their redds, feeding on stream detritus and small invertebrates for at least their first summer, and sometimes into the autumn period (McCormick et al. 1998). After the fry begin feeding on larger prey they are known as parr, and will move further from their redds but usually remain within the same natal stream or tributary system, with movement "mainly associated with attaining the maximum amount of food or a suitable habitat while avoiding predation..." (McCormick et al. 1998) (pp. 78). Parr may remain in freshwater for anywhere from 2-8 years– depending on genetics, environmental conditions, and latitude– remaining within a fairly limited 1300m^2 home range (Aas et al. 2010; Hansen and Quinn 1998) for the duration of this growth period.

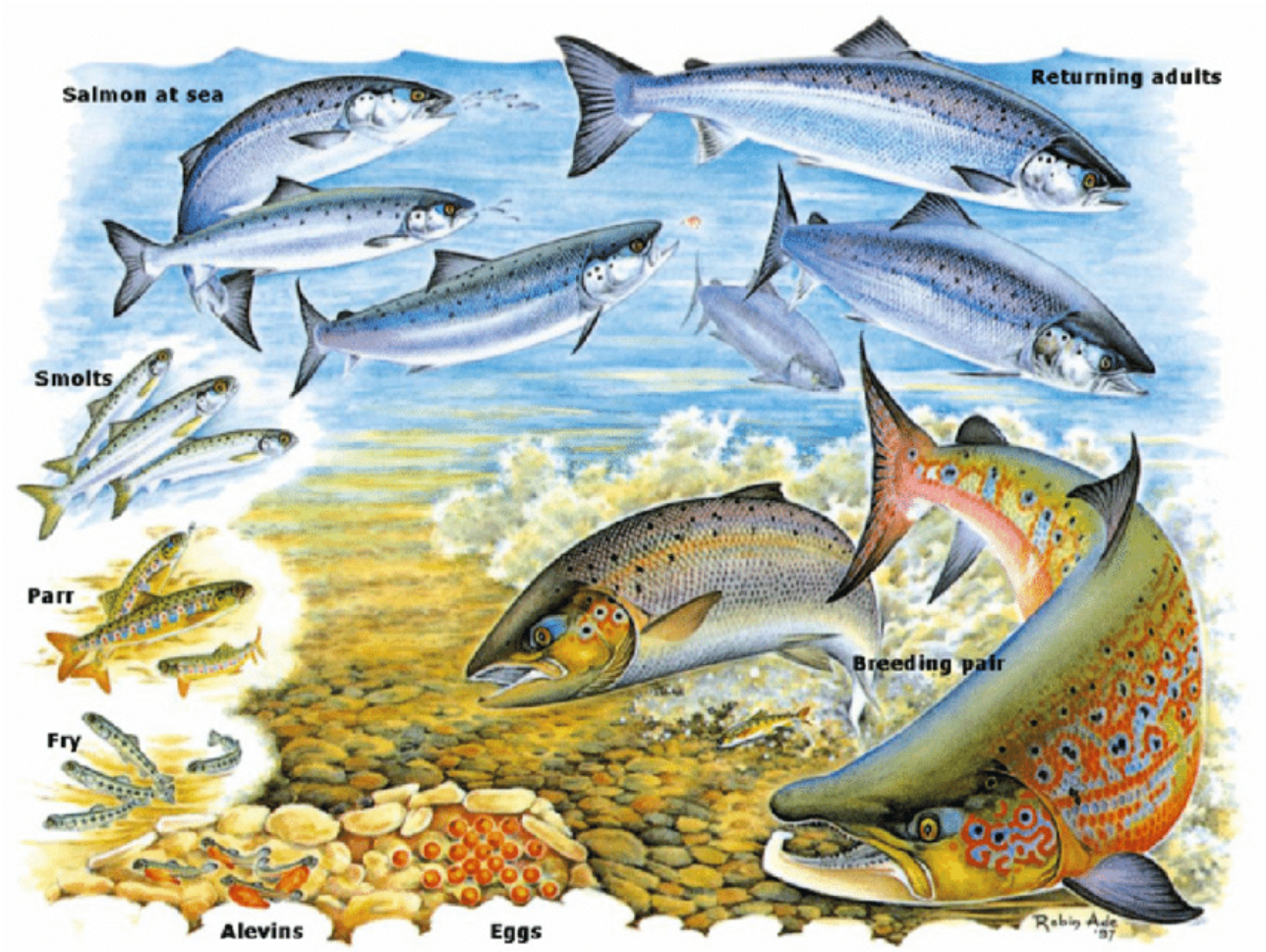


FIGURE 5.1: Illustration of the Life Cycle of Atlantic Salmon - Image © Atlantic Salmon Trust and Robin Ade (Ade 1997)

The transformation from freshwater to saline-tolerant fish occurs during the so-called "smolting" process, whereby parr that have reached certain developmental milestones become smolts capable of migrating to ocean feeding grounds (McCormick et al. 1998). While smolting is triggered by environmental cues to some degree, the fish must have reached an adequate size to begin the process and the survival rate of post-smolts in marine environments is directly correlated to their size-at-smolting (McCormick et al. 1998; Turrero, García-Vázquez, and Leaniz 2014). Smolting can be dependent on water temperature and flow rate, but one of the largest environmental influences on smolting is photoperiod, or day length, which results in later smolting ages as you move further north in latitude (Hansen and Quinn 1998; McCormick et al. 1998). The physical smolting process itself generally occurs over a 3-6 week period, but the descent downstream from natal rivers through estuaries and out to the open sea may take several months (McCormick et al. 1998). This is due, in part, to the reliance of post-smolts on nightly ebb tides for travel and favorable estuarine environmental conditions– some may move quickly through coastal or fjord areas out to the ocean, but other individuals may take several months to exit estuarine environments.

Post-smolt salmon that have reached the ocean enter a stage of dramatically rapid growth, with many fish increasing in weight by a factor of 1000 or more as they reach adulthood (Hansen and Quinn 1998; Rikardsen and Dempson 2010). When entering the ocean these post-smolts are generally approximately 15-20cm fork length (length measured from tip of nose to middle caudal fin ray), and, unlike other migratory salmonid species they can successfully feed on fish as soon as they enter the ocean– maximising nutrient intake (Rikardsen and Dempson 2010). North Sea populations of salmon appear to move northward with the shelf edge current, migrating from their natal streams around the basin toward the northern boundaries and into the open North Atlantic ocean (Hansen and Quinn 1998). The migration speed and distance of Atlantic salmon is highly variable, but they have a calculated minimum progression rate of 7-30km per day for some populations, and individual salmon originating from Russian rivers have been found as far away as ocean waters west of Greenland (Hansen and Quinn 1998; Thorstad et al. 2010). Recent tagging studies of post-smolt Atlantic salmon have shown clear differences in feeding grounds of salmon from differnent geographic origins, with those from Ireland, Spain and Iceland primarily feeding off of East Greenland, and those from Norway and Denmark generally migrating northwards towards the Norwegian, Barents, and Greenland Seas (Rikardsen, Righton, et al. 2021). There were small amounts of overlap observed between Danish and Irish populations, but for the most part the two European-origin groups did not share the same feeding grounds in the open ocean, and those from more southern latitudes preferred the warmer (5-16°C) waters south of Greenland (Rikardsen, Righton, et al. 2021).

After spending anywhere from 1-5 years feeding in the ocean, post-smolts are considered fully mature adults and will return to spawn in their natal streams (Hansen and Quinn, 1998). Salmon which return after only one year are colloquially referred to as *grilse* while others are generally called multi-sea-winter (MSW) salmon (Chaput 2012). Spawning periods vary by country, but, with the notable exception of Scotland, where salmon may arrive year-round, returning adults generally enter river systems in from late spring to early summer and will spawn in the autumn-winter period (Rikardsen and Dempson 2010). Adult salmon will spend a short period of time outside of their natal rivers, eventually entering once water levels and conditions are ideal (Thorstad et al. 2010). Females dig down into the river substrate to create the aforementioned gravel redds where they release anywhere from 450-750 eggs per pound (~.45kg) of body weight (Mills 2003), while males position themselves over redds to release sperm and fertilize the deposited eggs (Fleming and Einum 2010). After successfully spawning both male and female Atlantic salmon will attempt to return to the ocean, as they are iteroparous (multiple spawners) unlike all Pacific salmon species which are semeloparous and always die from their energy intensive spawning activities (Thorstad et al. 2010). Atlantic salmon which return to the ocean after spawning are referred to as *kelts*, and may complete the spawning migration upwards of seven times, but usually only survive 1-2 returns (Thorstad et al. 2010). Under normal circumstances approximately 65-75% of Atlantic salmon do die after spawning, from reasons ranging from predation and human fishing efforts, to disease and nutrient exhaustion (Sear et al. 2022; Thorstad et al. 2010).

5.2.2 Atlantic Salmon Physical Characteristics

Throughout their life cycles Atlantic salmon undergo a variety of morphological changes which result in distinctive physical characteristics as they progress from juvenile to adult fish. The vast majority of these are exterior changes in markings, scale type, and coloration and have little to no effect on skeletal structure, and therefore generally cannot be seen within the archaeological record. Some changes, however, do occur within the skeleton and can be used to identify salmon from different life stages. Chapter 3 describes some of these features and the zooarchaeological methodology for identifying them, especially when compared to osteologically similar brown trout (*Salmo trutta*).

Most juvenile salmon (alevins, fry, parr and smolts) can be skeletally defined by size only, and even then only for those stages with fully ossified skeletal elements. Research suggests that Atlantic salmon vertebrae begin developing by first feeding (approximately 8 weeks) and are fully developed by the end of the fry stage (Nordvik et al. 2005; Thorstad et al. 2010). Total length estimations for size at age of death can be estimated for salmon bones using a regression formula applied to vertebral measurements, first described by Watt, Pierce, and Boyle 1997. It is understood that the minimum total length for smolts is generally 7cm (Thorstad et al. 2010), therefore archaeological vertebrae with a calculated total length of 7cm or less may be assumed to be fry or parr. Those with a calculated total length between 7cm and 15cm would most likely be smolts, and those 15cm-30cm could be considered post-smolts (Thorstad et al. 2010).

Adult stage salmon (post-smolts, returning adults, and kelts) see some of the most significant growth and changes within their skeletal system, resulting not only in a drastic increase in overall size, but in new bone formation. Both male and female post-smolts and adult salmon grow rapidly during their time at sea, reaching reported total adult lengths ranging from 45-135cm, with individuals of up to 160cm reported in fishing literature (Buller 2007; Thorstad et al. 2010). The largest archaeological salmon individual recorded as part of of this thesis is represented by a single vertebrae from the 5th-8th century Nieuw Rhijngeest-zuid 2014 excavation in Oegstgeest, Netherlands, with a calculated total length of 130cm.

One of the male Atlantic salmon's unique skeletal features involves the alteration, absorption, and growth of both a new set of "breeding teeth" and a new skeletal element, the kype, or dentary hook (Figure 2). While completing their return migration to natal streams in preparation for breeding male salmon begin absorbing their present set of feeding teeth, following an observed pattern of one functional tooth followed by 2 teeth in states of absorption or development (P. Eckhard Witten, Rosenthal, and Brian K. Hall 2004). This can result in returning male salmon appearing to have only 1/3rd of their normal number of teeth, which may be visible in the archaeological record if the fish are caught prior to spawning. In addition to replacement of teeth, male spawning salmon go through significant changes in cranial bone shape and structure, resulting not only in the kype formation but in elongation of the rostrum and widening of the supraethmoid (see Chapter 3). The kype (Figure 2) is generally considered to be a newly formed skeletal element as it is not just a cartilaginous cap on the existing dentary, but a projection of both cancellous and cortical bone (P Eckhard Witten and Brian K Hall 2003). The kype permanently changes the shape and function of the dentary and premaxilla, even after being partially absorbed post-spawning.

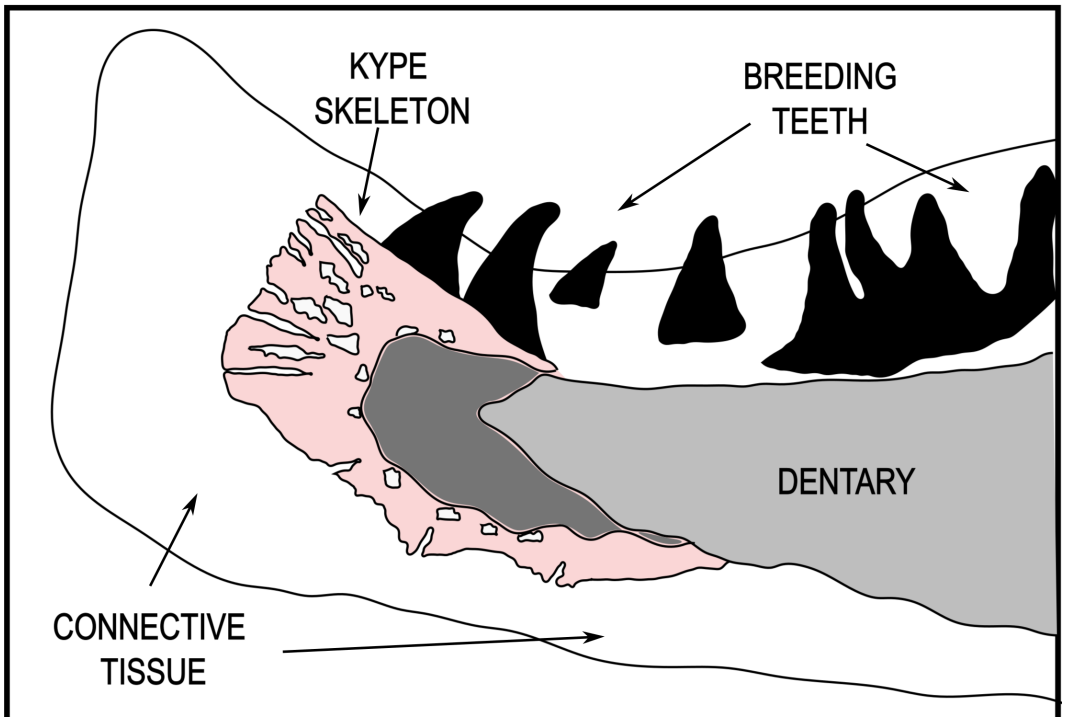


FIGURE 5.2: Diagram showing the kype structure and associated dentary features. After Witten and Hall (2002)

5.2.3 Brown Trout and Sea Trout

While the default ecotype behaviour of Atlantic salmon is anadromy, Brown trout (Salmo trutta) are generally perceived as a freshwater-only fish, thriving in riverine and lacustrine environments. However, there is a large degree of behavioural plasticity seen across the species, with internally migratory (potamodromous) ecotypes that remain entirely in freshwater, populations which briefly venture into coastal estuarine areas, and those which are truly anadromous and make a full seaward journey and return to their natal streams to spawn just as most Atlantic salmon do (B. Jonsson and N. Jonsson 2007). These behaviourally anadromous Salmo trutta are known as sea-run or sea trout, and undergo a similar smolting and maturation process as Atlantic salmon, growing far larger than their freshwater resident relatives (B. Jonsson and N. Jonsson 2007). Though there are several genetically distinct lineages of Salmo trutta across their comparatively large geographic range, it is thought that the majority of anadromy is instigated by environmental constraints and not genetic factors (B. Jonsson and N. Jonsson 2007). The behavioural "decision" to migrate seaward is dependent on juvenile freshwater growth rates and metabolism, and appears to factor in the migratory investment, and potential fitness return (B. Jonsson and N. Jonsson 2007). Fry that eventually become anadromous sea trout do not have to be born from anadromous parents, and anadromous and freshwater-resident trout can, and do, interbreed (B. Jonsson and N. Jonsson 2007). Jonsson and Jonsson 2007 describe this level of phenotypic plasticity as a "bet-hedging strategy", which allows individual fish to "decide" on a behavioral strategy that will ultimately benefit them the most. It appears that anadromous sea trout most often come from fast-growing populations, but are influenced to migrate because their natural inclination for fast growth cannot be sustained in an energetically limited environment (B. Jonsson and N. Jonsson 2007). Sea trout display the same physiological changes as Atlantic salmon, with a switch

to “pelagic camouflage”—silver, white and black coloration, and ability to tolerate salt water (B. Jonsson and N. Jonsson 2007).



FIGURE 5.3: Illustration comparing the marine appearance of Atlantic salmon (top) and anadromous sea trout (bottom). The main distinctions between the two fish are 1. notched tail seen in salmon, compared to the triangular shape of sea trout, and 2. the presence of dark spots below the lateral line in sea trout - Image © Sportsfiskarna, the Sportfishing and Fishery Conservation Association of Sweden

Sea trout experience a drastic increase in growth upon entering the marine environment, often tripling in size within the first year (B. Jonsson and N. Jonsson 2007) While the average mass of freshwater resident Salmo trutta remains between 50-150g, a sea trout can reach anywhere from 300-4000g– rivalling the size of some Atlantic salmon (B. Jonsson and N. Jonsson 2007). This is especially important to consider in ichthyoarchaeological analysis, as the instinct is to identify large *Salmo* sp. vertebrae as salmon and small ones as trout based on conventional size differences (Watt, Pierce, and Boyle 1997). Atlantic salmon and sea trout inhabit the same riverine environments during their early developmental stages, exhibit similar feeding patterns when at sea, and return to spawn at similar times of the year (depending, of course, on latitude and other environmental factors) (B. Jonsson and N. Jonsson 2007). This, coupled with their similarity in appearance (Figure 3), makes differentiation between their bones especially important and also raises questions of whether medieval fishers and consumers would have differentiated between the two species to the same degree that we do today (see Chapter 6).

5.3 *Salmo* sp. Osteobiology and Stable Isotope Ecology

5.3.1 Fish Bone Structure

The development of certain fish bones can differ significantly from the formation of similar structures within mammals and birds. A deeper understanding of the chemistry behind bone formation is important to aid interpretations of stable isotope ecology and proteomics– two methods of analysis employed within this thesis.

Osteobiology is the study of the biological and chemical composition and structure of bone tissues, is a interdisciplinary field involving the study of, among others, anatomy, evolutionary ecology and palaeontology. Understanding the chemical makeup of fish bone, and how it differs from mammalian and avian bone, may provide more insight into collagen preservation in archaeological contexts. Additionally, the osteobiology of teleost fishes and, specifically, Atlantic salmon and brown/sea trout, is important for this thesis as it provides a deeper understanding of the chemical environment that stable isotopes are deposited into during the growth of an individual fish. The stable isotope ecology of fish in general, and salmon in particular, is defined by known variations in stable carbon and nitrogen ratio values that differ between marine and freshwater environments, as well as trophic levels. The following subsections will discuss the bone histology, chemistry, and stable isotope ecology of teleost fishes as a whole, and *Salmo* as a genus.

There are over 28,000 species of fish within the infraclass *Teleostei* comprising over 96% of all bony fish (Norris and Lopez 2011), including salmonid species like Atlantic salmon, brown trout and sea trout. Teleosts are characterized by several physiological differences from the remaining small percentage of other fishes, especially with regards to their skeletal structure and chemistry (Arratia 2015). Aside from their common traits of an unpaired vomer and mobile premaxilla, teleost fish also generally have far less dense bone constructed from a system of bony struts rather than the typical cancellous bone seen in other vertebrates (Arratia 2015). Almost all vertebrate bone contains three kinds of cells, each with specific functions in metabolism, function, and growth– osteoblasts, osteoclasts, and osteocytes (Davesne et al. 2019). Teleost fishes, however, are split into two distinct groups of bone composition, acellular and cellular, with acellular fish being anosteocytic (without osteocytes) (Davesne et al. 2019).

The majority of Euteleosts (a clade within Teleostei to which all salmoniformes belong) present with acellular bone, however some families have apparently reacquired the ability to produce osteocytes and are classed as cellular (Davesne et al. 2019). It is posited that anadromous fishes are more inclined to reacquire cellular bone chemistry, which clarifies why Atlantic salmon and Brown trout are cellular teleosts (Davesne et al. 2019). Szpak 2011 states that the influence on bone preservation of cellular vs. acellular fish is currently unclear, however studies on the impacts of these bone types on bulk stable isotope analysis have shown potential differences that need to be accounted for (Bas and Cardona 2018; Szpak 2011). Davesne et al. reviewed the chemical and structural properties of over 600 species of teleost fishes in order to understand more about the development of acellular bone, and concluded that while it can adequately perform all the required structural and mechanical functions it is less efficient at maintaining mineral homeostasis (Davesne et al. 2019). The major impact of cellular bone composition on archaeological *Salmo* sp. fish is seen in their skeletal demineralization, remodelling and resorption activities during spawning activities, known as halastasis (Davesne et al. 2019). Halastasis is mostly directed at the formation of the dentary kype, but also results in skeletal and dental resorption during the energetically taxing spawning period that salmon and sea trout undergo, which may impact bulk isotope values (see Section 5.3.2 below) (Davesne et al. 2019; P Eckhard Witten and Brian K Hall 2003; P. Eckhard Witten, Rosenthal, and Brian K. Hall 2004).

5.3.2 *Salmo* sp. Stable Isotope Ecology

The structure and function of fish bone plays a key role in its ultimate stable isotope composition, and therefore the application of bulk stable isotope analysis to archaeological fish bones. While the impacts of acellular vs. cellular bone composition have yet to be fully studied, it is clear that cellular bone shows at least some variation in both δ^{13}C and δ^{15}N values among elements in the same individual (Bas and Cardona 2018). This phenomena is seen in other vertebrates, and is related to different tissue turnover rates seen in different skeletal elements as

well as the specific amino acid profile of a given set of collagen (Bas and Cardona 2018). This results in researchers suggesting caution when comparing bulk stable isotope values from cranial and vertebral elements in cellular bone fish like those in the genus *Salmo* (Bas and Cardona 2018). In that regard, the remodelling that occurs in anadromous Atlantic salmon and sea trout as a result of the kype formation process could potentially affect the bulk nitrogen values of male spawning individuals caught after their migration period. Within that subset of anadromous *Salmo* sp. fish we would expect to see lower overall δ^{15}N values in kype and other cranial elements, as a result of higher rates of the intensive bone remodelling– the formation of new bone material, which naturally lacks all previous isotope deposits, lowers the overall average across the bone in question (Fahy et al. 2017). That being said, it is unlikely that this remodelling would affect the bulk nitrogen values obtained from the vertebral elements of *Salmo* sp fish, which make up 90.9% of all *Salmo* sp. bone samples in this thesis. Similarly, the current range of known differences between *Salmo* sp. elements is small enough that questions of intra-skeletal variability should not preclude entirely the use of different skeletal elements.

It is generally assumed that high δ^{13}C and high δ^{15}N can be treated as signals of a marine environment, while high δ^{15}N and low δ^{13}C are assumed to signal a freshwater environment (Guiry 2019). These assumptions, however may not be as clear-cut as once thought as the basal food web which supports freshwater and estuarine fish can have a much wider range of isotopic compositions than previously thought (Guiry 2019). δ^{13}C values in particular can be comparatively broad across freshwater resident populations of Atlantic salmon, as demonstrated by Guiry et al. (2019), which needs to be accounted for when looking at archaeological *Salmo* sp. fish which may represent a variety of ecotypes ranging from lake resident to ocean-going. Similarly, there are demonstrable isotope differences between both anadromous *Salmo* sp. ecotypes, Atlantic salmon and sea trout. While large piscivorious (fish eating) brown trout from riverine or lacustrine environments will show enriched δ^{15}N values, they will still be lower than those seen in anadromous brown trout and, when combined with the presence of typically "marine" δ^{13}C values, can be used to discriminate between the two forms of this species (McCarthy and Waldron 2000). Interestingly, the δ^{15}N signatures of anadromous sea trout will also be consistently higher than those seen in anadromous Atlantic salmon specimens (see Chapter 8). Researchers have concluded that higher trophic level feeding is a main driver of these higher marine δ^{15}N signals seen in anadromous sea trout (Etheridge et al. 2008; McCarthy and Waldron 2000).

Bulk stable isotope analysis of Atlantic salmon which have spent their adult life feeding in the ocean should result in typically marine signatures, with anadromous salmon of northwestern European origin displaying a baseline mean δ^{13}C of -16.16 ± 0.34‰ and baseline mean δ^{15}N of 10.53 ± 0.79‰ (Almodóvar et al. 2020; MacKenzie et al. 2011; O'Toole et al. 2020; Trueman 2022). Figure 4 below shows the mean δ^{13}C and δ^{15}N values obtained from the scales from over 1900 modern and historical anadromous Atlantic salmon individuals, as well as modern baselines for both anadromous sea trout and freshwater trout (McCarthy and Waldron 2000; Svensson et al. 2014). Scale and bone-derived collagen in Atlantic salmon are comparable as they both represent long-term averages of nutrient intake and feeding which should reflect the most intense periods of feeding which, in anadromous salmon, occurs in the marine environment (Guiry et al. 2020).

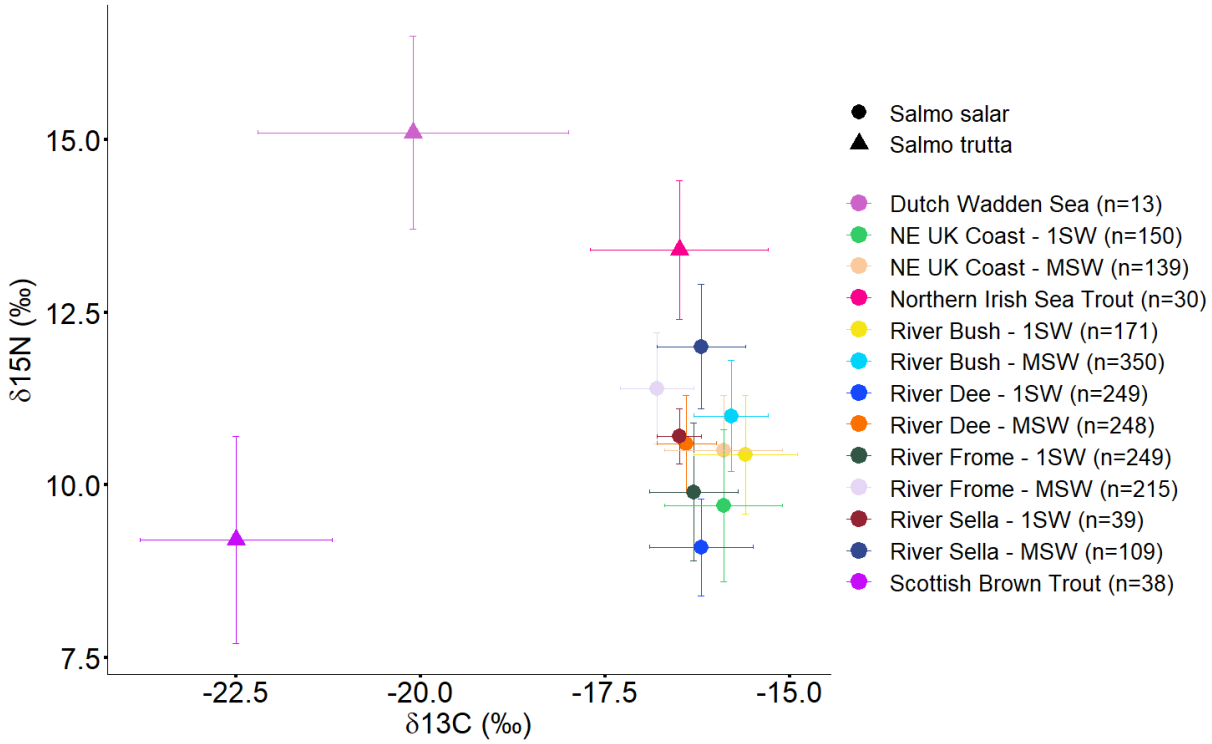


FIGURE 5.4: Visualization of mean bulk δ^{15}N and δ^{13}C values from modern and historical salmon, sea trout and freshwater trout harvested from rivers and lochs located in Spain (Sella), Northern Ireland (Bush, Faughn and Dennet), England (Frome), Wales (Dee), Scotland (Lochs Tay, Langavat, A'Ghriama, Merkland, Eck, Rannock and Talla) the Northeast UK Coast, amd the Dutch Wadden Sea. (Almodóvar et al. 2020; MacKenzie et al. 2011; McCarthy and Waldron 2000; O'Toole et al. 2020; Svensson et al. 2014; Trueman 2022)

The range of δ^{13}C values seen within these published data is quite small, with the average means only differing by 1.2‰ from a maximum of -15.6‰ and a minimum of -16.8‰, and no discernible geographic influence on variation between these mean values. The baseline mean δ^{15}N values, on the other hand, are more varied and this is influenced by several different factors in *Salmo* sp. fish. One is size and age at capture, and there is an observable trend in Atlantic salmon that results in an increase in δ^{15}N values, and, subsequently, trophic level, as the fish increases in size (Tsutaya et al. 2022). It is therefore expected that older, and larger, fish will show higher overall δ^{15}N values; demonstrated by the baseline data showing older multi-sea winter (MSW) fish with consistently higher mean δ^{15}N values (11.1 ± 0.8‰) than their one sea winter (1SW) counterparts (9.9 ± 0.8‰). Another factor that may impact δ^{15}N values is spawning, when salmon migrate from their ocean feeding groups back to their freshwater natal streams. Upon entering freshwater the salmon do not feed, which results in the catabolism of the animal's own body tissues, protein and lipids (Bowes, Lafferty, and Thorp 2014; Doucett et al. 1999). Doucett et al. found that fasting did affect both the δ^{15}N and δ^{13}C values from liver and muscle tissue in spawning Atlantic salmon (Doucett et al. 1999). For archaeological salmon bones, this may result in enriched δ^{15}N values seen in spawning adults (Bowes, Lafferty, and Thorp 2014; Doucett et al. 1999). Further study looking at possible correlations between increased stress, resorption, remodelling, sex, and δ^{15}N values may highlight significant differences between individuals, and one potential method of investigation would be targeted incremental isotope analysis of vertebrae and dentary/kype elements (Matsubayashi et al. 2017). This method has been successfully applied to modern masu salmon (*Oncorhynchus masou*, however application to

archaeological material would require unusually large vertebral specimens and the development of a drilling protocol that would maximise collagen extraction from different life stages (Matsubayashi et al. 2017). For now, the δ^{15}N values from archaeological *Salmo* sp. reported in this thesis should be seen as a lifetime average and taken as true, in order to have the most interpretive value.

The final consideration when discussing the stable isotope ecology of archaeological *Salmo* sp. fishes, is whether or not the observed typically-marine signatures are obtained from anadromous fish from the species *Salmo salar* or *Salmo trutta*. Anadromous *Salmo trutta* (sea trout) share the same behavioral trait as salmon, with a migration from freshwater to marine environments in search of richer feeding opportunities resulting in more typically marine δ^{13}C than seen in populations of trout which remain in freshwater environments. Three populations of *Salmo trutta* provide baseline mean δ^{13}C values of -18.3 ± 1.6‰ for sea trout, mean δ^{13}C values of -22.5 ± 1.3‰ for freshwater trout, mean δ^{15}N values of 14.25 ± 1.2‰ for sea trout, and mean δ^{15}N values of 9.2 ± 1.3‰ for freshwater trout (Figure 3). The mean δ^{15}N values for brown trout and Atlantic salmon are fairly comparable at approximately 10.53 ± 1.79‰ for the Atlantic salmon samples and 9.2 ± 1.3‰ for brown trout. However, sea trout show enriched δ^{15}N values, with a higher mean value of 14.25 ± 1.2‰, resulting in an average difference of 5.05‰ – on the order of one trophic level higher (J. Barrett et al. 2008; Schoeninger and DeNiro 1984). This difference is the basis for a combined biomolecular approach to identifying anadromous sea trout within the archaeological record, that is more fully explored in Chapters 8 and 9 of this thesis.

5.3.3 Preservation of *Salmo* sp. Bones

Preservation of *Salmo* sp. bones within the archaeological record is a key barrier to fully understanding the role of both salmon and trout in the Medieval Period using both osteological and biomolecular analysis methods. The most commonly repeated explanation for the poor preservation seen in the bones of *Salmo* sp. fish is related to the supposedly high fat content of these fish and their bones. Nearly a dozen reports and archaeological papers repeat this claim, with the justifications based around the idea that fat is stored in the comparatively open structure of their bones and diagenetic processes in soil transform lipids to fatty acids Beerenhout 2011; Enghoff 1986; Esser 2000; Jane, Nislow, and Whiteley 2014; F. Kerklaan 2016; Franka Kerklaan 2012; Lepiksaar and Heinrich 1977; Lepiksaar and Larsson 1982; Robinson et al. 2009; Spitzers 1998. Its likely that the preservation of *Salmo* sp. bones in northwestern Europe is influenced by a variety of factors, including inherent characteristics of bone chemistry, lipid content, and local soil moisture and acidity levels.

5.4 Historical Ecology

The last three decades have seen a significant amount of work to assess the importance of fish as food, commodity, and cultural medium to human groups living in northwestern Europe during the Medieval Period. Approaches have ranged from surveys of ichthyoarchaeological material (e.g. J. H. Barrett, Locker, and C. M. Roberts 2004a,b; J. H. Barrett, Nicholson, and Cerón-Carrasco 1999; J. H. Barrett, D. Orton, et al. 2011; Brinkhuizen 1979; Enghoff 1996; Galik et al. 2015; Häberle and Hüster Plogmann 2019; Harland 2006; Jagt et al. 2012; Makowiecki et al. 2009; Maltin and L. Jonsson 2018; D. C. Orton, Morris, et al. 2014; Oueslati 2019; Prummel and Heinrich 2005; Van Neer and Ervynck 1996; Williot and Castelnaud 2011) and reviews of documentary and literary sources (e.g. Bennema and Rijnsdorp 2015; Boe, Verhaeghe, and Archeologisch Patrimonium (Belgium) 1997; R. C. Hoffmann 1996, 2015; Holm 1996; Kowaleski 2000, 2003, 2010; Poulsen 2010; Sicking and Abreu-Ferreira 2009; Wolter 2015), to assessments of anthropogenic impacts on local ecologies (R. C. Hoffmann 1996, 2005; Langouët and

Daire 2009; Lenders et al. 2016). A common theme within this body of literature involves taking a broad view of marine and freshwater ecosystems from a particular geographic and temporal perspective, with targeted assessments of individual taxa generally focused on some of the most commercially important fish, such as gadids and herring (J. H. Barrett, D. Orton, et al. 2011; J. H. Barrett and D. C. Orton 2016; Enghoff 1996; Limburg et al. 2008; Maltin and L. Jonsson 2018; D. C. Orton, Makowiecki, et al. 2011; D. C. Orton, Morris, et al. 2014; Star et al. 2017). Looking specifically at the historical ecology of a particular taxon allows for a deeper understanding of distinct periods of change in their exploitation and provides a framework for interpreting biomolecular results from archaeological material in a way that may benefit modern ecology and conservation efforts. This section will cover the key features of Atlantic salmon historical ecology in the North Sea Basin throughout three distinct periods of activity– medieval exploitation, early modern commercial fishing and decline, and modern conservation. It will focus primarily on anthropogenic changes to salmon environment and their overall importance to culture and economy, rather than fishing techniques, cooking methods, or documentary evidence for salmon consumption (see Chapter 6).

5.4.1 Medieval (500-1500CE) Exploitation

The exploitation of aquatic resources was a major economic driver behind fluctuations in socio-political power in Northwestern Europe during the broadly Medieval Period, c. 500-1500 CE (e.g. J. H. Barrett, Locker, and C. M. Roberts 2004a; R. Hoffmann 2000; R. C. Hoffmann 1996, 2005). The river and estuarine systems that drain into the North Sea were not only a source of natural aquatic resources like animals, plants, fresh water, salt, and building materials but also key sites of environmental control. The control of water and the aquatic environment during the Medieval Period came in many forms, ranging from large-scale hydraulic engineering and agricultural projects, to local management of water mills, drinking water, and access routes (e.g. Grewe 2000; R. Hoffmann 2000; R. C. Hoffmann 2005; Holt 2000; Rynne 2000; Squatriti et al. 2000; TeBrake 2000). The environmental history of the waterways of Europe during the Medieval Period is succinctly summarized as consisting of "patterns of impact and response" by Hoffmann (1996, pg. 632), with economic and technological developments across the region mapping neatly onto documented changes in ecosystems and resource exploitation. The mechanisms behind these environmental changes were highly dependent on time period and region, but include anthropogenic modifications resulting from intensive cereal-based agriculture as well as damming of rivers for water powered mechanical systems (R. C. Hoffmann 1996). Shifts in resource exploitation patterns were a natural result of these changing environmental conditions, and key evidence for historic changes in freshwater fishing practices can be found in documentary, literary and artistic records (R. C. Hoffmann 1996). Specific documentary evidence for declines in so-called 'prestige' fish like sturgeon, salmon and pike demonstrate that, by the 13th-century, human groups across Europe had long been practicing "economic manipulation and transformation of aquatic organisms and systems" (R. C. Hoffmann 1996).

The historical evidence for declines in fish stocks due to anthropogenic environmental change has encouraged archaeological study of the topic, with many ichthyoarchaeological reviews and assessments focusing on using fish assemblages to understand localized changes in economy or culture (e.g. J. H. Barrett, Nicholson, and Cerón-Carrasco 1999; J. H. Barrett, D. Orton, et al. 2011; Brinkhuizen 1979; Enghoff 1996; Galik et al. 2015; Häberle and Hüster Plogmann 2019; Harland 2006; Jagt et al. 2012; Makowiecki et al. 2009; Maltin and L. Jonsson 2018; D. C. Orton, Morris, et al. 2014; Oueslati 2019; Prummel and Heinrich 2005; Van Neer and Ervynck 1996; Williot and Castelnaud 2011). Deeper insights into broader geographic trends in medieval fishing across Northern Europe stem from a series of reviews intending to explore ichthyoarchaeological evidence for the proposed medieval rural-to-urban transition that was concentrated around the 10th and 11th centuries CE (Hodges 1989).

Extensive surveys of ichthyoarchaeological evidence from English medieval sites resulted in the identification of a "fish event horizon", centered at a period of transition from the 10th-11th centuries CE (J. H. Barrett, Locker, and C. M. Roberts 2004a,b). Broadly speaking, this 'fish event horizon' involved the widespread decline in freshwater and anadromous fish exploitation across the reviewed area, coinciding with a marked increase in presence of marine fish taxa (J. H. Barrett, Locker, and C. M. Roberts 2004a). It is proposed that three main variables may have contributed to this drastic change in fishing patterns; environmental change, technological innovation, and the influence of Christian fasting practices (J. H. Barrett, Locker, and C. M. Roberts 2004b). While these initial reviews of archaeological data were restricted to 127 English fish bone assemblages, the conclusions have proven applicable to a much broader geographic range; with evidence for shifts from primarily freshwater to marine fishing found in ichthyoarchaeological assemblages across Western Europe (J. H. Barrett 2016; J. H. Barrett, Locker, and C. M. Roberts 2004a,b; J. H. Barrett, D. Orton, et al. 2011; Lotze 2007; Maccarinelli 2021; Oueslati 2019; Van Neer and Ervynck 2016). By the mid-14th century CE it is proposed that a "pan-European fish-trade network" of sorts had emerged, with import/export links between the bustling urban hubs of Northern Europe commonplace for economically important fish species like Atlantic salmon (J. H. Barrett and D. C. Orton 2016).

A major barrier to taxon-specific archaeological reviews of *Salmo* sp. fish in Northwestern Europe is the issue of relative preservation; compared to most other fish taxa exploited by human groups throughout the region, *Salmo* sp. bones simply do not preserve as well and are not often present within the archaeological assemblages at a given site. Given the supposed importance of Atlantic salmon, as well as large extant populations of Brown trout across North Sea basin rivers, the lack of *Salmo* sp. remains seen in the region is intriguing. A review of commercial exploitation and proto-conservation of Atlantic salmon in medieval Scotland discussed results from published and archival documentation of salmon commerce in the study area, the scant zooarchaeological records, and contemporary literary descriptions of fishing sites and methods from the period (R. C. Hoffmann 2015). In medieval Scotland salmon were "ubiquitous features of conspicuous consumption", which continued to hold a high position of importance in northern and western European cultures even after the previously discussed transition from primarily freshwater to primarily marine resource exploitation (R. C. Hoffmann 2015). Interestingly, the reviewed Scottish documentary and ichthyoarchaeological record is framed as an anomalous holdout of robust salmon stocks when compared to the rest of North-western Europe, and Hoffman ascribes this to a combination of regulatory efforts by local and regional authorities, less unintended anthropogenic change of salmon habitat due to agricultural intensification, and a Scottish preference for building water mills on artificial bypass channels rather than the main body of a river (R. C. Hoffmann 2015).

This last point, regarding human modification of riverine environments through damming and diking, has been touched upon briefly by most authors investigating environmental changes in North-western Europe (R. C. Hoffmann 2005; C. Roberts 2007; Wolter 2015, e.g.), but most directly addressed by Lenders et al 2016. Historical evidence for anthropogenic environmental modification in the Palaeo-Rhine catchment area, which includes the Rivers Rhine, Meuse, Scheldt, Thames and Seine, contextualizes changes in historic salmon populations in the region (Lenders et al. 2016). This taxa-specific review concluded that ichthyoarchaeological remains from the Netherlands, Belgium and France show a strong decline in exploitation of Atlantic salmon in the Early Medieval Period, and used a ratio of N(salmon)/N(pike) increases to quantify the evidence reviewed (Lenders et al. 2016). A sharp decrease in the number of sites with salmon remains relative to those showing pike remains was identified in the Early to Late Medieval Period, as well as a post-Late Medieval increase in the same ratio (Lenders et al. 2016). Consistent with Hoffman's (2015) interpretation of medieval Scottish salmon stocks, Lenders et al. interpret this late increase as being related to imports of salmon from Scotland rather than an actual rebound in local stock populations in North-western Europe (Lenders et al. 2016). The major proposed mechanism behind

these observed declines is related to the ecological impact of watermills, dams, dikes, and other anthropogenic river modifications implemented across the Paleo-Rhine catchment during the Medieval Period (Lenders et al. 2016). The evidence demonstrates a strong negative correlation between the increase of anthropogenic river modifications and perceived decrease in Atlantic salmon stocks within the study area (Lenders et al. 2016). The offered reasons for this high impact range from increased siltation and lowered oxygenation in dammed waters, to an overall reduction of adult salmon able to successfully navigate to and from their natal streams (Lenders et al. 2016).

Assessing the true impact of human exploitation on salmon populations in the Medieval Period remains difficult, but methods to approach the issue can be found in recent research combining historical population data with bulk stable isotope analysis. A single population approach, focusing on the River Spey in Scotland, utilized a combination of sedimentary bulk stable isotope analysis and historical catch records, to determine whether known fluctuations in returning salmon populations were due to climatic changes, local ecosystem processes, anthropogenic effects, or a combination thereof (Sear et al. 2022). Sedimentary samples were taken from Loch Insh and Loch Vaa, two inland lochs located along the course of the River Spey in the Scottish Highlands. Samples were selected after total organic carbon/nitrogen was determined, and then analyzed for $^{15}N/^{14}N$ ratios, resulting in a $\delta^{15}N$ value to be compared to the standard atmospheric N_2 (Sear et al. 2022). To contextualize the sedimentary isotopic values, the authors conducted a review of historical catch data for Atlantic salmon from four Scottish salmon rivers from a time period spanning 1770CE-2000CE, in order to create a baseline for returning salmon volume in the study area (Sear et al. 2022). Several periods of decline and resurgence in reported catch numbers were identified, with a period of particularly low salmon catches in the late-18th-early 20th centuries correlating with an observed genetic bottleneck in River Spey salmon during the same period (Nikolic et al. 2009; Sear et al. 2022). This pattern of decline in the Early Modern period has mostly been ascribed to a combination of the Northern European climatic anomalies seen in the Little Ice Age, and alternating periods of human commercial exploitation and conservation of salmon (Sear et al. 2022). Sedimentary analysis was aimed at determining the proportion of total ecosystem $\delta^{15}N$ which could have reasonably been derived from Atlantic salmon, after Hill et al.'s method of calculating marine derived nutrients (MDNs) to freshwater environments like rivers and lochs (Hill, Stanford, and Leavitt 2009; Sear et al. 2022). It was established that the nitrogen record of the sediment cores sampled from both Lochs were especially enriched relative to the calculated background nitrogen expected in the samples, and determined that it was likely due to MDNs– which, in this case, the only MDN source would be Atlantic salmon returning to spawn (Sear et al. 2022). The observed fluctuations in $\delta^{15}N_{SED}$ were then compared to known climatic events during the 2000-year period the sediment cores covered, and it was concluded that there was a rapid collapse in numbers of returning Atlantic salmon to the River Spey area from approximately CE 1000-1250, which continued until approximately CE 1850 (Sear et al. 2022). This identified decline corresponds with those highlighted by Lenders et al. (2016), however rather than being clearly connected to human activity, Sear et al. maintain that the fluctuations in $\delta^{15}N_{SED}$ from Atlantic salmon is due to both natural environmental changes and anthropogenic sources (Sear et al. 2022).

5.4.2 Medieval to Post-Medieval Conservation

The periods of decline in the Early and Late Medieval periods identified by Sear et al. and others (J. H. Barrett 2019; Lenders et al. 2016; Sear et al. 2022), lead into the increasingly complex Early Modern (c. 1500-1850) and Modern (c. 1850-present) periods of changing salmon ecology. They were both characterized by what may be termed as "conservation" movements and "industrial" salmon fisheries, which resulted in subsequent rises and falls in salmon stocks across Europe. The environmental changes discussed in Sear et al., include the Little Ice

Age, the cold multi-century post-glacial period which spanned approximately 1450-1850 CE and was particularly impactful on the local climate of Northwestern Europe (Lamb 1972; Masson-Delmotte et al. 2021; Sear et al. 2022). Changes to how humans manipulated the freshwater and marine environment in order to both maximize catches and protect stocks were evident across the study area as early as the 14th-century (R. C. Hoffmann 2015), and historical evidence for what might be termed "conservation" practices coincides with the reported declines in salmon abundance due to river damming, weir construction, overfishing, and climatic shifts (J. H. Barrett 2019; J. H. Barrett, Nicholson, and Cerón-Carrasco 1999; R. Hoffmann 2012; R. C. Hoffmann 2010, 2015; Lenders et al. 2016; Sear et al. 2022). As early as the 1300s legislation was introduced in Scotland to prohibit fishing salmon at certain times of year not just for the benefit of the noble or ecclesiastical owners of fishing rights, but for the general health of the salmon population (R. C. Hoffmann 2015). Similar regulations were enacted in what are now areas of Italy, England, Germany, and the Netherlands concerning the need for passages in mill dams and existing fishing weirs that would allow at least some salmon and trout to pass easily through in order to spawn (Bennema and Rijnsdorp 2015; R. C. Hoffmann 2010). By the Late Medieval/Early Modern period there were observations being made by naturalists like Adriaen Coenen about the recent fluctuations in abundance of salmon in local environments (Bennema and Rijnsdorp 2015). Coenen specifically wrote about salmon stocks in the Netherlands, but was clear that there had been overall declines in salmon caught in the North Sea, even while numbers in Dutch rivers like the IJssel and Maas remained strong (Bennema and Rijnsdorp 2015). Writing in 1578, Coenen observed that salmon had been extremely expensive when his own parents were young, becoming more accessible in his youth and again increasing in price by the contemporary period (Bennema and Rijnsdorp 2015). While he did not directly ascribe these declines and resurgences in salmon stocks to any anthropogenic or climatic actions, it's clear that fishers and naturalists were aware of changes in fish availability between environments (Bennema and Rijnsdorp 2015).

The output of commercial fisheries for salmon in estuarine, riverine, and marine environments ebbed and flowed as the Early Modern period progressed. This resulted in a curious dichotomy wherein the collapse of local stocks in places like the Netherlands (Lenders et al. 2016) occurred at the same time that populations in Scotland, England, and Germany reportedly rebounded or remained stable (De Groot 1992; R. C. Hoffmann 2015; MacLeod 1968). It is during this Early Modern period of simultaneous abundance and decline that trans-Atlantic urban myths arose about salmon being so common that it was relegated to the position as a poor person's or servant's food in England, the United States, and Scotland, particularly during the 17th-18th centuries (Brushfield 1897; Chase 1861; MacLeod 1968). But despite the supposed bounty of salmon during these periods, by the mid-19th century there began concerted state-level efforts to record statistics about catches in rivers and estuaries of England, Scotland, the Netherlands and Germany (De Groot 1992; MacLeod 1968; Robertson 2001).

These programs of catch recording appear to have been motivated not just by an economic worry about the productivity of the various salmon industries, but also by a sense of environmental responsibility for the fish. In England, Ireland, Wales and Scotland governmental takeover of riverine resources was implemented as early as the 1860s, with a major motivation being the wellbeing of salmon (MacLeod 1968). In fact, the Royal Commission on salmon for England and Wales was appointed upon the fundamental principals of not just preserving salmon numbers and movement, but preventing pollution in the rivers they inhabited (MacLeod 1968). As catches declined in both Germany and the Netherlands, changes to fishing technology were adapted to slow the population loss, with seine netting forbidden by the early 20th century (De Groot 1992). However, despite these late-19th and early-20th century efforts at conservation, the resulting local rebounds in fish stocks only led to a repetitive cycle of, as MacLeod put it in 1968, "indifferent half measures" (MacLeod 1968) across the North Sea basin area. Denmark, Norway, Scotland, Ireland, Germany and England all had active, if not particularly robust, sea fisheries

for Atlantic salmon during the first half of the 20th century, with those off the coast of Norway and the Faroe Islands not stopping until the mid-1980s (Dadswell et al. 2022; De Groot 1992; MacLeod 1968). These sea fisheries are a particular concern for conservation of salmon stocks because of the key role that marine feeding plays in not only the growth and survival of individual fish, but the health and productivity of local populations.

In 1983 the Convention for the Conservation of Salmon in the North Atlantic Ocean was held in Reykjavik in order to assess and plan for the conservation of Atlantic salmon across the North Atlantic region (NASCO 2019). North Atlantic EU members countries, Norway, Sweden, Denmark, Finland, the Union of Soviet Socialist Republics, Canada and the USA were all party to the convention and most ratified the creation of the North Atlantic Salmon Conservation Organization (NASCO) (EEC 1983). The ratified treaty from 1983 represents one of the first international efforts to codify the conservation of Atlantic salmon in the North Atlantic, and specifically forbade fishing for salmon beyond 12 nautical miles of the member countries coastlines, with two exceptions in Greenland and the Faroes (EEC 1983). To assess salmon conservation status each year, the International Council for Exploration of the Seas (ICES) has formed a Working Group on North Atlantic Salmon (WGNAS) which directly reports to NASCO, allowing for continually updated evaluations of salmon habitat, threats to salmon survival at sea and in riverine environments, and local and regional population numbers. While the efforts of NASCO and the WGNAS are concentrated primarily on the marine habitat of Atlantic salmon, the late 20th century saw the creation of many state-level and non-governmental organizations focusing on the preservation of salmon's freshwater habitat. The Atlantic Salmon Trust, Danmarks Center for Vildlaks, Association Internationale de Défense du Saumon Atlantique, Der Atlantische Lachs, Fisheries Management Scotland, and Norske Lakseelver are just some of the NGOs with official observer status at NASCO meetings (NASCO 2006).

Despite these state and international level efforts, the collapse of Atlantic salmon populations has either already occurred in some areas, or is imminent (Dadswell et al. 2022). There have been international movements to enhance stocks through breeding and hatchery programs, decreases in overexploitation, and the restoration of riverine habitats but the overall downward trends continue (Dadswell et al. 2022; NASCO 2019). There are many proposed causes for the inability of salmon populations to fully recover, including the impacts of anthropogenic climate change, illegal, unreported, and unregulated fisheries (IUU), and the rise of intensive Atlantic salmon farming (Dadswell et al. 2022; NASCO 2019). A particularly interesting recent discussion of these causes comes from work by Dadswell et al., which proposes that these artificial factors may be enhanced by natural characteristics of Atlantic salmon populations which make them particularly susceptible (Dadswell et al. 2022). Dadswell et al. reviews reports of interannual variations in adult salmon returning to spawn, and concludes there is a natural 9-10 year cycle which, when interfered with by artificial means, can result in the interruption of adult salmon survival and productive spawning (Dadswell et al. 2022). The authors identify several periods of cyclical disruption, decline in adult returns and mean size, and, ultimately, local stock collapse (Dadswell et al. 2022).

These observed patterns of modern salmon decline and collapse are, for the most part, based on historical catch and fisheries data. While clearly useful in determining long-term trends in salmon historical ecology, it is also clear that archaeological data could greatly supplement these modern approaches to the problem of salmon conservation. Extending the baseline of knowledge back to the Medieval Period allows us to connect past variations in Atlantic salmon population and exploitation to those of the modern era. The isotopic and species abundance information detailed in this thesis (Chapter 9) will provide even more environmental evidence to consider when questioning the current approaches to salmon conservation.

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Chapter 6

Medieval Perceptions and Representations of *Salmo* sp. Fishes

6.1 Introduction

This chapter serves a dual purpose– as both the locus for new documentary and historical analysis and as a reflective space for interpretative exploration and cross-disciplinary considerations. The main focus of this chapter is medieval conceptions of *Salmo* sp. fishes– mainly anadromous salmon, anadromous sea trout, and freshwater trout– with the aim of interrogating how medieval people from various cultural and geographic locations and social groups interacted with and thought of these fish. This chapter presents several reviews of non-archaeological material, ranging from documentary sources of tax and purchase records to symbolic and representational imagery of fish produced during the period from approximately 500-1600 CE. The following sections contain in-depth discussions of representations of salmon, sea trout and freshwater trout including linguistic evidence for these fish, medieval categorizations, and portrayals of the different species and ecotypes in a variety of literary, documentary, and artistic modes.

6.2 Medieval Conceptions of *Salmo* sp. Fishes

Identifying and categorizing parts of the natural world is a human instinct that is certainly as ancient as spoken language, and likely extends beyond that into the very beginnings of our cognitive development. Unsurprisingly, nomenclature and etymology of the various words for salmon and trout are particularly complex. While the modern English word "salmon" and medieval cognates like "samoun", "samowne", "samon", "saumon", etc. are certainly derived from the Latin *"salmō"*, the origin of this word are uncertain– there are no native salmon species in Italy, and folk etymologies claiming that it comes from the root word *"salire"* (to jump) are incorrect (Andrews 1955; Vaan 2008). There is more evidence that Roman settlers in northwestern Europe more commonly referred to salmon instead as *"esox"* or *"isox"*, from the proto-Celtic *"*esoxs"* (Andrews 1955). Interestingly, this word still survives in the world of fish nomenclature, both in the Modern Welsh word for salmon *"eog"* and as the scientific name for another large prestige fish– *Esox lucius*, or the Northern pike. There is a much more clear etymological history for the Germanic and Slavic words for these fish, seen in forms like "lachs", "lax" and "losos"– which can be traced to the Proto-Indo-European reconstruction *"*laḱs-"* (D. Adams 1985; Mallory 2021). This direct lineage spawned a controversial– and likely white supremacist– theory (*lachsargument*) about the Indo-European homeland being centered in northern Europe (Diebold 1976; Mallory 2021; Thieme 1954). This now-disproven argument was based on the existence of a word for Atlantic salmon, a species which is endemic to the North Atlantic and Baltic, but not to the Pontic-Caspian steppe– the location with the most linguistic, genetic, and archaeological evidence for the Indo-European homeland (Mallory 2021), but ultimately refers to the "wrong" fish. The true irony here is that, while nearly all modern derivations of the reconstructed PIE word refer exclusively to Atlantic salmon, it is highly likely that *"*laḱs-"* and it's cognates actually referred to a morph or subspecies of trout, such as the Caspian trout (*Salmo caspius* or *Salmo trutta caspius*) (D. C. Adams, Rohlf, and Slice 2013; Mallory 2021). Most forms of trout in classical and medieval times were derived from the Latin *"trūcta"*, (likely borrowed from Ancient Greek *"trktēs"* or "nibbler" (Andrews 1955)), resulting in both medieval and modern forms like "trutta", "truite", "trught", "trouhte", etc. There is one alternate form, seen in the modern German "forelle" and Dutch "forel", which actually goes back to the Proto-Germanic *"*furhnō"*, which is likely related to the Proto-Indo-European root *"*perḱ-"* meaning "speckled"– referring, of course, to the spotted patterns found on most trout species, but, as with the salmon term *"*esoxs"*, which survives today in the common and scientific names of other fish, e.g. perch (Kroonen 2013).

These etymological trails through deep time all lead to the two modern English forms of reference for these

fish – salmon and trout. When thinking about these species at the beginning of this thesis, I was working within a strict binary of assumptions– salmon were predominantly migratory ocean-going fish and trout were freshwater. I was aware, perhaps like the average medieval consumer may have been, that there were some salmon which stayed in rivers or lakes, but for the most part these definitions were pretty rigid. As the results of this thesis have unfolded, I have begun to wonder whether the concept of "salmon" and "trout" might have been more fluid in the broadly Medieval Period than we think of the fish now. After all, it's clear that fish of good quality and size could be from either species and one of many different ecotypes. In the modern era we generally separate the fish based mostly on genetics and phenotypic classification, but to the average person much of this detail is superfluous. To the non-specialized eye (both modern and medieval) a silvery fish with fatty pink-red flesh, which travels out to the ocean and returns again to the river, undergoes a physical appearance change, and grows to extraordinary size is a salmon. Similarly, a fish which has a similar body shape and some vaguely similar coloring, but remains in a river or lake, grows to a medium size, and is a fierce fighter when caught on a line is a trout. Contemporary imagery of salmon in Western society bring to mind the ubiquity of farmed fish in grocery stores, dining on sashimi and poke bowls, travelling to remote rivers to battle the elements and prove yourself as a fisher, and watching live-streams of Alaskan bears munching on salmon roe. The average person may not know that Pacific and Atlantic salmon are from two different genera, but they will recognize their importance in a number of ways. Contemporary imagery of trout is a little less clear-cut, and the fish are usually coupled with salmon and discussed in terms of sport fishing or unusual recipes to try. Thinking historically, salmon conjure images of kings and feasts, while trout are perhaps not thought of at all. That being said, however neat this interpretation of "salmon = prestige, migratory" and "trout = common, stationary", relegating these species to binary categories is supporting centuries-old stereotypes about the "Dark Ages" and Medieval Period as a time of unspecific language, unskilled labor, and apathy for the natural world. After all, the vernacular and formal dialects of Latin used across medieval Europe, as well as local languages like Old French, Norse, English, and Dutch, all contained a variety of terms attested in documentary and literary records that referred to migratory salmon, lake salmon, sea trout, lake trout, and sea trout (see Sections 2.2 and 2.3). In addition to the variety of words and phrases used to describe the fish, there is also the question of how individuals in different social groups interacted with and conceived of salmon and trout. Looking at these interactions through an ethnoichthyological lens (Mahugnon Benjamin Hounkanrin et al. 2022) can help interrogate how three distinct groups saw salmon and trout– fishers, common consumers, and control classes.

It's clear that fishers themselves had a high degree of knowledge about sea trout, salmon and trout– along with the many other fish commonly caught during the Medieval Period. Small-scale subsistence fisheries relying on locally available species characterized the world of Early Medieval fishing in northwestern Europe (Barrett, Locker, and Roberts 2004a,b; R. Hoffmann 2000; R. C. Hoffmann 2023). Early subsistence fishers, supplementing their own harvests or livestock with available game, contributed to the institutional knowledge that would lead to the rise in specialist or so-called "artisan" fishers, many of whom were contracted via indenture or feudal obligation to local landowners to supply fish for households and market alike (R. Hoffmann 2000). Throughout the Early and High Medieval Period there is direct evidence for members of the various ruling classes, from Charlemagne (r. 768-814 CE) to Simon de Montfort - Duke of Leicester (1256), requiring and expecting to have skilled fishers on their private estates in order to supply them with food and surplus fish (R. Hoffmann 2000). Fishers, especially those targeting migratory species like salmon, needed to have the ecological knowledge to successfully capture fish in the right environment, season, and using the most efficient techniques (R. Hoffmann 2000). Additionally, as the growth of commercial fisheries expanded after the 11th-century marine fishing intensification, fishers and those who processed and sold fish on the market would need to properly represent their catch. As

salmon were consistently valued higher than sea trout or freshwater trout (see Section 2.3), precise identification of fish was key.

If the fish caught were destined for a marketplace like early trading emporia (e.g. Johan van Oldenbarneveltlaan or ASR 9 Posthuset sites) or urban multi-use sites (e.g. Coppergate)– the next stage of salmon/trout-interactions involved direct consumers. These may have been skilled laborers, artisans, servants, or any number of social and class identities that emerged during the medieval European urban revolution, where populations exploded, cities expanded and more and more people demanded more and more fish (R. Hoffmann 2000; R. C. Hoffmann 2023; Moore 2000). Questions of what was called salmon, sea trout, and trout at a medieval market are difficult to assess as little to no records exist outside of tax documents (see Section 2.2). This returns us to the question of whether the average consumer would know the difference between a migratory sea trout or salmon when presented in a whole state, and even freshwater trout may be confused for either of the two ecotypes when presented in fillets or otherwise processed. Hoffmann (2000) cites an Early Medieval preference for whole fresh fish of all kinds, rather than those preserved by salt, drying or oil, and he lists associations with poverty and ill-health as possible reasons for the overall resistance to buying preserved fish during these periods (R. Hoffmann 2000; R. C. Hoffmann 2023). It may be the case that, especially with regard to fish of the various *Salmo* sp. ecotypes, consumers were initially resistant to purchasing fish that had been filleted, processed, salted, and barrelled because once altered from their whole state and adulterated with preserving agents, it becomes increasingly difficult to tell salmon, sea trout and freshwater trout apart. All three fish have relatively high fat contents, firm-medium textured flesh, which varies from light pink to deep red depending on the individual's diet and uptake of the carotenid astaxanthin (Schmeisser et al. 2021). After all, wanting to be certain about what exactly you're getting when you purchase a fish is not a foreign concept even in today's globalized supply chain and supermarkets– fish fraud runs rampant, and genetic and biomolecular methods applied in archaeology have increasingly been used to verify the species of commercially sold fish in recent years (Cawthorn, Baillie, and Mariani 2018; Crego-Prieto et al. 2012; Deconinck et al. 2020; Dierickx, Presslee, and Harvey 2023).

The final group were members of various control classes, including rulers, nobility/landowners, and ecclesiastical institutions. They were the recipients of many of the earliest catches of salmon, sea trout and other fish sourced by specialist fishers, and even as the medieval urban revolution commenced and direct consumerism was on the rise these groups still received a large amount of fish (R. Hoffmann 2000; R. C. Hoffmann 2023). This was especially true for high value fish like salmon, and the nobility and ecclesiastical institutions likely conceived of these fish as part of a complex system of control where they conveyed not only direct sources of income and food, but also prestige and favor (R. Hoffmann 2000; R. C. Hoffmann 2005, 2023). The importance of salmon is evident in literary and artistic records, of course (see Sections 2.3 and 2.4), but is particularly visible in the exhaustive documentary records of salmon as key parts of trade, taxes, and gift exchanges.

6.3 Salmon in the Historic Archive

6.3.1 Documentary Records

The majority of the literate population in Early and High Medieval Europe were members of religious institutions, royal courts, or specialised scribes of some kind (Houston 2002), so it is no surprise that the majority of written documents referring to salmon, sea trout, and trout are restricted to ecclesiastical, high status, and mercantile settings. At least one publication is available which reviews the pre-industrial tax and purchase records of fish products by institutions within these settings, but it is geographically restricted to North Northumber-

land (Osler and Porteous 2010). In order to gain a slightly better understanding of the breadth of documentary records available which specifically deal with *Salmo* sp. fishes, a very preliminary review (See Appendix D) of seven publications which contain English tax, purchase, and gift records from Durham, Leicester, London, Lynn, Southampton, Torksey and Winchester was conducted (Bateson 1899, 1901; Fowler 1898, 1899, 1901; Gras 1918). In total, 107 entries specifically discussing *Salmo* sp. fishes were recorded, ranging from the year 1228-1524. The parameters used for recording an entry were based around whether there was an associated price, whether a cost-per-unit or tax fee, and whether the cost was only for the *Salmo* sp. fish and not part of a larger list of purchases or goods. An additional 36 entries were recorded of other fish and their associated prices and/or fees from the same periods, in order to served as a direct comparison and add more context for observed changes in *Salmo* sp. prices. These fish included herring, stockfish (mainly cod), eels, lampreys, and turbot, among others, and, as with the *Salmo* sp. fish, their manner of preparation and unit of sale was recorded as well.

The vast majority of records are for salmon of some kind, with a wide variety of recorded spellings and preparations listed (Table 1), included salted, calvered (dressed with vinegar, oil and spices), and stopped (stuffed) salmon. Very few records of trout were made, and when they do appear they are generally grouped together with salmon, with other freshwater fish, or with multiple preparation forms as in the case of the 1442 entry on the Durham *Rotuli Celerariorum* (cellarer's rolls) for "trutes sals et trutes rec. [recentibus, i.e. freshly caught]" (Fowler 1898). In all sources consulted only a single reference to sea trout was found– a 1388 entry in the cellarer's rolls of Durham Abbey recording a purchase of five "Salmon Troutys" purchased for 12 pence (approx.£41.98 GBP in 2023). All entries for units of salmon purchased, gifted or otherwise received are either from the account rolls of the Abbey of Durham dating between 1299-1524, or from the records of the municipal corporation of the city of Leicester, dating between 1264-1379. The remaining entries refer to taxes and customs levied on salmon shipments, recorded between 1421-1467 and referring to duties taken in Torksey, Lynn, London, Southampton and Winchester during these periods. These duties are generally reported in terms of the total value for an entire shipment of mixed goods, which would then have the petty custom applied (Gras 1918), but there are several instances where a shipment is entirely of salmon. For example, the merchant Frowlyk Clevyghous brought a shipment of 12 barrels (one *last*) of salmon to London in 1421 which was valued at £8, roughly equivalent to £7,172.25 in 2023. By the mid-15th century most entries for the ports of London, Lynn and Southampton deal in terms of barrels of salmon, likely preserved in salt or oil, and the average price-per-barrel (in 2023 GBP) was approximately £542.08 in 1421, £671.29 in 1444 and £447.79 in 1467 (Gras 1918).

Word or Phrase	Translation	No. of Entries
Salmon, salmon., salmone, salmonibus, salmonis, samowne	Atlantic salmon (singular and plural)	82
Poudred salmon., salmon. poudred, salmon. poudrt., salmonibus pulv'	Poudred or poudré salmon (lightly dusted with salt)	7
Salmon. calver	Calvered salmon (dressed with oil, vinegar and spices)	3
Salmon sals., salmonibus salsis, salmonum salt, salso salmon.	Salted salmon	6
Salmon. sals. et pouder'	Salted and poudré salmon	1
Salmon. stopp., Stopedsalmon	Stopped salmon (stuffed)	3
Seyme salmon. salt	Seyme or seym salmon, salted (packed in lard)	1
Salmonibus recentibus	Freshly caught salmon	1
Salmon. Troutys	Salmon-trouts, or sea trout	1
Trutes sals et trutes rec.	Salted and freshly caught trout	1
Other Significant Phrases	**Translation**	
Quilibet salmon	all salmon - referring to a tax or levy on all salmon entering a port	NA
Salmon-fee	Refers to a fee first paid to the Lord Mayor of Leicester for his services in 1334, initially equivalent to 1 mark (160 pence). Separate from payments for his dinner or other expenses.	NA

TABLE 6.1: Glossary of words and phrases used to refer to *Salmo* sp. fishes in the sources consulted

The fact that these Late Medieval records deal primarily in collective units of processed salmon rather than individual fish is indicative of the industry-wide expansion of fisheries beginning in the 11th-century that eventually led to hundreds and thousands of barrels of herring and stockfish being shipped across the Baltic and North Seas to and from England by merchants from as far away as Talinn and as close by as Calais (Kleineke 2006; Orton et al. 2011). However, as observed by Hoffmann (2000; 2023), the preference during the earlier Medieval Period was for either whole fresh fish or single preserved fish, and this is reflected in the earlier data from 1264-1449 CE represented below in Figure 1.

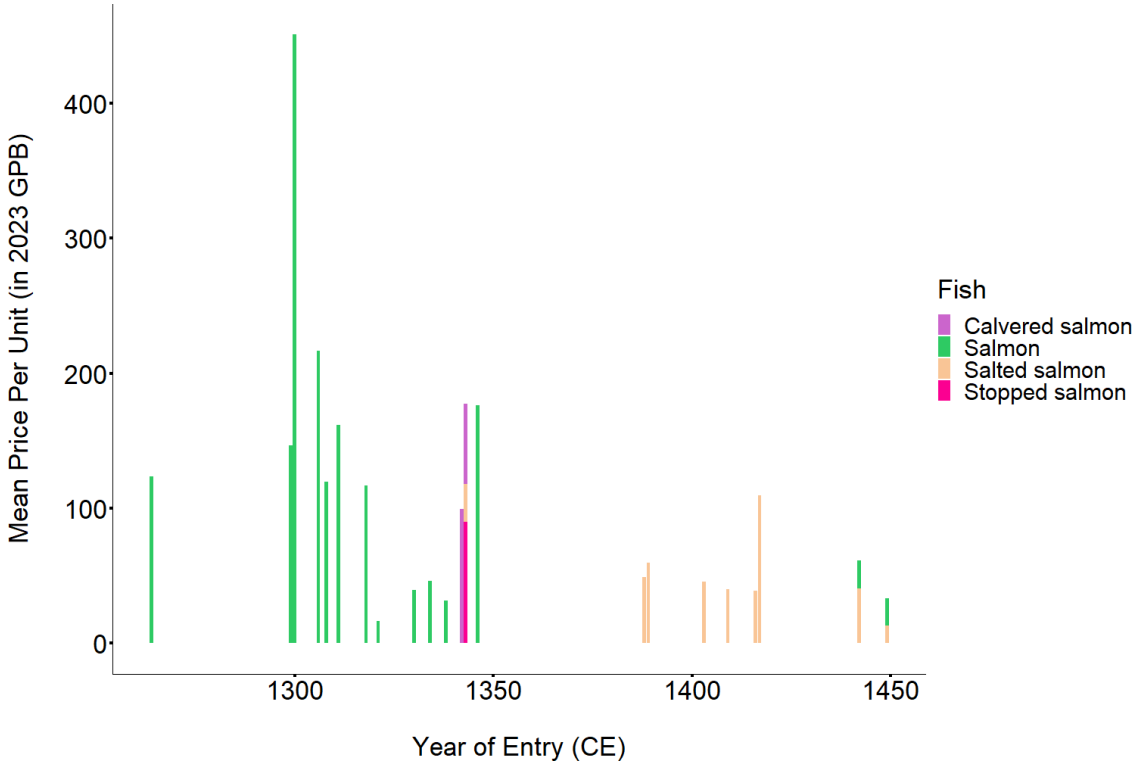


FIGURE 6.1: Records of whole salmon prepared and sold in a variety of ways between the years of 1264 to 1449 CE, with price per unit calculated and presented in terms of value in 2023 sterling (GBP)

The data briefly explored here come from the Corporation of Leicester records, spanning 1264-1346 CE, and the Account Rolls of the Abbey of Durham, spanning 1308-1524 CE (Bateson 1899, 1901; Fowler 1898, 1899, 1901). Price-per-unit of whole individual salmon were calculated based on the reported values within the records and converted to 2023 GBP using tools produced by the National Archives and Bank of England to provide a rough estimate of modern day purchasing power (Archives 2017; England 2023). Mean price-per-units were calculated based on number of fish and entries for each given year, and the data were further divided into four subgroups based on preparation– calvered salmon, salted salmon, stopped salmon and, of course, fresh whole salmon. The overwhelming majority of records indicating the purchase, sale or gifting of fresh whole salmon can be found pre-1350 CE, and all processed forms of salmon only begin to occur in 1342 CE. This is not to say that salted, calvered, or stopped salmon could not be found prior to this date– in fact both the Leicester and Durham sources have a few mentions of each type in earlier periods (Bateson 1899, 1901; Fowler 1898, 1899, 1901). However, in terms of sheer

numbers it seems that this preliminary data support Hoffman's assertion that whole fish was preferred in the earlier Medieval periods, and it's likely that a more in-depth review would confirm the extent of this preference. In addition to the apparent preference for whole salmon earlier, the average cost-per-unit of these fish is far higher– at £137.16 per fish in the 1264-1350 period compared to £56.14 per salted/calvered/stopped fish in the 1342-1449 period.

The question remains, why did the preference for whole salmon appear to die out as the 14th-century progressed? Was it simply a question of changing tastes, less prestige afforded to salmon, or something else? It's likely that a combination of factors influenced this shift, chief among them declines in local salmon populations which led English markets to outsource salmon from further and further afield. Fresh salmon could only be transported so far in the Medieval Period, and must be either very recently caught and quickly transported– as in the 13th-century 150km "fast-horse relays" attested to in France– or shipped in a purpose-build vessel with circulating water– like the Dutch "waterschip" (R. C. Hoffmann 2023). As the Medieval Period progressed, trade expanded, and demand for salmon continued it may have been far easier to salt, calver, or stopp a single fish and/or barrel of salmon and import it than to source a whole fish from local waters. Concerns over local scarcity of salmon are reflected in proto-conservation efforts made by both royal and corporate interests, with evidence for bans on taking salmon at certain times, restrictions on particular equipment, and permit systems being instituted in medieval Scotland, France, the Netherlands, Germany, Spain and England (R. Hoffmann 2000; R. C. Hoffmann 2015, 2023). When these factors are combined with the increased availability of fish like cod and herring, which could be easily accessed by all levels of society as the Medieval Period progressed, it's easy to see how this would create an economic and social environment where preserved imported salmon was cheaper and more accessible across classes, while whole fish remained the "ubiquitous features of conspicuous consumption" in elite and ecclesiastical settings (see Section 3.3).

6.3.2 Literary References

An exhaustive analysis of all literary references to salmon, trout and sea trout spanning the medieval to Early Modern period is not possible, nor practical, given the limitations of translations, transcriptions, and manuscript availability. That being said, four main categories of literary sources discussing and/or mentioning these fish can be identified – Monastic and/or lay texts and chronicles, Norse sagas and poetry, cookery and household management books, and fishing guidebooks/bestiaries. Table 2 lists the general characteristics of sources consulted in this thesis, which include references from contemporary writers in England, Scotland, wider Scandinavia, France, Germany, Belgium, the Netherlands and Denmark written or recorded between c. 990 and 1663 CE.

Text Name	Author	Date	Text Type	Description of Entries	Location
Aelfric's Colloquy	Aelfric of Eynsham	c. 990	Monastic teaching tool	Salmon - discussion of sea fishing	England
Lausavisur 1	Sigvatr Þórðarson	c. 995-1045	Skaldic stanza	Trout - fishing activity	
L'Estoire des Engleis	Geffrei Gaimar	c. 1140	History	Salmon - fishing activity and prestige association	England
Topographia Hibernica	Giraldus Cambrensis	c. 1188	History, bestiary	Salmon and sea trout - fish habitat and behavior	Ireland
Heimskringla	Snorri Sturluson	c. 1230	Saga	Salmon - geographic description	Scandinavia
Orkneyinga Saga	Anonymous	c. 1240	Saga	Sea trout or trout - Aurridafjord place name	Orkney
Promptory of the Little Clergy	Anonymous	c. 1244	Dictionary	Salmon - preserving and preparations	England
De rerum natura	Thomas de Cantimpré	c. 1244	Natural history, bestiary	Salmon and trout - fish habitat and behavior	Flanders
Harmsól	Gamli Kanóki	c. 1250-1300	Skaldic verse	Salmon - kenning	Iceland
Fiska Heiti	Anonymous	c. 1250-1325	Catalogue of poetic terms	Salmon, sea trout, male salmon, trout	Scandinavia
Ragnars saga loðbrókar	Anonymous	c. 1250-1325	Saga	Sea-trout - Kenning	Scandinavia
Volsunga Saga	Anonymous	13th century	Saga	Salmon - mythic tale	Iceland
Brennu-Njáls Saga	Anonymous	13th century	Saga	Salmon - fishing activity	Iceland
Egil's Saga	Anonymous	13th century	Saga	Salmon - fishing activity and geography	Iceland
Gísla saga Súrssonar	Anonymous	13th century	Saga	Salmon - fishing activity	Iceland
Laxdale saga	Anonymous	13th century	Saga	Salmon - list of fish	Iceland
Le Viandier de Taillevent	Guillaume Tirel	c. 1300	Cookery book	Salmon and trout - one entry each	France
De naturen bloeme	Jacob van Maerlant	c. 1340	Natural history, bestiary	Salmon - fish habitat and behavior	
Ein buch von guter speise	Konig vom Oldenwald	c. 1350	Cookery book	Salmon and trout - one entry	Germany
The treatyse of fysshynge wyth an angle	Juliana Berners	c. 1388	Fishing guide	Salmon and trout - fishing activity and methods	England
The Forme of Curye	Anonymous	c. 1390	Cookery book	Salmon and trout - one entry each	England
Le Ménagier de Paris	Anonymous	c. 1393	Household management guide	Salmon, sea trout, and trout - seasons and menus	France
Liber Cure Cocorum	Anonymous	c. 1430	Cookery book	Salt salmon, salmon, trout - Fast day menu	England
A noble boke off cookry	Anonymous	c. 1467	Cookery book	Salmon and trout - multiple entries	England
Wel ende edelike spijse	Anonymous	c. 1450-1500	Cookery book	Salmon - three entries	Netherlands
Book of Kervynge	Wynken de Worde	1508	Terminology pamphlet	Salmon and trout - butchery	England
Een notabel boecxken van cokeryen	Anonymous	c. 1510	Cookery book	Salmon - one entry	Netherlands
Visboek	Adriaen Coenen	c. 1580	Fish bestiary	Salmon and trout - fishing activity, behavior, habitat	
The Good Huswife's Handmaide for the Kitchin	Anonymous	1594/97	Cookery book	Salmon - three entries	England
Koge Bog	Anonymous	1616	Cookery book	Salmon - four entries, including curing	Denmark
The Compleat Angler	Izaak Walton	1653	Fishing guide	Salmon and trout - fishing activity, behavior, habitat	

The earliest identified non-Classical text which discusses salmon is the Colloquy of Aelfric of Eynsham, a prolific 10th-century abbot and chronicler operating mostly out of Dorset (Harris 2003). This work is not a bestiary or history, but a teaching tool developed to teach incoming monastic students, with mock discussions between specialist laborers and artisans printed in both Latin and Old English. The text includes a conversation with a fisher,

who is asked what fish they catch and in which environments, which contains an explicit reference to salmon as marine fish, grouped with herring, sturgeon, flatfish dolphins, and crustaceans (Garmonsway 1938; Harris 2003). Aelfric was certainly not an expert on fishing, and specialist fishers were likely not consulted on their experiences, but this brief mention does provide some information about monastic knowledge about salmon habitat and fishing. Aelfric only refers to salmon within the Colloquy text, but later monastic historian Giraldus Cambrensis, writing c. 1188 CE about Ireland, makes explicit references to multiple separate *Salmonidae* fishes– salmon, freshwater trout, sea trout, and what is likely some kind of whitefish in the genus *Coregonus* (Cambrensis 2000). This text, with it's descriptions of fish behavior and habitat is a precursor to one of the most significant medieval natural histories and bestiaries, *De natura rerurm*, written c. 1244 CE by Thomas de Cantimpré, a Flemish Dominican friar (Cantimpré 1250), which greatly informed a later (c. 1270 CE) commissioned natural history by Jacob van Maerlant, *De naturen bloeme* (Maerlant 1270). The natural history text by de Cantimpré discusses behavior, habitat, size and popular conceptions of salmon as well as freshwater trout– which he characterizes a similar in shape to salmon but with less flavor and more fragile flesh– and has an extensive bestiary with some of the earliest illustrations of both fish (see Section 2.2.3) (Cantimpré 1250). Earlier than both the *De natura rerum* and *De naturen bloeme*, the *Estoire des Engleis* written by Geoffrey Gaimar c. 1140 CE contains an early reproduction of the romantic story of Havelok the Dane, and within this is not only an early description of fishing for salmon with a net by the Anglo-Scandinavian Havelok, but also the earliest reference to salmon as a prestige fish associated with the highest classes;

> "...they were served the best food that king or emperor would eat: cranes, swans, venison, salmon, lampreys and sturgeon, and plenty of fine wine." (Geffrei 1889)

The final monastic text which provides information on salmon differs from the others in that it is not a natural history or chronicle, but a Middle English-Latin dictionary attributed to Geoffrey the Grammarian and first published around 1440 CE, but potentially based on much earlier texts (Way 1843). It's here that we find context for many of the preparations of salmon mentioned in documentary sources (Section 2.2.2), including *"calvur"* salmon, a *"cawdelle"* of salmon, and the butchery term a *"ioll"*, or jowl/cheek, of salmon (Way 1843).

The second major source of references to salmon, trout and sea trout can be found in the broadly Scandinavian corpus of skaldic poetry and sagas, which generally cover historical and mythological subjects related to the expansion of Norse power across the North Atlantic. The examples listed in Table 2 all date to the 13th century, with the exception of a fragmentary stanza (*lausavísur*) attributed to the skald Sigvatr Þórðarson, c. 995-1045 CE (Fulk 2012). This short poetic stanza offers the oldest example of a Norse description of fishing for trout in estuarine areas using a line and hook (Fulk 2012). Interestingly, this stanza specifically uses the word *"aurriða"*, which is translated as referring to freshwater trout in the 12th-century *Fiska heiti*, which contains a standardized list of poetic terms for fish which also includes salmon (*Lax*), sea-trout (*birtingr*), and male salmon *hœingr* (Gade and Marold 2017). Whether these terms were strictly defined throughout the period, or used only in poetic contexts and not common speech, is unknown, and other translators of Norse skaldic poetry and sagas translate the same root word, *"aurriða"* as sea trout rather than freshwater trout (Anderson 1873; Anonymous 2018; Fulk 2012). These translations make more sense given the estuarine context described in the Þórðarson stanza and the local fish biogeography of Orkney, the focus of the c. 1240 CE *Orkneyinga Saga*, which describes the *Aurriðafjörd*, or sea trout firth/fjord, being visible from the the site of Orfjara, aka Earl's Bu (Anderson 1873; Anonymous 2018; Fulk 2012). Other Norse sources make only passing references to salmon and trout, mostly as kennings, or stock metaphors, for the sea or ocean and descriptions of desirable geographic locations (Attwood 2007; Green 1893; Press 1889; Ross 2017; Sturlason 1225). The remainder of the Norse sources contain brief references to fishing activity, both mythological and historical, as well as the tools used to catch salmon, including nets, spears, hooks

and lines (Anonymous 1888; G. DaSent 1866; G. W. DaSent 1861; Fulk 2012).

The cookery and household management books (Table 2) provide a varied and interesting look at the culinary uses of salmon, sea trout and trout throughout the High Medieval to Early Modern period, c. 1300-1616 CE. Though the books recorded or printed post-1500 cannot necessarily be considered representations of medieval cookery, they can be viewed as records of recipes which were likely in use during earlier periods, and terms and preparations mentioned in these English, Danish and Dutch texts do appear in earlier ones– like references to a *"chynne"* of salmon, salmon cooked in pastry, and instructions for baking, boiling and roasting salmon and trout (Anonymous 1616; Muusers 2002; Wallace 1594; Worde 1508). The oldest transcribed cookery book which mentions salmon and trout is the *"Viandier"* de Taillevent, likely first recorded c. 1300 CE and attributed to Guillaume Tirel (Tirel 1892). Fairly simplistic preparations of trout and salmon are presented here, with instructions for boiling, baking and roasting both fish, and served with either a heavily spiced Cameline or Yellow Pepper sauce (Tirel 1892). The use of ginger, cinnamon, vinegar, pepper, and saffron to spice salmon and trout is repeated throughout the cookery books presented here, including in the German *"Buch von guter spiese"* (c. 1350), the English *"Noble boke off cookry* (c. 1467), the Dutch *"Notabel boecxken van cokeryen"* (c. 1510), English *"Good Huswife's Handmaide for the Kitchin"* (c. 1594), and Danish *"Koge Bog"* (c. 1616). In fact, the only recipe that does not mention any of these is the c. 1390 *"Forme of Curye"*, which instructs the maker of a "Vyande Cypre of Samoun" (Cypriot Style Salmon), to season only with salt, sugar, and color with alkanet to give the resulting minced salmon and almond dish a red hue (Hieatt and Butler 1985). Other French, Danish, and English texts from the Late Medieval-Early Modern period discuss not only the preparation of salmon and trout, but the best seasons to purchase fish, examples of which fish to serve on fast days, and methods for preservation (Anonymous 1616; Hieatt and Butler 1985; Morris 1832; *The Goodman of Paris [Le Menagier de Paris]* 1928).

The final category of Late Medieval-Early Modern texts is those which are explicitly focused on describing fishing methods and categorizing fish– two from England and one from the Netherlands. The oldest example of a fishing "guidebook", and only text attributed to a woman, is the *"The treatyse of fysshnge wyth an angle"* possibly first recorded by Dame Juliana Berners– a prioress and chronicler on hawking, hunting, heraldry and fishing– sometime after 1388 CE (Woodward and Burnett 1892). This guidebook to fishing with an angle is focused primarily on freshwater fishing, describing methods of fly fishing and line fishing for trout and salmon in riverine environments (Woodward and Burnett 1892). Interestingly the author of this text, whether its Dame Juliana Berners or some other contemporary, takes pains to mention that salmon can be caught in fresh water, but that it is difficult due to their preference for the deepest parts of the river and reluctance to bite while spawning (Woodward and Burnett 1892). This early guidebook on fishing certainly influenced Izaak Walton's 1653 text *"The compleat angler"*, which contains extremely comprehensive descriptions of habitat, behavior, appearance, season, fishing methods and life span for salmon, freshwater trout, and sea trout (Walton 1653). Finally, a slightly earlier text is the *"Vis boek"*, completed c. 1580 CE by Dutch naturalist and fishmonger Adriaen Coenen (Coenen 1580). This text is primarily interesting for it's exceptional illustrations– there is no accessible transcription or translation of the manuscripts, however it's clear that there are entries describing salmon and sea trout, as well as an illustration depicting the kype development of male spawning salmon (see Section 2.2.3 below) (Coenen 1580).

6.3.3 Artistic Representations

The final point of discussion about depictions of salmon, trout and sea trout in Medieval and Early Eodern art concerns artistic representations, which includes a massive variety of symbolic carvings, illustrations, sigils and heraldry, and still life paintings. As with literary references it is impossible, and impractical, to catalogue ev-

ery visual reference to these fish from the European Medieval Period, but a cursory review of their appearance throughout the period is helpful in understanding their importance.

The earliest visual depictions of salmon-like fish during the period can be found on Pictish monumental stele, or symbol stones, from the 5th-9th centuries CE– over 200 of these can be found across Scotland from Anworth on the Solway Firth to Shetland (Alcock 1988; Noble, Goldberg, and Hamilton 2018; Thomas 1963). Fish are a repeated symbol motif that at least a dozen of these stones display, most of them interpreted as salmon or trout based on their overall body shape and physical features like an adipose fin (Gordon 1964). There has been continuous debate over the meaning behind these symbol meanings, with historians, linguists and archaeologists interpreting them as everything from markers of salmon fishing rights and place/family names, to mythological stories and even fringe theories of a language system (Alcock 1988; Gordon 1964; Noble, Goldberg, and Hamilton 2018; Samson 1992). What is interesting is that isotopic evidence from the Pictish human burials does not suggest a high reliance on marine protein like fish, despite the high incidence of salmon symbolism in their art (Curtis-Summers 2016). Nevertheless, numerous stones, including those found at Gairloch, Kintore, Golspie and Dunrobin (Figure 2), depict salmon or trout– in fact, the last of these specifically shows a male spawning salmon with it's kype (Unknown 2023a,b,c,d).

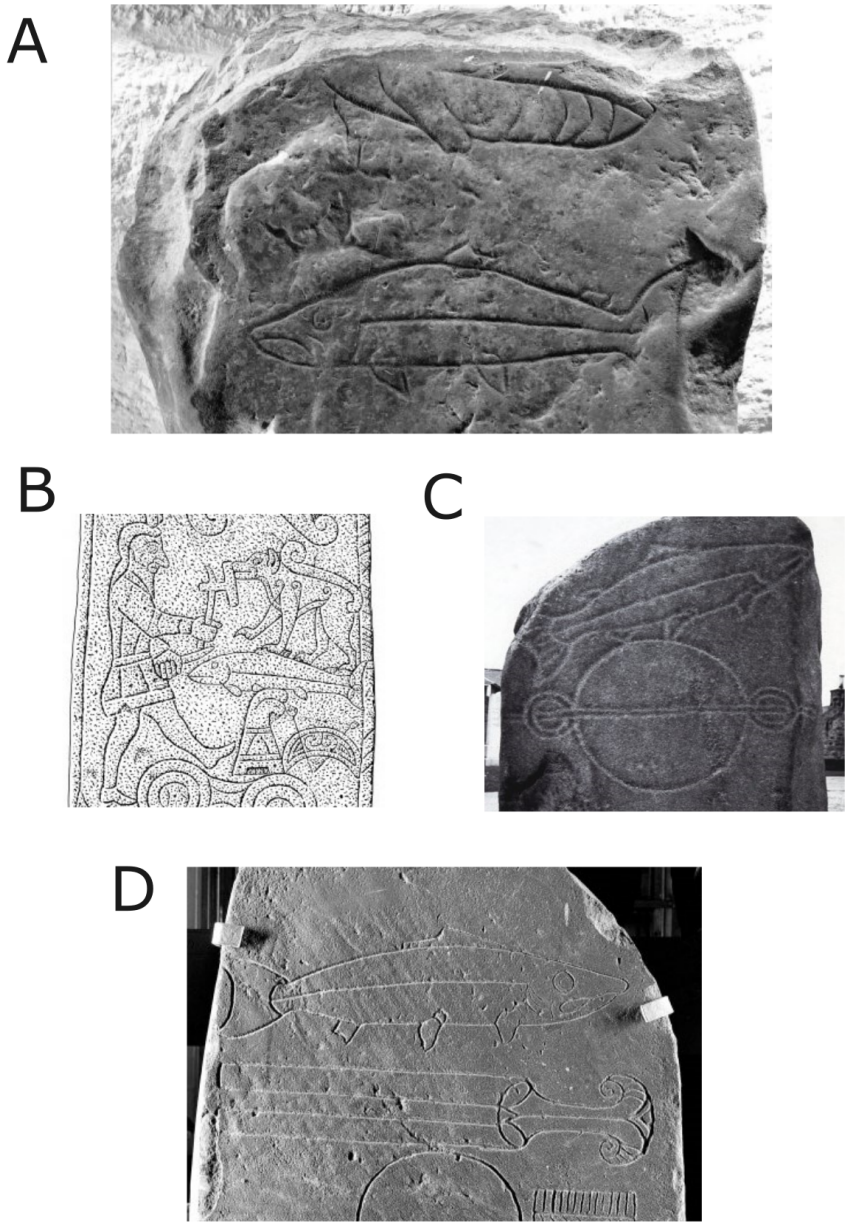


FIGURE 6.2: Four pictish monumental stele depicting salmon-like fishes. A. The Gairloch Stone (detail), showing a salmon below what is likely an eagle, another common animal motif, B. The Golspie Stone (illustration detail), showing a salmon leaping over water, C. The Kintore Stone (detail), and D. The Dunrobin Stone (detail), showing a male salmon with it's kype positioned over a sword. Photos courtesy of Canmore, the National Record of the Historic Environment managed by Historic Environnment Scotland.

Illustrations in bestiaries and natural history texts are the best source of salmon and trout depictions from the High-Late Medieval Period, and the previously discussed texts (Section 2.2.2) show these fish in several states. The *Topographia Hiberniae* provides the oldest of these, both likely produced c. 1188-1223 CE, and show a

salmon leaping with it's tail curled behind it (Figure 3C and 3D) (Cambrensis 2000). The next oldest illustrations come from a manuscript of Thomas de Cantimpré's *De natura rerum* dated to 1280 CE, which show a salmon and a trout, both with accompanying descriptions (Figure 3A and 3B) (Cantimpre 1280). The final three medieval illustrations are in versions of van Maerlant's *De naturen bloeme*, dated to c. 1300-1325, 1340-50, and 1450, all of which depict salmon (Maerlant 1300, 1340, 1450) (Figure 3E, 3F, and 3G).

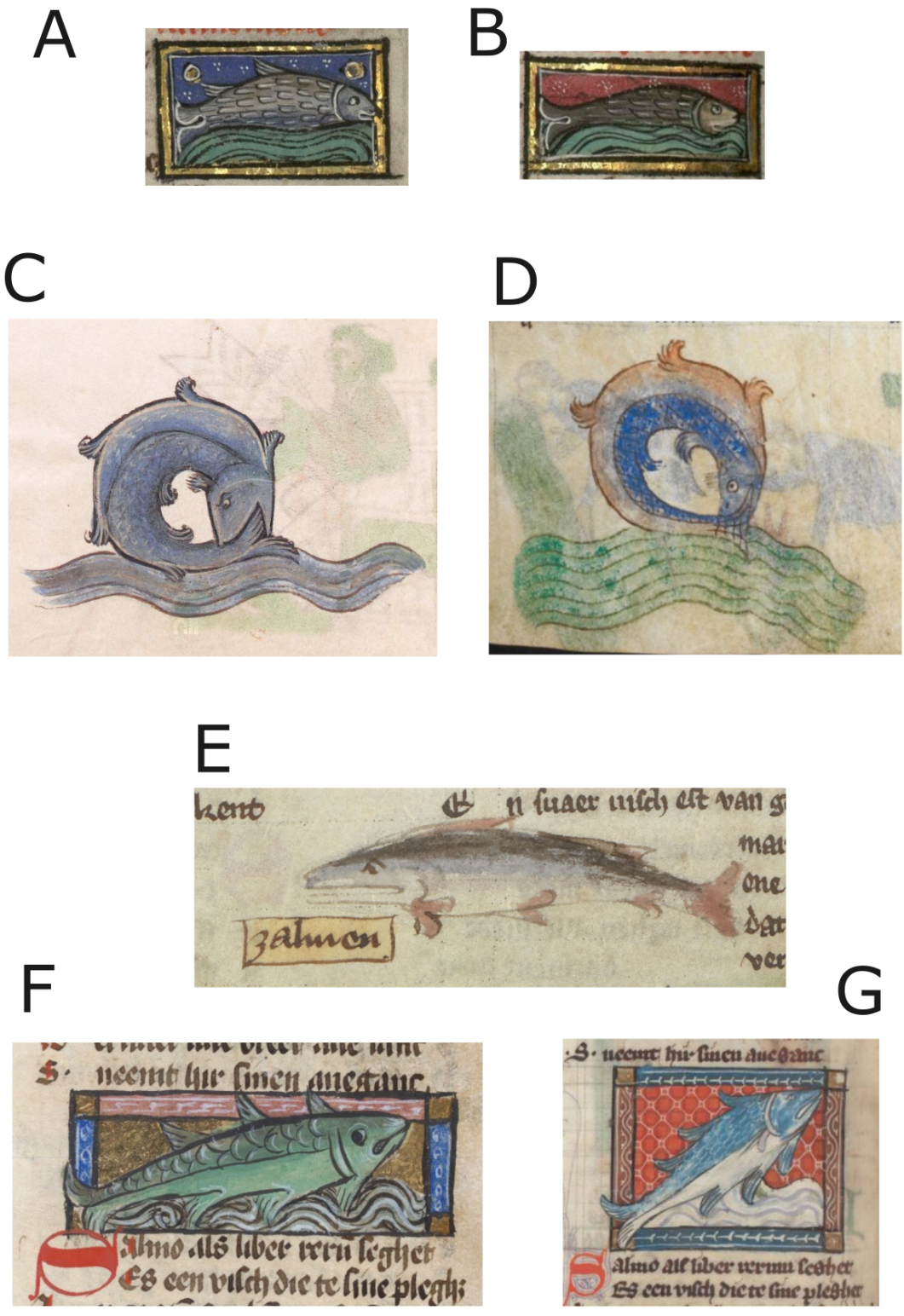


FIGURE 6.3: Seven medieval illustrations of salmon and trout found within manuscripts of *De natura rerum* (A and B), *Topographia Hiberniae* (C and D), and *De naturen bloeme* (E, F, and G). Images courtesy of the Bibliothèque municipale de Valenciennes, the Koninklijke Bibliotheek, and the British Library

The final series of textual illustrations are from Adriaen Coenen's *Vis boek*, and are far more detailed and accurate than the High-Late Medieval depictions seen in Figure 3, which is to be expected given its publication in 1580– a period when the naturalism and realism of proto-scientific and scientific drawings was intensifying in Western Europe (Smith 2006). The Coenen illustations are still hand-drawn with watercolours, in a style reminiscent of that seen in the latest *De naturen bloeme* manuscript from c. 1450 CE (Fig. 3E), with a heavier reliance on line drawing and ink shading than the other Medieval Period images. The *Vis boek* depicts a salmon (Figure 4A), a sea trout (Fig. 4B), a male spawning salmon with kype (Fig. 4C), as well as an illustration of fishers spearing and drying salmon on a river bank (Fig. 4D).

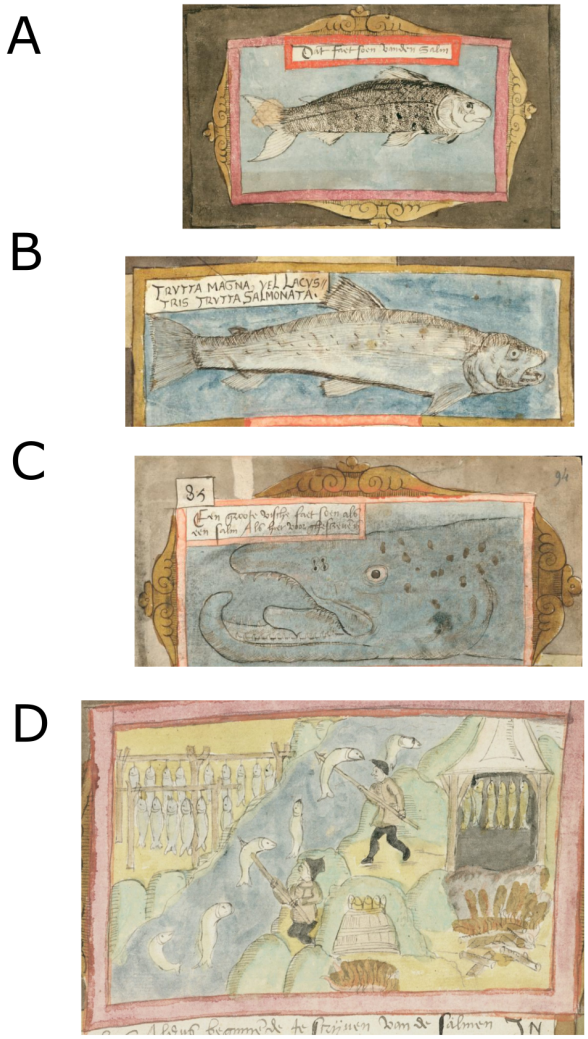


FIGURE 6.4: Four illustrations from Adriaen Coenen's *Vis boek*, published 1580 CE. Images courtesy of the Library of Congress.

Fish symbolism in Medieval and Early Modern heraldry was fairly extensively studied and recorded in the mid-19th to early 20th century, and salmon are a fairly common animal symbol used within the heraldry of west-

ern European towns and families (Fox-Davies 1909; Moule 1842; A. Wade 1912; W. C. Wade 1898; Woodward and Burnett 1892). Some of the most iconic uses of these fish in heraldry are connected with places and families which derive, or appear to derive, their name from the word "salmon" – the French historic houses of Salmon/Samoun, the English houses of Salmon/Salmond/Salmine, and the historic counties and principalities of Salm (and it's variations and derivatives) in Luxembourg, Belgium, Germany and France (Moule 1842). The earliest attestations of the salmon being used as the personal arms of an English branch of the Salmon family comes in the late 13th-early 14th century, associated with John Salmon the Prior of Ely (Moule 1842). The County of Salm, originally recorded in 1036 as a Lotharingian county, has had multiple variations on county and family arms, all of which have included at least one salmon throughout the years (Calmet 1725; Moule 1842). Interestingly, the County of Salm, and all it's subsequent derivatives, were not named for the Old German word "salm", meaning salmon, but for the River Salm, which has it's etymological roots from the Proto-Germanic and Proto-Celtic **salwa* meaning dirty or dark colored, and the association with the fish is in error (Graulich and Legros 1994). In the UK, the coats of arms of cities and towns closely associated with salmon rivers or commercial salmon fisheries very often have images of the fish in their historic and/or modern heraldry, including Kingston-upon-Thames, Peebles, Lanark, Bournemouth, and, perhaps most famously, the city of Glasgow (Moule 1842). The seals of the city and archbishopric of Glasgow (Figure 5) have included at least one salmon with a ring in it's mouth, referencing a miracle performed by the city's patron St. Kentigern, since at least 1484 (*Archbishop Blackadder's Seal* 2004; Moule 1842).



FIGURE 6.5: Seal of the first Archbishop of Glasgow, Richard Blackadder depicting the city of Glasgow's patron, St. Kentigern. A salmon (right) with a gold ring in it's mouth is held by St. Kentigern (left). Image source: Mitchell Library (GC 941.354 REN)

6.4 Conclusion

It is clear from the previous sections that *Salmo* sp fishes, especially the anadromous salmon, have been prominent in the linguistic, documentary, literary, and artistic records throughout the Medieval and into the Early Modern period. This, along with their presence at archaeological sites of many types, including monastic and high status settings, adds further credence to their reported importance as a "ubiquitous feature of conspicuous consumption" (R. C. Hoffmann 2023) during the Medieval Period. Changes in preferences for and cost of salmon and sea trout can be inferred from the preliminary analysis of documentary records presented in Section 3.1. Evidence for fishing methods and exploitation patterns of each of the ecotypes discussed here can be found within the literary examples discussed in Section 3.2, and the use of *Salmo* sp. fishes in both symbolic and representation art from the very earliest Medieval Period is further proof of their ubiquity in social, cultural and economic realms.

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Chapter 7

A Systematic Review of Ichthyoarchaeological *Salmo sp.* Identification Data from the Medieval North Sea

7.1 Abstract

This study uses a meta-analytical approach to investigate changes in exploitation of *Salmo* sp. fishes throughout the Medieval Period, observed via archaeologically recovered fish bone material from the North Sea basin. A review of published and unpublished archaeological fish bone data was undertaken to explore changes in presence and absence of fish from the genus *Salmo*, including the economically and culturally important Atlantic salmon (*Salmo salar* and brown/sea trout (*Salmo trutta*) species. Archaeological number of individual specimen (NISP) data from eight modern-day countries with access to the North Sea were included in this dataset of 1270 contexts from 410 archaeological sites. In order to understand more about both patterns of *Salmo* sp. exploitation by human groups and identification in the archaeological record, variables including taxonomic identification, site type, time period, report decade, and collection methods were investigated. Observations from this study support past archaeological research into an 11th-century CE "fish event horizon", with drastic increases in overall fish NISP and presence of *Salmo* sp. fishes seen during a c. 950-1200 CE period. In addition to the results of this meta-analysis, a review of identification methods for *Salmo* sp. fishes is presented, as well as a case study on complementary zooarchaeology by mass spectrometry (ZooMS) analysis. This ZooMS study represents the largest dataset of accurately identified medieval archaeological *Salmo salar* and *Salmo trutta* remains from Europe, and provides evidence for regionally-distinct patterns of *Salmo* sp. exploitation during the period.

7.2 Introduction

7.2.1 Research Aims

Fish of the *Salmo* genus, including migratory *Salmo salar* (Atlantic salmon) and both the migratory (sea trout) and freshwater (brown trout) ecotypes of *Salmo trutta*, have played various roles in human diet and culture across their combined range in Northwestern Europe for at least 40,000 years (Turrero, García-Vázquez, and Leaniz 2014). Remains of Atlantic salmon, and the closely related brown trout/sea trout (*Salmo trutta*), have been found in contexts varying from Magdalenian caves in Belgium and France, to 11th-century Benedictine monasteries and urban domestic rubbish from the 15th century Delft (Guillaud, Cornette, and Béarez 2016; Jorgensen 2015; Van Neer, Wouters, and Germonpré 2007). While both species are physically comparable, broadly fished and have a similar taste and texture, the brown trout, and its migratory "sea trout" ecotype, has never quite managed to capture the imagination of human cultures like the Atlantic salmon has. One of the oldest examples of Palaeolithic fish carvings can be found at Abri du Poisson, a roughly 25,000 year old depiction of a salmon-like fish (Peyrony 1932; Zotkina and Cleyet-Merle 2017). Salmon and salmon-like fish appear in Pictish symbol stones, medieval illuminated manuscripts, and historic and modern heraldic imagery across Northwestern Europe (Cambrensis 2000; Cantimpré 1250; Siebmacher 1999; Wade 1898). While the Atlantic salmon never reached the widespread economic importance of marine fish like cod or herring, it's role was well established in various social, economic, and cultural contexts, including what is broadly referred to as the European Medieval Period, taken here to range from roughly 500-1500CE.

Literary and documentary sources discussing the use and management of Atlantic salmon and, to a lesser extent, sea trout, are found in legal statutes, tax records, work orders, financial accounts, cookery books, educational texts, and scientific treatises (e.g. J. H. Barrett and D. C. Orton 2016; Cambrensis 2000; Fowler 1898; Fulk 2012; Garmonsway 1938; Gras 1918; Hieatt and Butler 1985; Richard Hoffmann 2000; R. C. Hoffmann 2015, 2023; Maerlant 1270; C. Roberts 2007; Tirel 1892). Reviews of medieval fisheries report that declines in Atlantic salmon populations were noted by fishers, administrators and medieval scholars between the 8th to 14th centuries in

France, Belgium, the Netherlands, England, Germany and parts of Scotland (R. C. Hoffmann 2015; Lenders et al. 2016; C. Roberts 2007). These reported declines were addressed by legal regulations in some cases, like the example of a 1214CE Scottish statute enacted either by William I or Alexander II, addressing anthropogenic barriers to Salmon passage (R. C. Hoffmann 1996; C. Roberts 2007). Ample references to the preparation and culinary value of salmon and trout can be found in late-Medieval European cookery books and recipe records, with most coming from high-status environments like the court of England's Richard II or France's Charles V (Anonymous 1933; Hieatt and Butler 1985; Leone 1994; Tirel 1892). However, despite the apparent popularity and abundance of salmon and trout within the diet, cuisine, and economy of medieval NW Europe, the archaeological record does not, at first glance, appear to reflect the same abundance. Compared to other fish species exploited across the North Sea basin area, relatively few *Salmo* sp. bones are recovered from archaeological sites– even those sites with otherwise excellent bone preservation.

This preservation factor is further complicated by issues of differentiation between the species *Salmo salar* and *Salmo trutta*, which are so skeletally similar as to be indistinguishable in most cases. Additionally, while sea trout are genetically and proteomically identifiable as a migratory ecotype of *Salmo trutta*, they display physical and behavioral similarities to salmon. While all three ecotypes of importance are equally edible, there appears to have been a demonstrated preference for salmon and sea trout over freshwater brown trout in the Medieval Period – a trend which continues into modern times (EUMOFA, 2022; Watson, 2021). This preference is likely due to salmon and sea trout's higher fat and protein content, milder taste, and larger overall size. Accurate identification of fish species is key to understanding fishing choice, which may reflect abundance, socioeconomic status or relative fishery access. The choice of anadromous *Salmo* sp. fishes over freshwater-resident brown trout may shed insight into the relationship between medieval people of varying cultural affiliations and the so-called "King of [freshwater] Fish" (Watson 1996). In order to understand more about the importance of *Salmo* sp. fishes during this Medieval Period we have conducted a review of identification and taphonomic factors impeding study, as well as the currently available published fish bone data from medieval archaeological sites located in the North Sea basin. There are suggestions that fishing practices and habitat modification was already reducing the distribution of Atlantic salmon, and likely both forms of trout as well, by the 12th-13th centuries (Lenders et al. 2016), and zooarchaeological data is an invaluable source of information to supplement the limited quantitative historical data available. We examine the literature from archaeological and historical ecology studies, a large archaeological dataset compiled from sites located across northwestern Europe, and the results of a zooarchaeology by mass spectrometry (ZooMS) pilot study, in order to assess evidence for changing distribution and exploitation of Atlantic salmon, and the types of archaeological contexts where Atlantic salmon remains may be found.

7.2.2 Medieval Salmon Fishing

The North Sea during the Medieval Period was a hub for economic and social exchange, with an interwoven matrix of trade networks, military and colonial expansion, and ideological transmission. From early Scandinavian raids and settlements (Bencard, L. B. Jørgensen, and Madsen 1981; R. A. Hall 2014), to the commercial trade initiatives of the Hanseatic League (Mehler 2014) cities and towns surrounding the North Sea were key to the fluctuations of geopolitical power evident throughout the Medieval Period in NW Europe. Additionally, these settlements were often built on or near major rivers and estuaries, many of which supported, or continue to support, significant Atlantic salmon, sea trout, and brown trout populations. This results in a wide area of potential sites of *Salmo* sp. exploitation during the study period, which is aided by relative ease of access to archaeological resources from sites across the study area. Finally, the availability of documentary, artistic, and textual

evidence from medieval North-western European societies which explicitly reference Atlantic salmon, sea trout, and brown trout makes the North Sea an ideal point of focus for this review.

The extent of the North Sea Basin area includes 8 modern day countries, which represents hundreds of cultural and political units which shifted greatly throughout the Medieval Period. One feature which unites them is a broadly observed intensification of fishing efforts seen from the beginning of this period through to the post-medieval and modern age (J. H. Barrett, Locker, and C. M. Roberts 2004a; Inge Bodker Enghoff 2000; R. C. Hoffmann 1996). Beginning in the mid-10th century a definite increase in fishing activity and shift from freshwater to marine fish exploitation is seen in various locations across NW Europe, and is evident in both the archaeological and historical record (J. H. Barrett, Locker, and C. M. Roberts 2004a; J. H. Barrett and D. C. Orton 2016; J. A. Galloway and Murphy 1991; R.C. Hoffmann 2000). Termed the "fish event horizon" by Barrett et al. (2004), this period coincides with an increased religio-social reliance on fish in the diet of predominantly Christian medieval society, as well as new developments in fishing technology ranging from more sophisticated net systems to larger, higher capacity boats which allowed for longer travel to deeper waters (J. H. Barrett, Locker, and C. M. Roberts 2004b; R. C. Hoffmann 1996). Throughout the roughly 1000-year Medieval Period in NW Europe, there were distinct shifts from early subsistence level fisheries, with individual fishers providing almost exclusively for direct personal use, to more "artisan" small-scale fisheries (R.C. Hoffmann 2000; Richard Hoffmann 2000; R. C. Hoffmann 2023; Holm et al. 2019). These saw the advents of specialized fishers working to produce a surplus which could be locally sold or provided to elite sites like monasteries, and later these specialised fishers became the center of an exploding North Sea multi-species commercial fishery (Richard Hoffmann 2000; R. C. Hoffmann 2023; Holm et al. 2019; Moore 2000). Full-time fishery work involved the provision of fish for large urban centers, with a regional supply chain that manifested in the well-known herring and cod trades (e.g. J. H. Barrett 2016; J. H. Barrett, D. Orton, et al. 2011; Inge Bødker Enghoff 1996; Richard Hoffmann 2000; R. C. Hoffmann 2023; Moore 2000; D. C. Orton et al. 2014).

Technology was one of the driving factors behind this expansion, with key changes seen in both the type and size of tools like nets and weirs, as well as an apparent increase in the presence of hooks for line fishing as time goes on (Milner et al. 2008). The advent of floating surface nets allowing for increase catch of shoaling pelagic fish like herring, horse mackerel and garfish (J. H. Barrett and D. C. Orton 2016; Inge Bodker Enghoff 2000; Holm 1996; A. C. Wheeler, Jones, and R. Wheeler 2009), and massive beach seines used to catch demersal and migratory species like flatfish, pilchard, sturgeon, shad, sea trout and salmon are attested in documentary records from various North Sea Basin countries (Bennema and Rijnsdorp 2015; Desse-Berset 2011; R. C. Hoffmann 2015). Objects potentially used as net sinkers have been found at key medieval sites like Ribe and Coppergate (Inge Bodker Enghoff 2000; R. A. Hall 2014), and weirs ranging from small, individual traps to complexes spanning the width of a river or estuary were ubiquitous during the Medieval Period (Inge Bodker Enghoff 2000; J. A. Galloway and Murphy 1991; R. C. Hoffmann 1996; Kowaleski 2016; C. Roberts 2007).

While many fishing methods were applicable to more than one species at a time, fishers targeting migratory Atlantic salmon and sea trout generally utilized weirs, nets, or a combination of both to gather their catch. Weirs were generally either placed well upstream in rivers to catch migrating fish, or in estuarine environments where fish arriving from various directions could be directed into waiting baskets or nets as the tide rose or fell (Inge Bodker Enghoff 2000). Dedicated salmon and sea trout weirs were erected in both locations, with the intention of either trapping fish as they attempted to return to the ocean post-spawning, or to intercept them prior to entry of their native river system. It is a testament to the importance of the fish that individual salmon weirs have been highlighted in the documentary record through time, with some of the more famous incidents involving arguments over control, and even targeted destruction of, salmon weirs in Scotland and Germany (Richard

Hoffmann 2012; R. C. Hoffmann 1996). An important factor in the placement and maintenance of weirs was the season of the local salmon runs, both returning adults and departing smolts. Ocean migration of adult salmon is geographically, seasonally and, to some degree, genetically dependent and varies greatly across the breadth of the North Sea Basin area (L. P. Hansen and Quinn 1998; M. M. Hansen et al. 2014). This means the salmon run in neighboring countries can be drastically different, with salmon generally arriving in English rivers in the late summer while their northern cousins arrive in Scottish waters nearly all year round (Rikardsen and Dempson 2010). Similarly, the migration of sea trout is heavily reliant on local foraging conditions, as the trigger for brown trout to become sea trout is rooted in juvenile freshwater growth rates and the relative cost/benefit of migration to richer ocean feeding grounds (B. Jonsson and N. Jonsson 2007). This means that fishers targeting salmon and sea trout needed an in-depth knowledge of the local population's migration patterns in order to manage between the spring/summer smolting season and the locally-variable spawning arrival times.

Though the successful fishing of salmon is, at least in part, predicated on the successful management of a complex river ecosystem and knowledge of migratory habits, the longevity of the local population was not always prioritized. References to increased scarcity and cost of salmon appear in the documentary record as early as the 13th century (R. C. Hoffmann 2015), and historians propose declines in NW European stock of Atlantic salmon continuing through the end of the Medieval Period (De Groot 1992; R. C. Hoffmann 1996, 2015; Holm 2005). Hoffman discusses results from published and archival documentation of salmon commerce in the study area, the scant zooarchaeological records, and contemporary literary descriptions of fishing sites and methods from the period (R. C. Hoffmann 2015). Salmon were "ubiquitous features of conspicuous consumption", which continued to hold a high position of importance in northern and western European cultures even after the previously discussed transition from primarily freshwater to primarily marine resource exploitation (R. C. Hoffmann 2015). Hoffmann frames the later medieval Scottish salmon populations as anomalous holdouts of robust salmon stocks when compared to the rest of North-western Europe, and ascribes this to a combination of regulatory efforts by local and regional authorities, less unintended anthropogenic change of salmon habitat due to agricultural intensification, and a Scottish preference for building water mills on artificial bypass channels rather than the main body of a river (R. C. Hoffmann 2015).

Human modification of riverine environments through damming and diking is postulated to have had a significant impact on anadromous fish stocks during the Medieval Period (Lenders et al. 2016). Reviews of historical and archaeozoological evidence have demonstrated a possible connection between exploitation of Atlantic salmon in the Early Medieval Period and anthropogenic environmental change, identifying a sharp decrease in the presence of salmon remains relative to other freshwater fish (Lenders et al. 2016). One interpretation for these observed declines is related to the ecological impact of watermills, dams, dikes, and other anthropogenic river modifications implemented across the Paleo-Rhine catchment during the Medieval Period (Lenders et al. 2016). Lenders et al. demonstrate a strong negative correlation between the increase of anthropogenic river modifications and perceived decrease in Atlantic salmon stocks within the study area. The offered reasons for this high impact range from increased siltation and lowered oxygenation in dammed waters, to an overall reduction of adult salmon able to successfully navigate to and from their natal streams (Lenders et al. 2016).

While there have been reviews of changes in exploitation of fish like cod and herring through time and across broad geographic regions (J. H. Barrett 2019; J. H. Barrett and D. C. Orton 2016; Häberle and Hüster Plogmann 2019; D. C. Orton et al. 2014), Atlantic salmon have not had the same treatment. Lenders et al. 2016 did conduct a review focused on salmon, however the authors made some assumptions regarding the ease of identification and reliability of available data that are contradictory to the approach taken within this current review– as will be addressed below. Additionally, the restriction to the Paleo-Rhine catchment area limits the full efficacy of the

review. To address these issues we provide a broader discussion of issues of identification and interpretation, conduct a regional survey of archaeological sites with and without identified *Salmo* sp. remains, report results of preliminary ZooMS-aided research, and discuss further biomolecular study to fill in identified gaps in environmental information, as called for by Milner et al. (2008).

7.3 Archaeological Fish Bone

7.3.1 Sources of Faunal Data

Seven main sources of archaeozoological data were utilized for this review, consisting of six previously compiled databases plus an independent review of other major medieval archaeological sites from the North Sea Basin area (Albarella 2019; Albarella and Pirnie 2008; J. Barrett et al. 2018; Clavel 2001; Inge Bodker Enghoff 1999, 2000; Holmes 2017). Table 6.1 breaks down the data sources by country, highlighting the contributions by various coauthors to the compiled North Sea Archaeological *Salmo* dataset. These sources include review publications (Clavel 2001; Inge Bodker Enghoff 1999, 2000), reviews commissioned by Historic England Albarella and Pirnie 2008; Holmes 2017, contributions to the ongoing Northern Seas Synthesis project (J. Barrett et al. 2018), and targeted review of published medieval fish bone datasets.

Country	**Source of Data**
Belgium	Northern Seas Synthesis (van Neer & Ervynck)
Denmark	Enghoff 2000; Quinlan research 2021
England	Albarella & Pirnie 2008; Holmes 2017; Quinlan research 2019-2021
France	Clavel 2001; Quinlan research 2019-2021
Germany	Northern Seas Synthesis (Küchelmann); Enghoff 2000
The Netherlands	Northern Seas Synthesis (van der Jagt)
Norway	Northern Seas Synthesis (Hufthammer); Enghoff 2000
Scotland	Northern Seas Synthesis (Harland)

TABLE 7.1: Data sources by country

Material relating to site descriptions, location, chronology, fish bone NISP, and relevant information about *Salmo* sp. identification was extracted from both the published and unpublished datasets using both manual and programmatic data cleaning methods. A master spreadsheet was compiled, and eventually contained 1270 individual contexts from 410 archaeological sites. All sites included were selected using a defined set of criteria, which primarily excluded sites outside of the selected date range (500-1500CE) and geographic area (Figure 1).

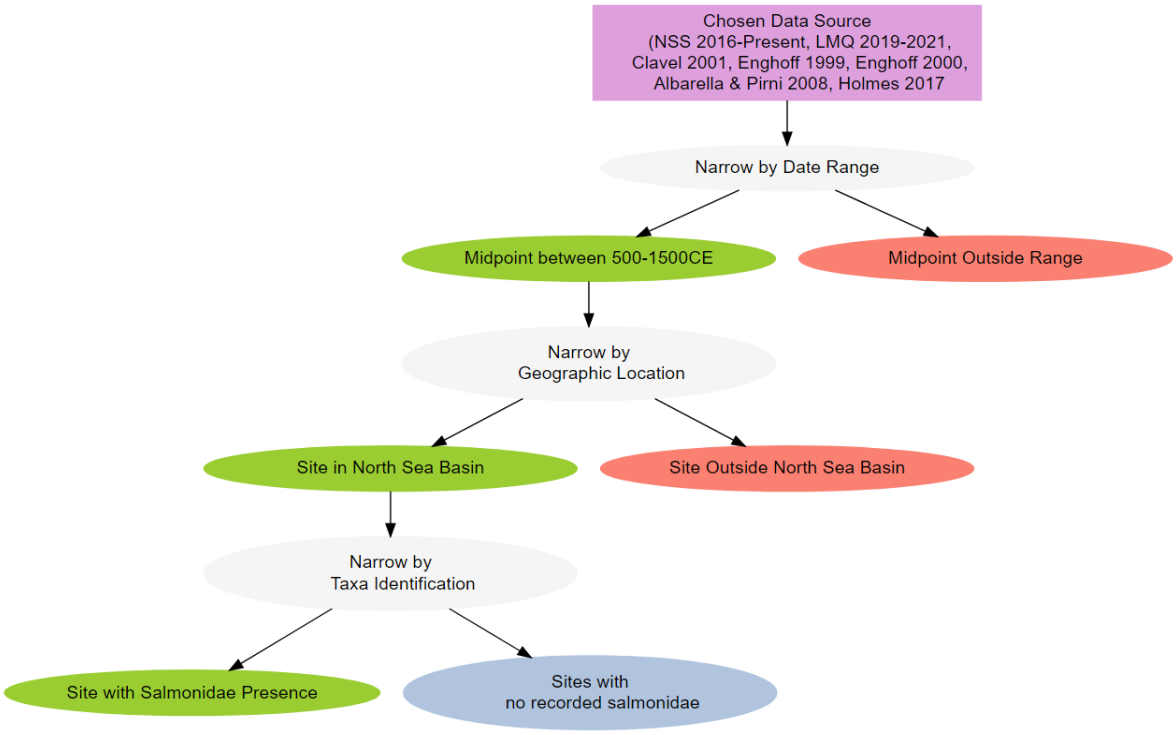


FIGURE 7.1: Flow chart of *Salmo* sp. review decision making. Sites from a variety of sources were first screened by date range, with sites which midpoints fell between 500-1500CE including in the study dataset. The dataset was then narrowed by geographic location, to include only sites in the North Sea Basin area. Finally, the entire dataset was divided into two groups, those with recorded *Salmo* sp. fish bones and those without. Both groups were included within the final dataset, and this division was only made for ease of data interpretation.

Species were assigned to one of four categories– Marine, Freshwater, Diadromous, and Mixed– in order to better understand proportions of fish of from different environments at these sites. Common marine species included cod, haddock, herring and flatfish, while cyprinids, pike, and perch dominated the freshwater category. All *Salmo* sp. fish were placed in the diadromous category along with eel and sturgeon, as the accurate differentiation of salmon, sea trout, and brown trout and is difficult. Fish placed in the mixed category mostly belonged to larger taxonomic groups that couldn't be narrowed down to a specific environment, like those identified as Clupeidae and Percidae. Only archaeological sites with midpoints within the study period of 500-1500CE were included in the review, and those with *Salmo* sp. remains were recorded separately from those with no recorded *Salmo* sp. remains. Geographic boundaries were assessed on a country-by-country basis, and sites within the research area were generally coastal or riverine sites, with relatively easy access to the North Sea itself, or which lay along one or more of it's tributary rivers.

7.3.2 Osteological Identification of Species

The primary barrier to accurately assessing the importance, abundance, and trends in Atlantic salmon, sea trout and brown trout exploitation during the Medieval Period is the difficulty in differentiating between the bones of salmon and the other species in the *Salmo* genus, the brown trout. There is some commentary in the available literature discussing specific differences between skeletal elements of Atlantic salmon and brown trout, with the

most commonly mentioned skeletal elements that show clear differences being the dentary, premaxilla, maxilla, supraethmoid, vomer, and atlas vertebra (Kacem and Meunier 2009; Norden 1961; Tchernavin 1938; Watt, Pierce, and Boyle 1997). The case of the ethmoid, dentary, maxilla and premaxilla is more dependent on sex and age, and so are not able to be used 100% of the time to distinguish between salmon and trout. The development of the "kype" or hooked beak is a characteristic of spawning male anadromous *Salmo* sp. individuals, including anadromous Atlantic salmon and sea trout. This kype is generally assumed to be a secondary sexual characteristic which may attract females during spawning, and may aid in defense from attacks made by other males (Tchernavin 1938; P Eckhard Witten and Brian K Hall 2003, 2002; P. Eckhard Witten, Rosenthal, and Brian K. Hall 2004). While the most prominent osteological changes seen in kype development involve the dentary, significant changes also occur within the supraethmoid, premaxilla and maxilla (Kacem and Meunier 2009; Tchernavin 1938; P. Eckhard Witten, Rosenthal, and Brian K. Hall 2004).

The ethmoid complex may be used to differentiate between breeding male and female salmon and sea trout, as there is a marked widening of the anterior portion of the supraethmoid, related to the development of the kype (Tchernavin 1938). Additionally, there is a demonstrated ability to develop a distinct hypethmoid portion of the ethmoid complex, which can aid in distinguishing between *Salmo salar* and *Salmo trutta*. As salmon lose their ossified maxillary teeth during the smolting process (Norden 1961), the presence of such teeth may be used to differentiate between post-smolt salmon and adult trout. There is a measurable difference between the ratio of height to width in the premaxillae of the two *Salmo* species, with salmon having a premaxillary height roughly 50% of the width, and freshwater brown trout having a premaxillary height roughly 70% of the width (Watt, Pierce, and Boyle 1997). Additionally, a convex thickening or bulge is often reported on the medial aspect of the premaxillae in brown trout, and is absent in salmon. One of the most reliable cranial bone diffentiation methods uses the characteristics of vomerine teeth. The vomer of the Atlantic salmon displays only a single row of teeth along its central shaft and head, forming a "T" shape, and may even lose these teeth during spawning due to bone reabsorption for kype formation and egg development (Kirczuk and Domagała 2011; Locke 1929; Tchernavin 1938). Conversely, all adult brown trout show two rows of well-rooted vomerine teeth, alternating in a zig-zag fashion, on both the central shaft and the head (Kirczuk and Domagała 2011; Locke 1929). The head of the vomer is differently shaped in both species, with the Atlantic salmon having a roughly pentagonal shape and the brown trout having a clear triangular vomerine head (Kirczuk and Domagała 2011; Tchernavin 1938). Finally, the atlas vertebra of both salmon and trout may be distinguished based on visible and metric differences, including vertebral height and waist, pore shape, and process shape (Feltham and Marquiss 1989) although this method is not reliable 100% of the time. Measurements obtained from the first vertebra can be reliably used to classify species with 90% certainty using a regression analysis that plots vertebral width against total calculated fish length (Feltham and Marquiss 1989).

7.3.3 Preservation and Taphonomy

A further complicating factor in differentiating Atlantic salmon, sea trout, and brown trout bones is the persistent taphonomic problem of element survival, which greatly affects the recovery of archaeological material for all ecotypes. While we have described at least five cranial elements which can be used to differentiate between salmon and trout, to various degrees, the survival rate of cranial bones is drastically reduced in both *Salmo* species. This is due in large part to overall recovery issues seen in *Salmo* sp. fishes, but which appears to be highly dependent on factors like location, soil characteristics, and recovery method. Some sites which yield high amounts of fish bone material, with otherwise excellent preservation and recovery, may show proportionally small *Salmo* sp. subsets– for example, the Townwall Site in Dover, UK has a recorded NISP of 91,504, but only 3 recorded *Salmo*

sp. bones (Nicholson 1996) .

Faunal data from several sites with a large number of recorded *Salmo* sp. remains were reviewed, and the vast majority of identifiable bones are vertebrae. For example, 256 *Salmo* sp. bones were recorded withing the available fish bone assemblage from the 16-22 Coppergate site in York, England, and approximately 86% of the *Salmo* sp. bones were vertebrae or vertebral fragments (n = 221). At the Ribe Posthuset site, 100% of the recorded sample (n=100) are vertebrae or vertebral fragments. Finally, at Earl's Bu, a Late Norse period feasting site located in Orphir, Orkney there were 115 recorded *Salmo* sp. bones, and 78.2% (n=90) are vertebrae or vertebral fragments. This preponderence of vertebral elements in archaeological assemblages of *Salmo* sp. bones is especially problematic for species identification. Apart from the first vertebrae, there is no consistently accurate published osteological method for differentiating the vertebrae of Atlantic salmon, sea trout, and Brown trout based on morphology.

7.4 Identification Methods Review

7.4.1 Geometric Morphometrics

One proposed method for developing a more reliable identification protocol for archaeological *Salmo* sp. remains is geometric morphometrics (GMM)– an approach which focuses on describing covariations with form using visual and statistical analyses (Adams, Rohlf, and Slice 2013; Cooke and Terhune 2015) By calculating the variation of fixed landmarks across a discrete sample of archaeological fish bone, an observation of statistical difference can be quantified (Guillaud, Cornette, and Béarez 2016; Huber et al. 2011). The proposed methodology is that with a large enough sample, and distinct enough variations in form between the vertebral centra of *Salmo salar* and *Salmo trutta*, one could identify species from a photograph. As of the date of publication there have been two archaeological studies conducted on the centra of various *Salmo* species which have focused on species identification. The first involves the analysis of vertebrae, focusing on all seven species of Pacific salmonids (*Onchorhynchus* sp.) conducted by Huber et al. (2011). While the researchers focus on a different genus of salmonids than the proposed research, their results and analysis remain relevant to the study. Their results showed that morphometric techniques using classification regression trees (CART) can accurately classify vertebrae to species anywhere from an average of 80 to 100% of the time (Huber et al. 2011).

The other study involving the identification of archaeological *Salmo* sp. fish using GMM techniques was conducted by Guillaud et al., in 2016. Their archaeological focus was on Magdalenian sites in France with a high abundance of undistinguished *Salmo* sp. remains, and they aimed to perform, optimize and quantify the results of analysis of the morphological distinctions between archaeological and modern *Salmo* sp. vertebrae specimens (Guillaud, Cornette, and Béarez 2016). For their analysis Guillaud et al. used 8 wild Atlantic salmon and 8 wild Sea trout as modern comparative specimens, as well as sampling a total of 87 *Salmo* sp. vertebrae from the La Taillis des Coteaux site in Antigny, France (Guillaud, Cornette, and Béarez 2016). While Guillaud et al. demonstrated 83% (trout) and 100% (salmon) rates of success for classifying vertebrae as belonging to *Salmo salar* and *Salmo trutta*, there is room for expansion and refinement of the identification protocols described by their research especially with regard to looking at regional differences.

7.4.2 Stable Isotope Analysis

A second analytical method that my prove useful for distinguishing between *Salmo* sp. ecotypes is bulk stable isotope analysis, specifically the study of ratios of C^{13} and N^{15} in preserved bone collagen. Bulk analysis of car-

bon and nitrogen isotopes can provide information on diet, environment, and trophic level (Pilaar Birch 2013; Zagrando et al. 2013), all important metrics for distinguishing between anadromous salmon, anadromous sea trout, and freshwater trout. δ^{13}C values in fish bone display a freshwater-marine split, with species living and consuming nutrients in riverine environments showing enriched δ^{13}C values, and those in marine environments showing depleted δ^{13}C values (Deniro and Epstein 1981). This is due in part to the isotopically distinct primary producers characteristic to nearshore, offshore, and riverine environments (Cherel and Hobson 2007; Deniro and Epstein 1981; Saino and Hattori 1987; Schoeninger and DeNiro 1984). Research on migratory trout ecotypes has indicated that sea trout display higher δ^{15}N (>11‰) and higher $\delta^{13}C$ (<-19‰) values when compared to freshwater-resident brown trout (McCarthy and Waldron 2000).

In addition to traditional bulk stable isotope analysis, a potential useful technique would involve the study of incremental isotope profiles from individual vertebrae. Incremental, or sequential, SI analysis involves sampling successive sections of bone or dentine which have been laid down in a chronological order by the nature of the tissue formation. This allows for a time-series of isotopic values from a single individual, showing changes and variations in isotopic values over the life of an animal. While this method has been applied fairly extensively to fish otoliths (Cook et al. 2016; Disspain, Ulm, and Gillanders 2016; Disspain, Wilson, and Gillanders 2012; Van Neer, Ervynck, et al. 2002), and has been used on elasmobrach vertebrae to reconstruct feeding ecology (Estrada et al. 2006; Kerr et al. 2006), very little work has been done to apply the method to teleost fishes. A landmark 2017 study determined that a stable isotope chronology could be determined using incremental stable isotope analysis of vertebral central from modern Masu salmon *(Onchorhynchus masou)* (Matsubayashi et al. 2017). Applications of this method to archaeological *Salmo* sp. remains would require selecting for the largest available vertebrae, as well as developing a sequential sampling method that would provide enough collagen for analysis as archaeological fish remains may only contain limited amounts of usable collagen. If successful, this method would be able to determine chronological dietary and environment change from the juvenile freshwater stage to the adult marine stage of a single fish.

7.4.3 Zooarchaeology by Mass Spectrometry

A final method for refining identifications of archaeological *Salmo* sp. fishes uses collagen peptide sequencing to conduct zooarchaeology by mass spectrometry, or ZooMS. This method utilizes the unique sequence of amino acid peptide markers found in bone collagen to distinguish between species, both taxonomically related and distant (Michael Buckley, Virginia L Harvey, et al. 2020; Collins et al. 2010; Kristine Korzow Richter et al. 2022) Collagen, unlike DNA, is a far more stable and abundant compound in bone material, and thus more likely to survive within the archaeological environment (Mike Buckley et al. 2010; Collins et al. 2010; Kristine K. Richter et al. 2011). This, coupled with it's cheaper and simpler extraction method, gives it a distinct advantage over other biomolecular species identification methods. ZooMS molecular barcodes for commonly found archaeological fish species were first published in 2009, and more have since been made available (Michael Buckley, Virginia L Harvey, et al. 2020; Collins et al. 2010; Virginia L. Harvey, LeFebvre, et al. 2022; Kristine Korzow Richter et al. 2022; Rick, Virginia L. Harvey, and Michael Buckley 2019). Species markers for Atlantic salmon and brown trout were identified by Richter et al. (Kristine K. Richter et al. 2011) and additions were made in subsequent publications (Michael Buckley, Virginia L. Harvey, et al. 2022; Virginia L. Harvey, Daugnora, and Michael Buckley 2018), however further study on the possibility of peptide marker variation in hybrids of *Salmo salar* and *Salmo trutta*, as well as the anadromous morph subspecies sea trout, may be required to clarify which markers are reliable. ZooMS analysis is, like stable isotope analysis, inherently destructive, and requires a portion of bone to be demineralized, gelatinized and digested with the enzyme trypsin Mike Buckley et al. 2010. However, unlike

bulk stable isotope analysis, which generally requires the destruction of a minimum of 100mg of bone material, ZooMS analysis can be successfully completed with as little as 10mg of bone material. Section 6 reports the results of a targeted large-scale identification study on archaeological *Salmo* sp. remains from a multi-site assemblage selected from the compiled North Sea Archaeological Salmo dataset detailed in Section 6.5 below.

7.5 Results of North Sea Archaeological Review

7.5.1 Data Overview

The North Sea Archaeological Salmo (NSAS) dataset (Appendix A) contains 1270 archaeological contexts, from 410 individual archaeological sites excavated in 8 modern-day European countries (Table 6.2). These sites span over a thousand years of human history, with the relevant contexts covering the entire Medieval Period and including distinct cultural traditions and political entities ranging from early Slavonic settlements along the Elbe to Anglo-Scandinavian urban centres along the English Ouse (Figure 2).

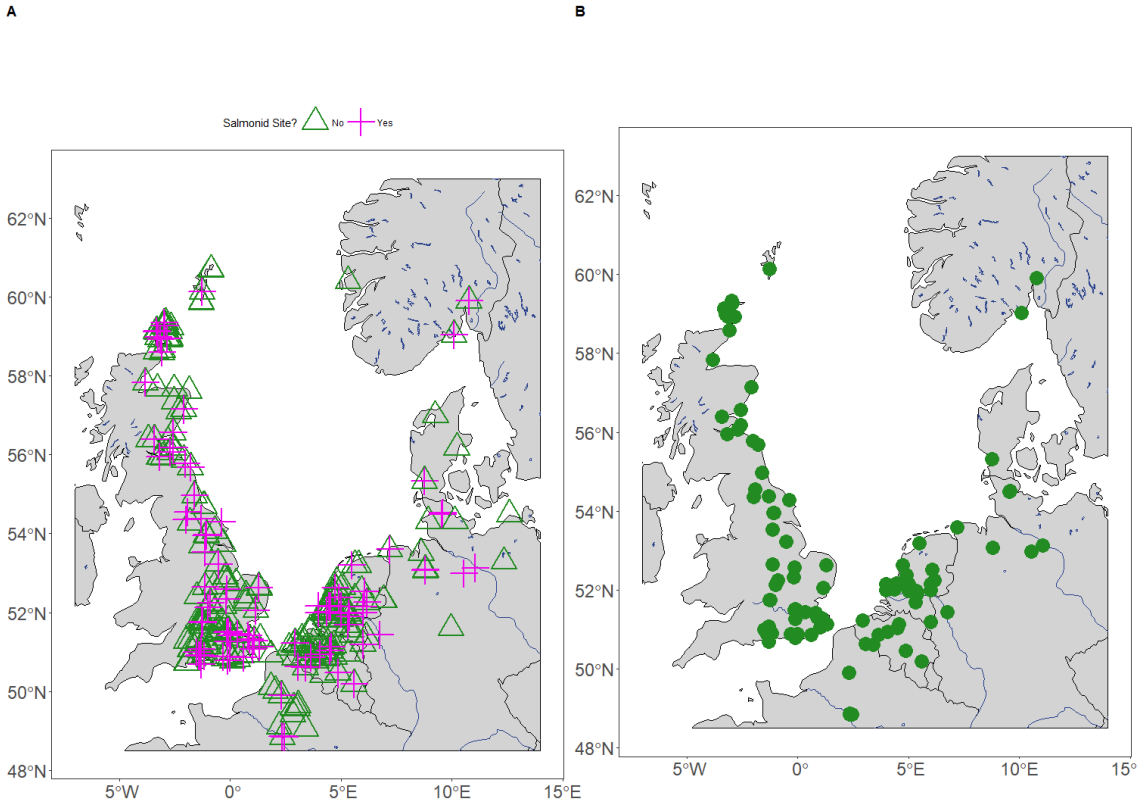


FIGURE 7.2: **A.)** All reviewed site contexts (n=1270), color and shape coded by whether there are *Salmo* sp. bones present at the site or not. **B.)** All reviewed site contexts with *Salmo* sp. remains present (n=254)

Country	Unique Contexts/Phases	Individual Sites
Belgium	403	65
Denmark	6	6
England	295	169
France	20	19
Germany	29	21
Netherlands	190	63
Norway	17	5
Scotland	310	63
Total	**1270**	**410**

TABLE 7.2: Archaeological Contexts and Sites included in the NSAS Review by Country

These reviewed medieval archaeological sites (500-1500CE) report well over one million total fish bones, with a NISP of 983379. Of the identified specimens (Figure 3), the overwhelming majority (74.6%) were marine, with that assemblage dominated by gadid species. The smaller diadromous, freshwater, and mixed categories (14.2%,6.2% and 4.9%, respectively) collectively represent a not-insignificant 246268 fish bones, and the data provides a fairly comprehensive overview of the state of aquatic resource exploitation during the Medieval Period (Figure 4).

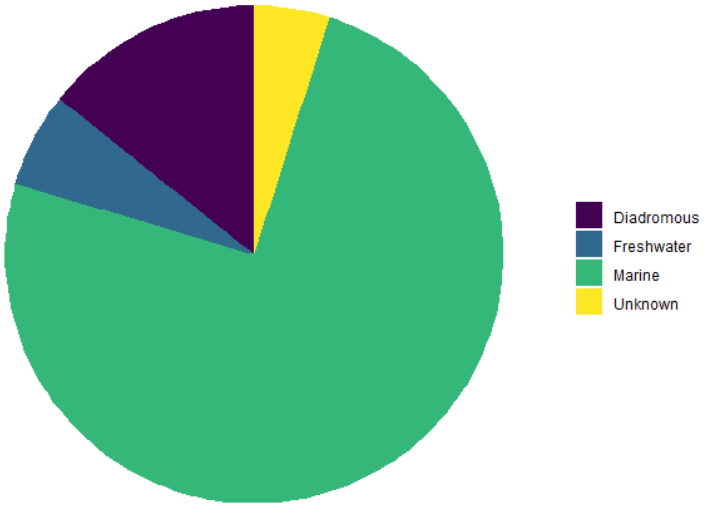


FIGURE 7.3: Chart Showing Proportion of Fish Bones Reviewed by Environmental Type

Briefly, the overall NSAS dataset reflects a clear pattern in intensification of marine fishing surrounding the proposed "fish event horizon" (J. H. Barrett, Locker, and C. M. Roberts 2004a), with the increase beginning in

the earliest part of the Medieval Period (600-750CE), and truly expanding in the 1050-1200 CE period. There is a visible decrease after this period, which may be due to a number of factors including site location, collection methods and preservation. Interestingly, the freshwater values also display an increase in NISP recorded during the 900-1050 period, which stays fairly steady until the post-1500 period. Diadromous NISP values are at their peak prior to the 1000CE fish event horizon, but do show a visible upswing within the 1050-1200CE period. Within that diadromous subgroup of fish from the NSAS dataset are the main *Salmo* ecotypes of interest for this review, Atlantic salmon, sea trout, Brown trout, and undistinguished *Salmo* sp. remains.

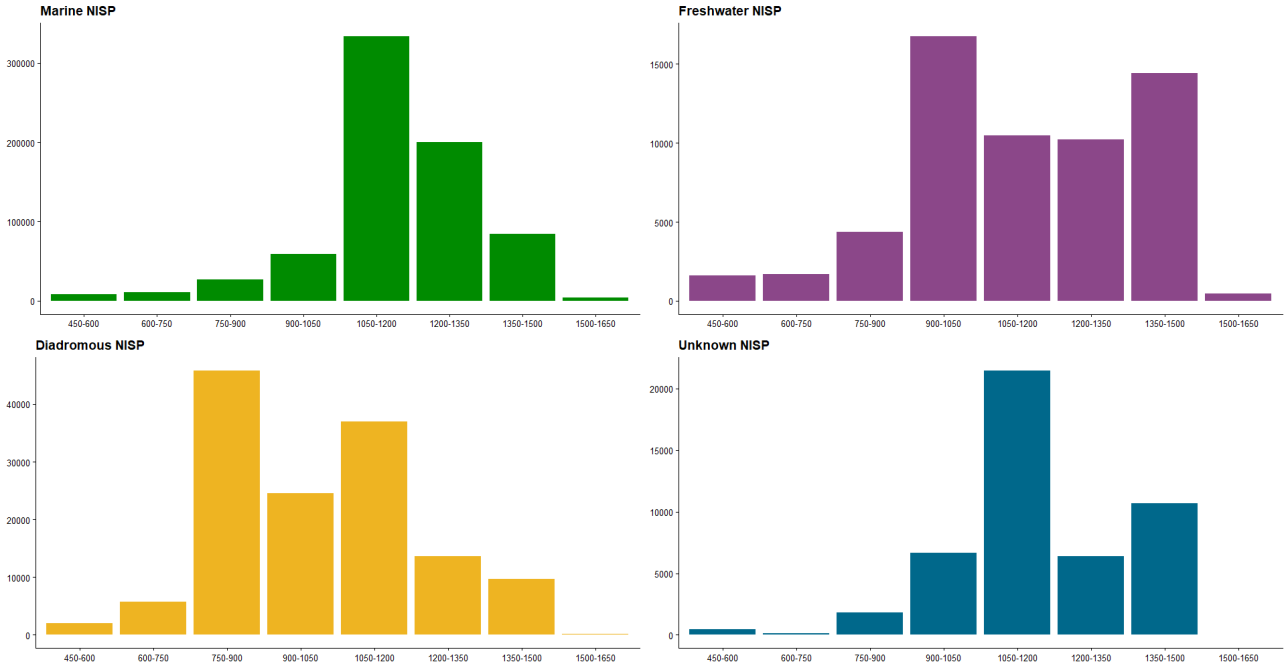


FIGURE 7.4: Comparisons of Different Fish Categories through Time for entire NSAS Dataset

7.5.2 Medieval *Salmo* sp. Assemblages

This review identified a total of 2515 individual *Salmo* sp. elements (Table 6.3) recorded from 146 archaeological sites. The following sections will go through the characteristics of the *Salmo* sp. assemblage from each North Sea Basin country included within this review, highlighting anomalous assemblages and general trends.

Country	Total Contexts	Total Sites	Total Salmo sp. NISP
Belgium	35	13	676
Denmark	3	3	306
England	104	68	878
France	6	6	27
Germany	9	9	145
Netherlands	41	21	364
Norway	5	4	42
Scotland	51	22	177
Total	**254**	**146**	**2515**

TABLE 7.3: *Salmo* sp. Identifications Recorded by Country

Belgium

The Belgian subset represents 13 total sites (8.9%), however it contains a disproportionate amount of the total *Salmo* sp. bones identified (26.9%). This is primarily due to the exceptional assemblage of identified salmon, trout and *Salmo* sp. bones recovered from the Chateau La Roche en Ardenne site, in the Luxembourg province of Belgium (Pigière, Van Neer, and Krznaric 2009; Van Neer, Wouters, and Germonpré 2007). Of the 676 *Salmo* sp. bones recorded in the Belgian subset, 598 of them are from this site, which is also the largest assemblage identified the entire North Sea Basin area. This site is a high status 11th-13th century château, occupied at various points by counts of La Roche, Namur and Luxembourg (*Histoire: Ville de la Roche-en-Ardenne* 2023; Pigière, Van Neer, and Krznaric 2009). Located at a bend in the Ourthe river, a known trout tributary of the River Meuse, its thought that many of the remains are in fact trout, however there are at least 11 bones in the assemblage which were confidently identified as salmon by the original analysts (Van Neer, Wouters, and Germonpré 2007). Because this site represents such an exceptional outlier in the Belgian subset, it has been removed from some graphical explorations of the data later in this report. The remaining Belgian sites, with a total *Salmo* sp. NISP of 78, are far more representative of the normal preservation and recovery of *Salmo* sp. bones at medieval sites. The Belgian subset is mostly represented by urban settlements, with a small amount of ecclesiastical and high states sites present. Geographically, all sites within modern day Belgian borders were included in the subset, as they all lay within reasonable distance of the North Sea or its tributary rivers.

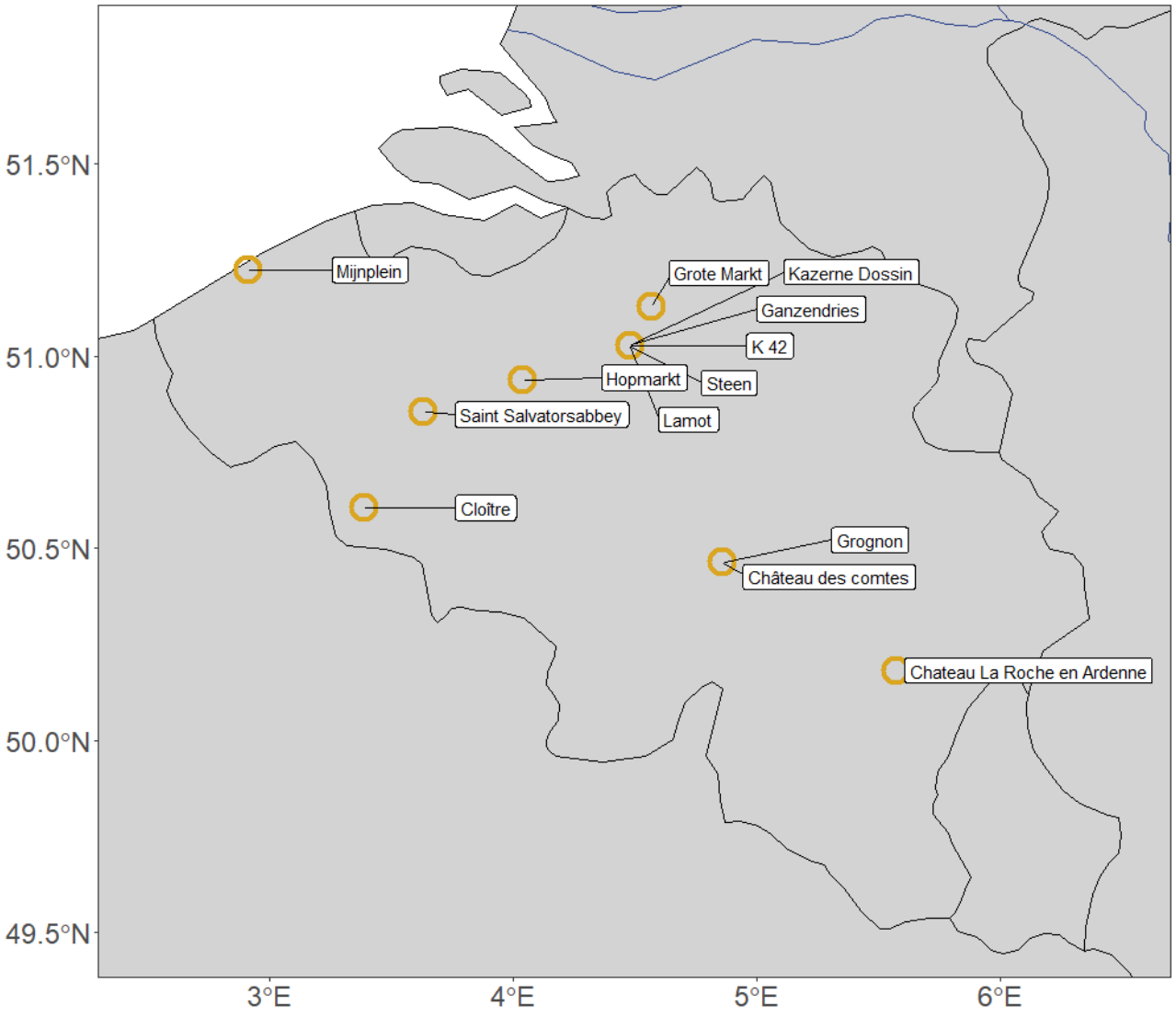


FIGURE 7.5: Map of Belgian archaeological sites with identified *Salmo* sp. remains (n=13

Denmark

The Danish subset is quite small, with 6 total sites and only three containing *Salmo* sp. remains. These three sites are all from the modern-day town of Ribe, which is one of the oldest continuously occupied settlements in Scandinavia, and the oldest extant town in Denmark. Two of the sites (ASR 13 - Lindegården and ASR 2090 - von Støckens Plads) are later occupations, dated between the 11th-14th centuries, and their *Salmo* sp. remains were first analyzed by the lead author. The other Ribe site (ASR 9 - Posthuset) is far larger, and represents the earliest 8th century occupation of the town (Bencard, L. B. Jørgensen, and Madsen 1981). The ASR 9 - Posthuset site had 200 *Salmo* sp. bones recorded by the original analyst (Inge Bodker Enghoff 2000), and was located in the central

marketplace of the settlement. The overall small size of the Danish subset precludes it from being treated as truly representative of medieval *Salmo* sp. exploitation in Denmark, but the presence of such a large assemblage at Ribe indicates at least some reliance on *Salmo* sp. fish for Early-High Medieval subsistence. When reviewing site data for the Danish subset only sites on the Jutland peninsula were included, as the islands of Zealand and Funen are more closely associated with Baltic Sea trade networks and access than the North Sea.

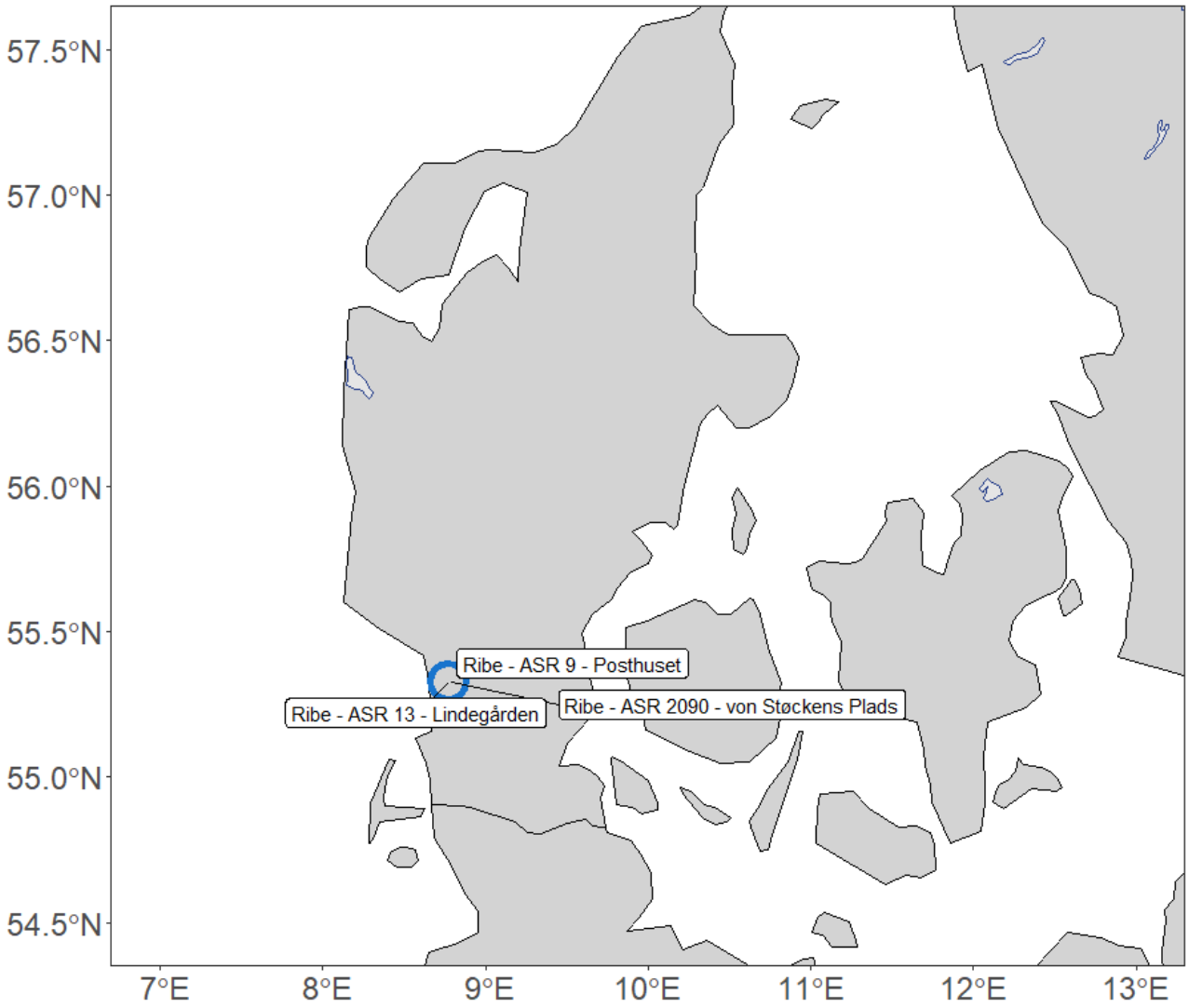


FIGURE 7.6: Map of Danish archaeological sites with identified *Salmo* sp. remains (n=3

England

The largest proportion of both identifications and sites reviewed comes from the English subset, with 35% of the total *Salmo* sp. bones from 46.6% of the total sites. The entire subset contains mostly urban settlements, supplemented by small amounts of ecclesiastical, high status, and rural settlements. Some of the largest assemblages of *Salmo* sp. fish are from sites from London (Dorter Undercroft - Westminster Abbey, n = 81), York (Coppergate and Fishergate, n= 260 and n=78), Durham (Barnard Castle, n=116), and Winchester (Staple Gardens, n=42). The vast majority of sites (n=59), however, have 10 or fewer individual bones recorded, with many showing only one or two bones. This subset most clearly demonstrates the observed issues with preservation and recovery of *Salmo* sp. bones from medieval sites, as it covers such a wide range of occupation periods, variety of site types, and breadth of geographic locations. When reviewing site data for the English subset all sites which lay east of 3°W were included, as to include most sites with access to eastern draining rivers like the Thames, Trent, Derwent and the Humber Estuary.

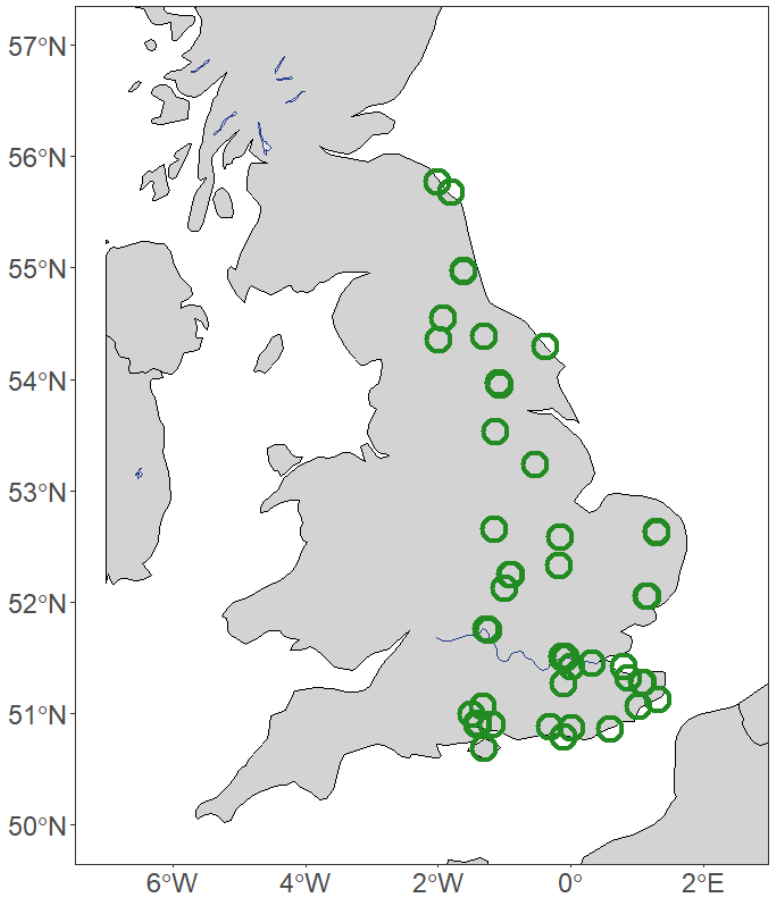


FIGURE 7.7: Map of English archaeological sites with identified *Salmo* sp. remains (n=68). Sites from England were too numerous to label within this figure, but full site names and descriptions can be found in APPENDIX A

France

The *Salmo* sp. subset from France was sourced entirely from Benoit Clavel's 2001 review of medieval faunal data, and represents a much later assemblage of sites (circa 900-1500CE) than most other countries. All sites

are located in northwestern France, in the Hauts-de-France and Île-de-France regions, with sites from the major cities of Amiens, Vincennes, Lille and Paris. The sites show only 27 *Salmo* sp. bones recorded, with over half (n=15) from the Capetian Manor at Vincennes (Clavel 2001). When compared to the other smaller subsets in this review, the French sites seem fairly typical in terms of low-preservation/recovery of *Salmo* sp. remains, and its expected that the addition of further sites would not change this representative sample.

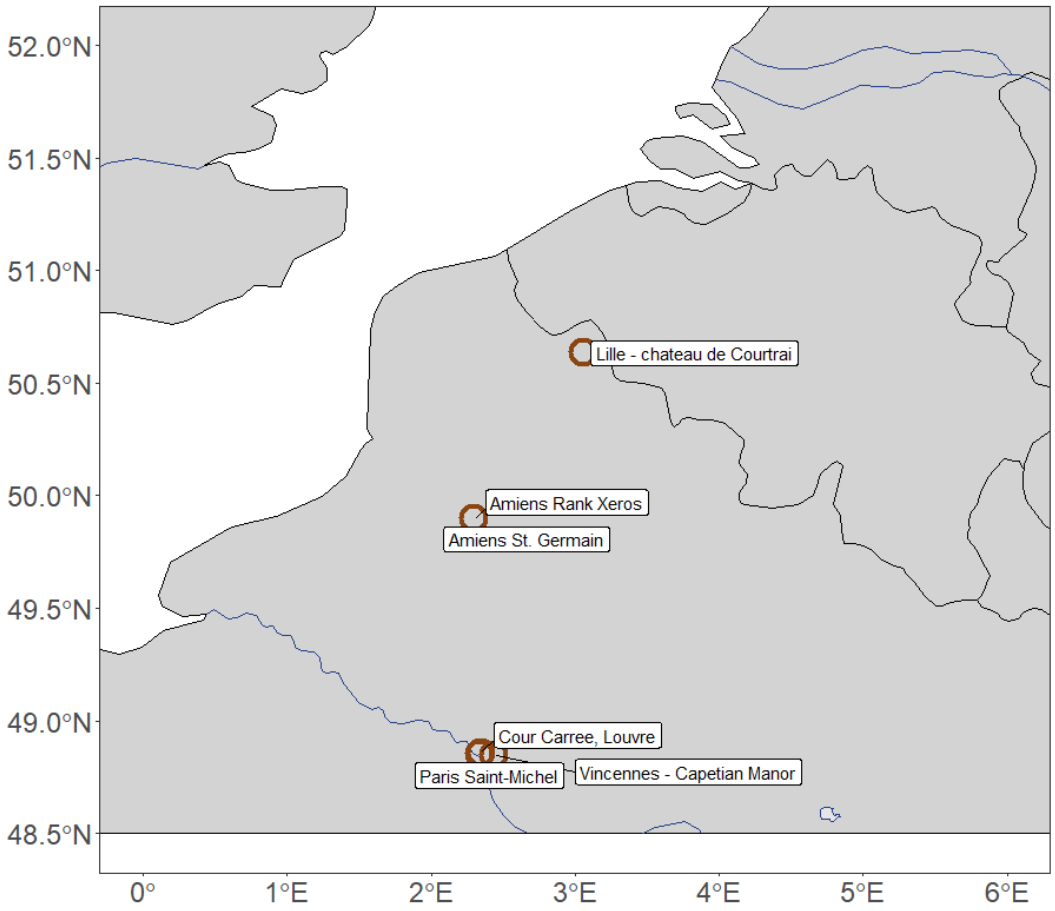


FIGURE 7.8: Map of French archaeological sites with identified *Salmo* sp. remains (n=6

Germany

The German subset of sites (n=9) all come from the modern day northern and western states of Bremen, North Rhine-Westphalia, Lower Saxony, and Schleswig-Holstein. Like the French subset, the sites also contains a fairly homogeneous *Salmo* sp. sample, with individual site NISPS ranging from 1-5 across nearly all the sites. The notable exception can be found in the Schleswig-Holstein site of Haithabu/Hedeby. A famous, formerly-Danish, trading settlement, first identified in the 19th-century, Haithabu/Hedeby lay at the base of the Jutland Peninsula, with easy access to both the North and Baltic Seas. The total fish assemblage from Haithaby/Hedeby is well studied, with a total NISP of 13,842 bones (Inge Bodker Enghoff 1999), with a large *Salmo* sp. assemblage of 129

recorded bones.

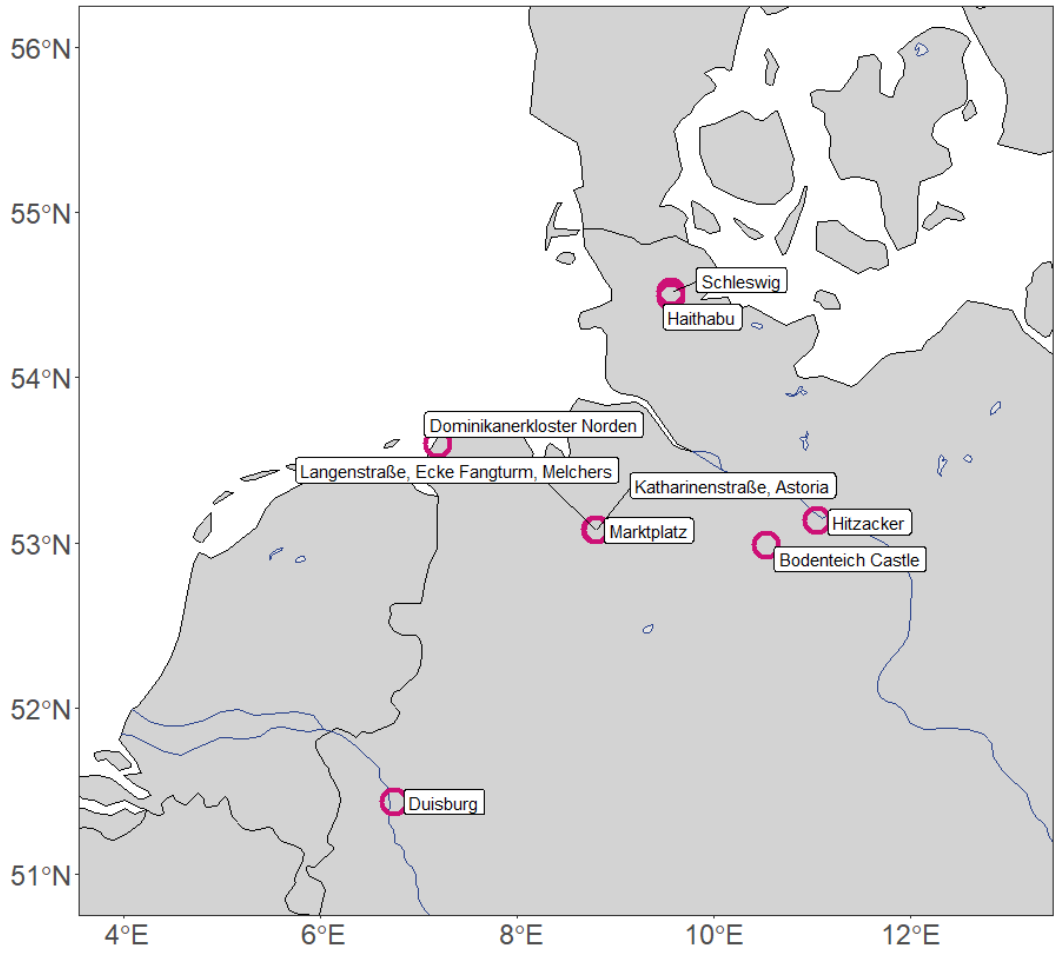


FIGURE 7.9: Map of German archaeological sites with identified *Salmo* sp. remains (n=9

The Netherlands

With 21 archaeological sites represented, the Dutch subset shows a more heterogeneous sampling of *Salmo* sp. remains, with 14 sites recording *Salmo* sp. NISPs lower than 10. The remainder show NISPs ranging from 25 at the ducal court and Franciscan friary in 's-Hertogenbosch (Kerklaan 2016) to 130 recovered from an Early Medieval trading settlement near Oegstgeest (Jagt and Laarman 2018). This largest assemblage was recovered from an early settlement (circa 475-725 CE), located only a few kilometers from the North Sea coast, and represents an ideal environment for early *Salmo* sp. exploitation. The Dutch subset as a whole is an excellent representation of the geographic ubiquity of *Salmo* sp. fishes at more than half the total sites from the Medieval Period, especially considering the complete absence of Atlantic salmon from Dutch rivers since 1960 (WWF 2001).

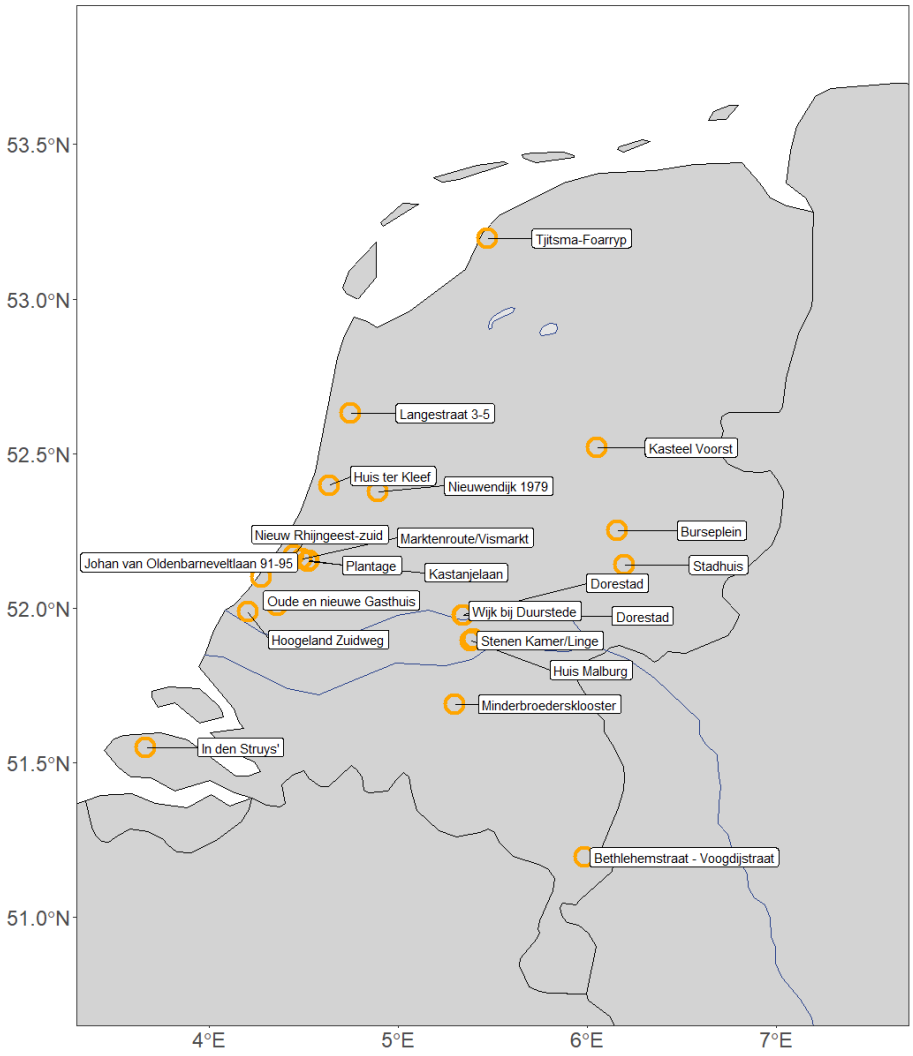


FIGURE 7.10: Map of Dutch archaeological sites with identified *Salmo* sp. remains (n=21

Norway

Another small subset, the collection of Norway sites reviewed (n=4) include three from Oslo and one from Larvik, a large town in the Vestfold and Telemark county of southern Norway. Only sites that lay south of approximately 62°N were included, as those further north are more closely associated with the Norwegian Sea. All Norwegian sites were recorded by the same analyst, R.W. Lie, and again show the consistently low *Salmo* sp. NISPs (between 2-9 bones) characteristic of most sites in the NSAS dataset. The largest recorded assemblage of *Salmo* sp. bones from Norway are from the Kanslergt 10 site in Oslo, which has a NISP of 27. Despite Norway's modern salmon population being one of the healthiest and robust in the Atlantic, and the presence of over 650 historic salmon bearing rivers (WWF 2001), the NSAS review shows an unexpectedly small proportion of archaeological *Salmo* sp. remains found at Norwegian sites.

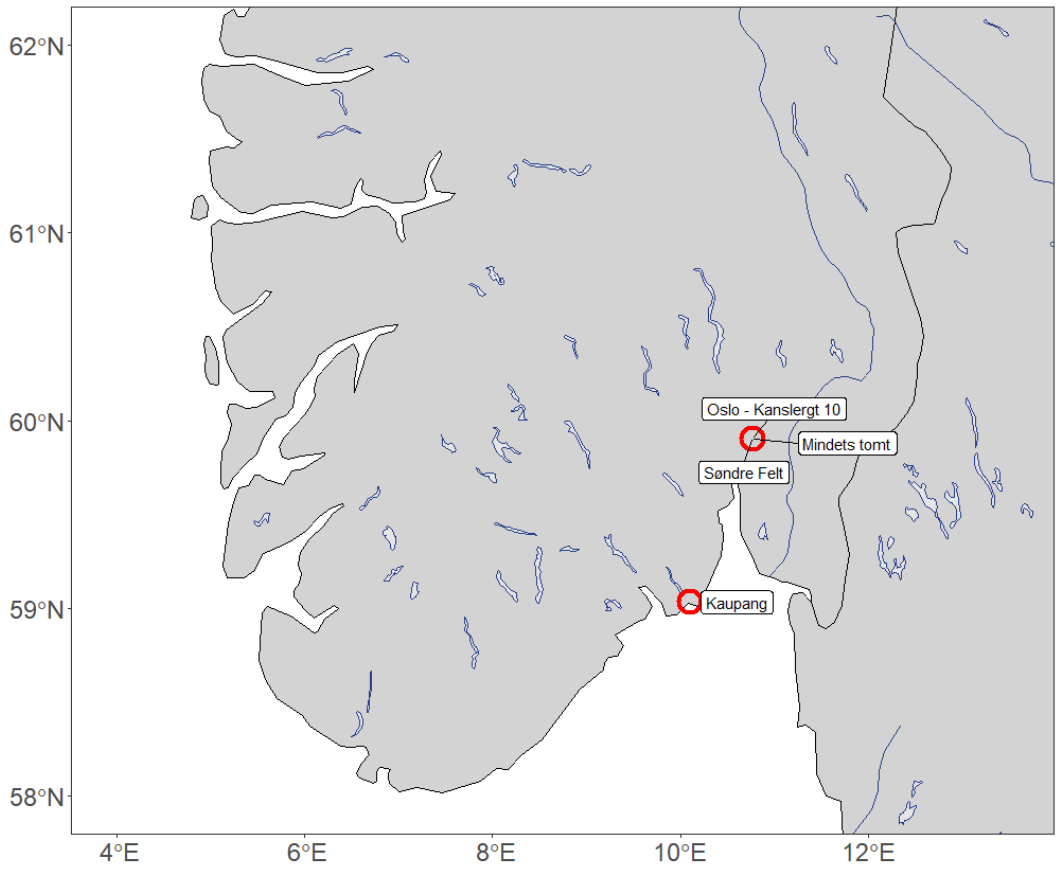


FIGURE 7.11: Map of Norwegian archaeological sites with identified *Salmo* sp. remains (n=4

Scotland

The Scottish dataset, like that of England and the Netherlands, is fairly comprehensive and robust, with over 75%(n=17) of sites showing the characteristic small assemblages of fewer than 10 identified *Salmo* sp. bones. The remaining sites with larger assemblages are nearly all in the Scottish Northern Isles of Shetland and Orkney, with the notable exception of Perth High Street (n=12). In fact, over half of the Scottish sites (59%) are from Orkney, including the largest assemblage of *Salmo* sp. fishes, recorded at the Earl's Bu site near Orphir (n=79). The Earl's Bu site is one of the largest assemblages of Viking Age and Late Norse fish bones recovered anywhere in Scotland (Harland 2006).

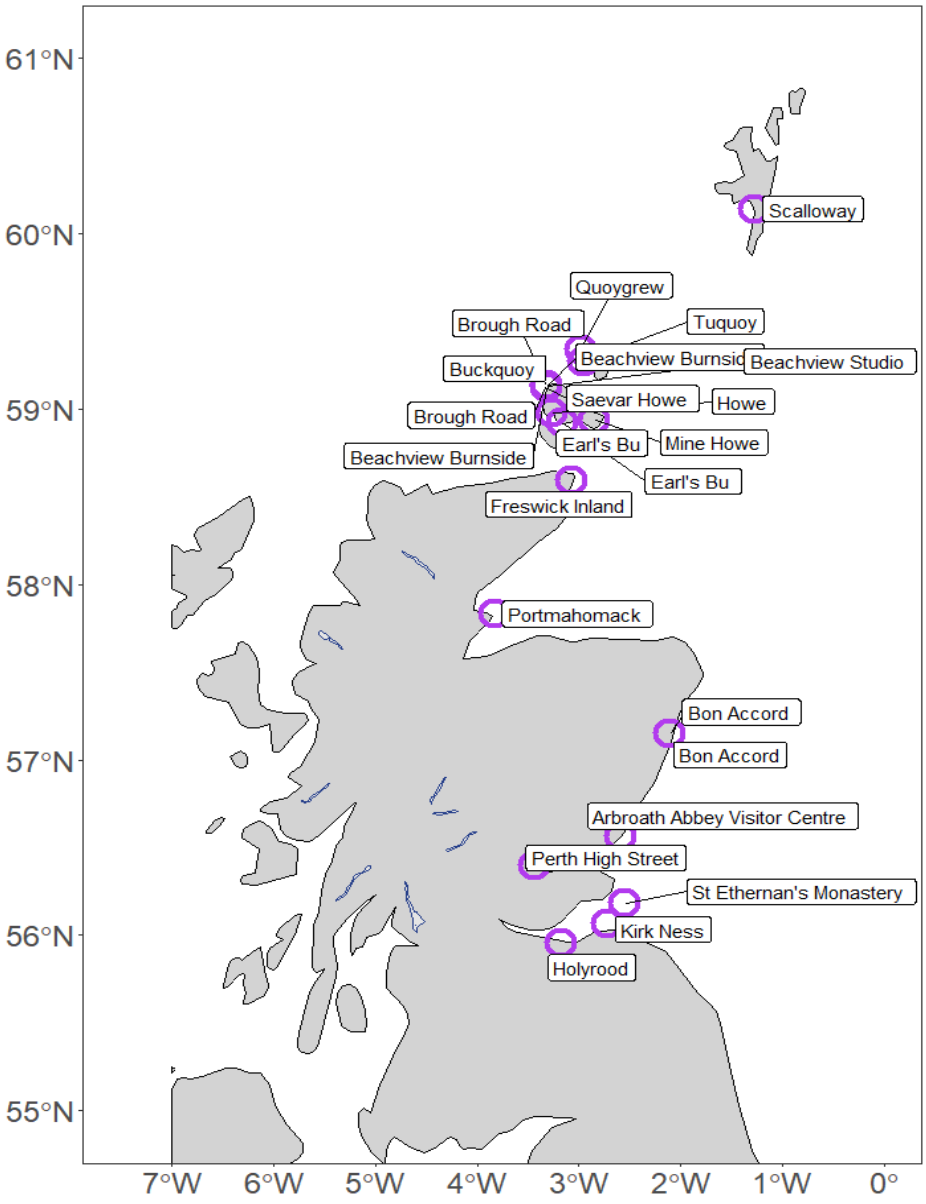


FIGURE 7.12: Map of Scottish archaeological sites with identified *Salmo* sp. remains (n=22

7.6 Identification of Archaeological *Salmo* sp. Remains using ZooMS

One of the major results of reviewing the assemblages of North Sea medieval fish bones for *Salmo* sp. remains is the compilation of a database that can be used to identify sites and individual bones to sample for further biomolecular testing. To this end, a total of 199 archaeological fish bones from sixteen archaeological sites located in England, Scotland, Denmark, and the Netherlands were sampled for ZooMS analysis– constituting approximately 7.9% of the identified *Salmo* sp. remains reported above. These samples were selected from assemblages identified during the review of *Salmo* sp. remains in the study area, and collected from storage depots, museums, and universities. Table 6.4 below shows the ZooMS identification results for the samples, 92.9% (n= 185) of which have been confirmed as either *Salmo salar* or *Salmo trutta*.

Site Name	***Salmo salar***	***Salmo trutta***	**% of *Salmo* sp. NISP**	**Gadus morhua**	***Esox lucius***	**Scophthalimidae**	**Cyprinidae**
16-22 Coppergate	54	4	22.65	1	1		
ASR 13 Lindegården		2	100.0				
ASR 2090 von Støckens Plads		4	100.0				
ASR 9 Posthuset	10	36	23.0				
Earl's Bu	9	14	29.1	8			
Heveskeklooster (HVSK)	1		100.0				
Huis Malburg (MAL97)	1		100.0				
Huize van den Kasteele			100.0		1		
In den Struys (IS Veere)	3		21.4			1	
Johan van Oldenbarneveltlaan (JOB84)	2		33.3				
Minderbroedersklooster (HTMK)	19		63.3				1
Nieuw Rhijngeest-Zuid (OBSP14)	14		12.6				
Oude en niuewe Gasthuis (ONG86)	2	1	75.0				
Plantage Leiderdorp (LE-PL-13)	1		12.5		1		
Stadhuis Zutphen (ZU-ST)	1		100.0				
Tjitsma Winjaldum (WIJ)	5	2	16.6				
TOTALS	**122**	**63**		**9**	**3**	**1**	**1**

TABLE 7.4: ZooMS results for 199 archaeological fish bones from sites around the North Sea basin area

The 7.1% (n=14) of samples that were not identified as either salmon or trout mostly represent misidentified cranial elements, uncertain identifications of species with similar morphology, and the results of a small

experiment on vertebral fragments from Earl's Bu. Table 6.5 below shows the breakdown of these non-*salmo* sp. identification results.

Sample ID	Site	Element	Original ID	ZooMS ID
EB_016	Earl's Bu	vertebral fragment	None	*Gadus morhua*
EB_017	Earl's Bu	vertebral fragment	None	*Gadus morhua*
EB_022	Earl's Bu	vertebral fragment	None	*Gadus morhua*
EB_024	Earl's Bu	vertebral fragment	None	*Gadus morhua*
EB_026	Earl's Bu	vertebral fragment	None	*Gadus morhua*
EB_027	Earl's Bu	vertebral fragment	None	*Gadus morhua*
EB_028	Earl's Bu	vertebral fragment	None	*Gadus morhua*
EB_061	Earl's Bu	preopercular fragment	Salmo sp.	*Gadus morhua*
LMQ_030	16-22 Coppergate	caudal vertebra	Salmo sp.	*Esox lucius*
LMQ_043	16-22 Coppergate	precaudal vertebra	Salmo sp.	*Gadus morhua*
NL_salmo_020	In den Struys	cranial fragment	Salmo sp.	Scopthalmidae
NL_salmo_037	Plantage	dentary	Salmo sp.	*Esox lucius*
NL_salmo_077	Minderbroedersklooster	dentary	Salmo sp.	Cyprinidae
NL_salmo_112	Huize van den Kasteele	ceratohyal	*Salmo salar*	*Esox lucius*

TABLE 7.5: Samples with ZooMS identifications other than *Salmo salar* or *Salmo trutta*

Previous analysts appeared to have had a difficult time differentiating between the cranial elements of *Salmo* sp. fishes and pike (*Esox lucius*, especially when the remains are fragmentary. This confusion is understandable, as the orders Esocidae and Salmonidae are genetically close, and display some morphological and osteological similarities (Betancur-R et al. 2017; Rondeau et al. 2014). The two cod (*Gadus morhua*) misidentifications, of a fragmentary preopercular and a precaudal vertebrae, were also likely due to analyst error and were selected for further ZooMS analysis because of suspected misidentifications. Eight vertebral fragments from Earl's Bu were sampled as part of a small experiment looking at unidentified pieces of bone that had splintered off from whole vertebrae at some point during post-excavation analysis or storage, and of these fragments 7 were identified as *Gadus morhua* and only one as *Salmo salar* (included in Table 6.5 above). Of the 185 samples that were confirmed to be from the genus *Salmo*, 122 were identified using ZooMS as *Salmo salar* and 63 as *Salmo trutta*. The vast majority of these (n=173) were vertebral elements of some kind (see Table 6.6), with a few cranial, appendicular, and indeterminate elements also contained within the sample.

Element	*Salmo salar*	*Salmo trutta*	TOTAL
articular	1		1
axis vertebra	2	2	4
caudal vertebra	43	37	80
ceratohyal	2		2
cleithrum	1		1
cranial bone	1	1	2
dentary	1		1
precaudal vertebra	40	18	58
rib	3		3
vertebral fragment	27	3	30
indeterminate	1	2	3
TOTAL	**122**	**63**	**185**

TABLE 7.6: *Salmo* sp. elements and associated ZooMS identifications

While the overall division of the *Salmo* sp. sample's ZooMS identifications is 65.9% *Salmo salar* and 34.1% *Salmo trutta*, the percent NISP breakdown by country and site reflects regional differences in the exploitation of Atlantic salmon and brown/sea trout (Figure 13, below, and Table 6.4, previously). The largest single assemblage of bones sampled for ZooMS analysis in this study was from the 16-22 Coppergate site located in York, England (n=60). The samples studied were selected from contexts which date to between 400-1720, though the vast majority (n=55) are from contexts dated between 850-1280CE, representing Anglo-Scandinavian, Anglo-Saxon, and Anglo-Norman occupations of the city (R. A. Hall 2014). Salmon dominated the assemblage from Coppergate, with 54 *Salmo salar* identifications and only 4 identified as *Salmo trutta*, and all were likely sourced from the nearby Rive Ouse, a modern day salmon river with a small, but recovering, Atlantic salmon and sea trout population (Environment Agency 2017). The Earl's Bu site from Orphir, Orkney is a high-status Norse period site with samples taken from contexts dated between 750-1200CE. Unlike Coppergate in England, the Earl's Bu identifications are predominantly *Salmo trutta* (n=14), with only 9 *Salmo salar* bones present. The presence of salmon is interesting, however, as Orkney has not historically had a native Atlantic salmon population, due to it's lack of the deep, fast-flowing rivers where migratory salmon prefer to spawn (Thomson 2015). This implies that the Norse settlers at Earl's Bu imported Atlantic salmon from somewhere in Scandinavia or mainland Scotland, possibly to use as part of documented feasting activity at the site (Anonymous 2018). The trout from Earl's Bu are likely sea trout, the migratory ecotypes of *Salmo trutta* which are still found in abundance in the small *burns* and lochs of the Orkney Islands (Thomson 2015).

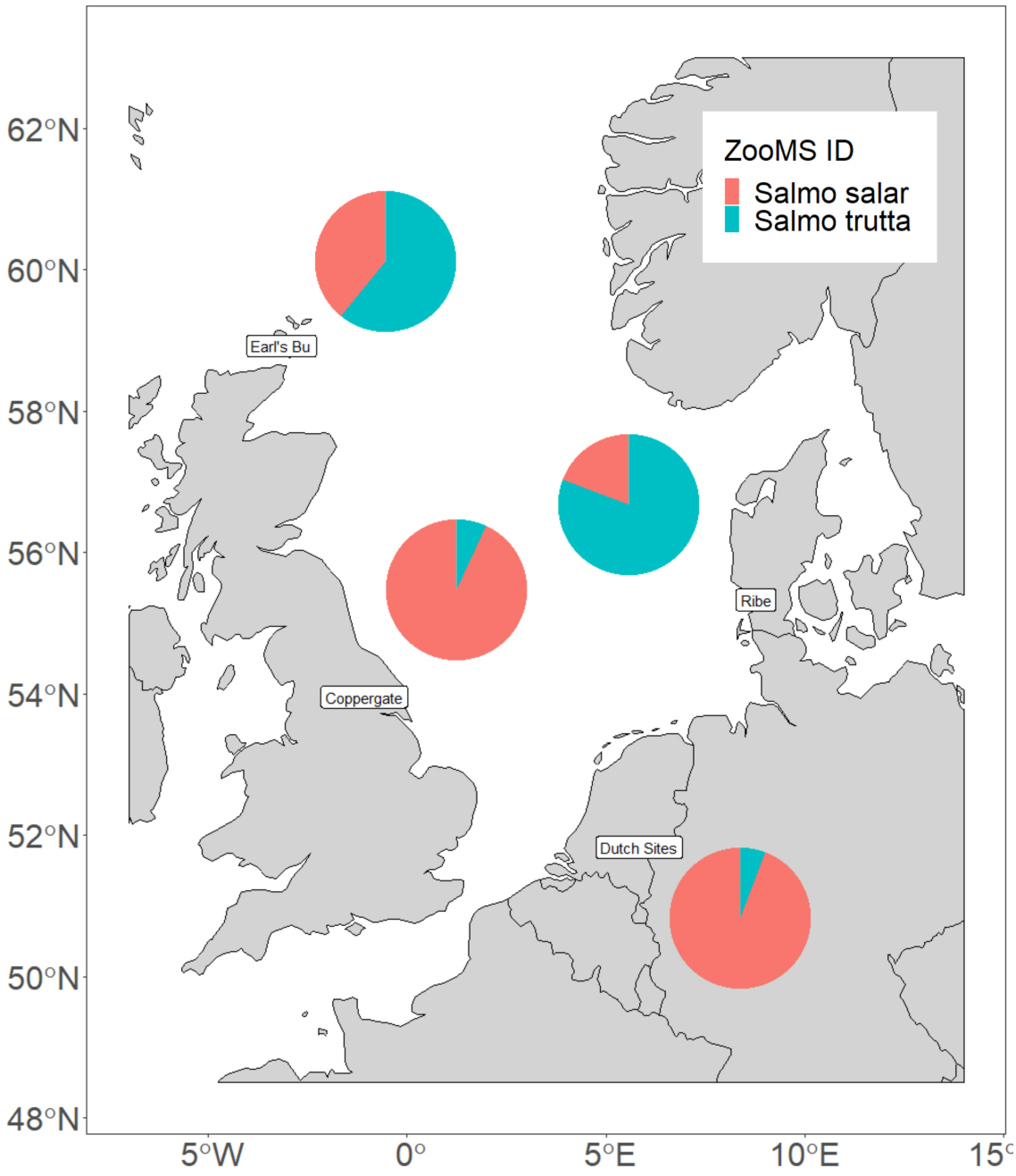


FIGURE 7.13: ZooMS Samples by Country

The assemblage of *Salmo* sp. samples from Denmark were taken from three separate excavations from Ribe, the site of an early medievcal marketplace and later medieval town, located in South-west Jutland on the North Sea coast. The majority of samples (n=46) were from the large and well-publicized ASR 9 Posthuset excavation, which dates from between 700-1200 CE. Most of the samples from the ASR 9 Posthuset site date from the earliest period of the site, when it was a communal space dedicated to craft manufacturing and market activity (Bencard, L. B. Jørgensen, and Madsen 1981; Sovso 2022). Like Earl's Bu in Orkney, the majority of samples (n=36)

were identified as *Salmo trutta* via ZooMS analysis, however, unlike Orkney, the Ribe Å (Ribe River) has historically supported a significant population of both Atlantic salmon and brown/sea trout (Geertz-Hansen and J. Jørgensen 1996). The other two sites in Ribe (ASR 2090 von Støckens Plads (1000-1200 CE) and ASR 13 Lindegården (1200-1300 CE)), both located across the river in the later medieval town settlement, only had 2 and 4 samples analysed, respectively. However, all six of these bones were assigned *Salmo trutta* identifications using ZooMS. The predominance of *Salmo trutta* samples from the three Ribe sites may reflect a larger local population of brown/sea trout during the Medieval Period, or even a preference for these fish amongst the inhabitants of the area.

Finally, the assemblages of *Salmo* sp. samples from the Netherlands (n=52) shows a similar dominance of salmon identifications to that seen at the Coppergate site in England, though in this case they are spread across 10 individual sites from seven of the country's twelve provinces. The majority of these sites (n=7) contained very few *Salmo* sp. bones, and 3 or fewer samples were taken from them (see figure 14B). The bones from these seven sites made up 23.1% of the Dutch sample (n=12 bones), and all but one of them were identified as *Salmo salar* via ZooMS analysis. The two larger assemblages were sampled from sites located in Oegstgeest, South Holland and 's-Hertogenbosch, North Brabant and represent an early urban center (Nieuw Rhijngeest-Zuid, n=14) and a High Medieval Franciscan monastery (Minderbroederskloosterster, n=19), respectively. The OBSP14 site, located in Oegstgeest, is broadly dated to between 475-725 CE and represents one of the earliest proto-urban centers in the Netherlands, with it's most intensive period of use occurring before the more-well-known 7th-century trading center of Dorestad near Utrecht (Es and Verwers 2010). The OBSP14 site has a reported 130 *Salmo* sp. elements, however only a portion of these were available for biomolecular sampling which resulted in a relatively small sample of 14 bones– all identified as *Salmo salar*. The Minderbroederskloosterster site is located in 's-Hertogenbosch, and, while the Franciscan's had arrived in the city as early as 1228 CE, the contexts sampled from this site date to a very narrow 50-year period between 1375-1425CE (Genabeek 2016). Of the 25 *Salmo* sp. bones from the site, a total of 19 were subsampled and subjected to ZooMS analysis, with all identified as *Salmo salar*. This representative sample, combined with the fact that this is a late-Medieval monastic context, supports conclusions about ecclesiastical demand for Atlantic salmon (see Discussion below).

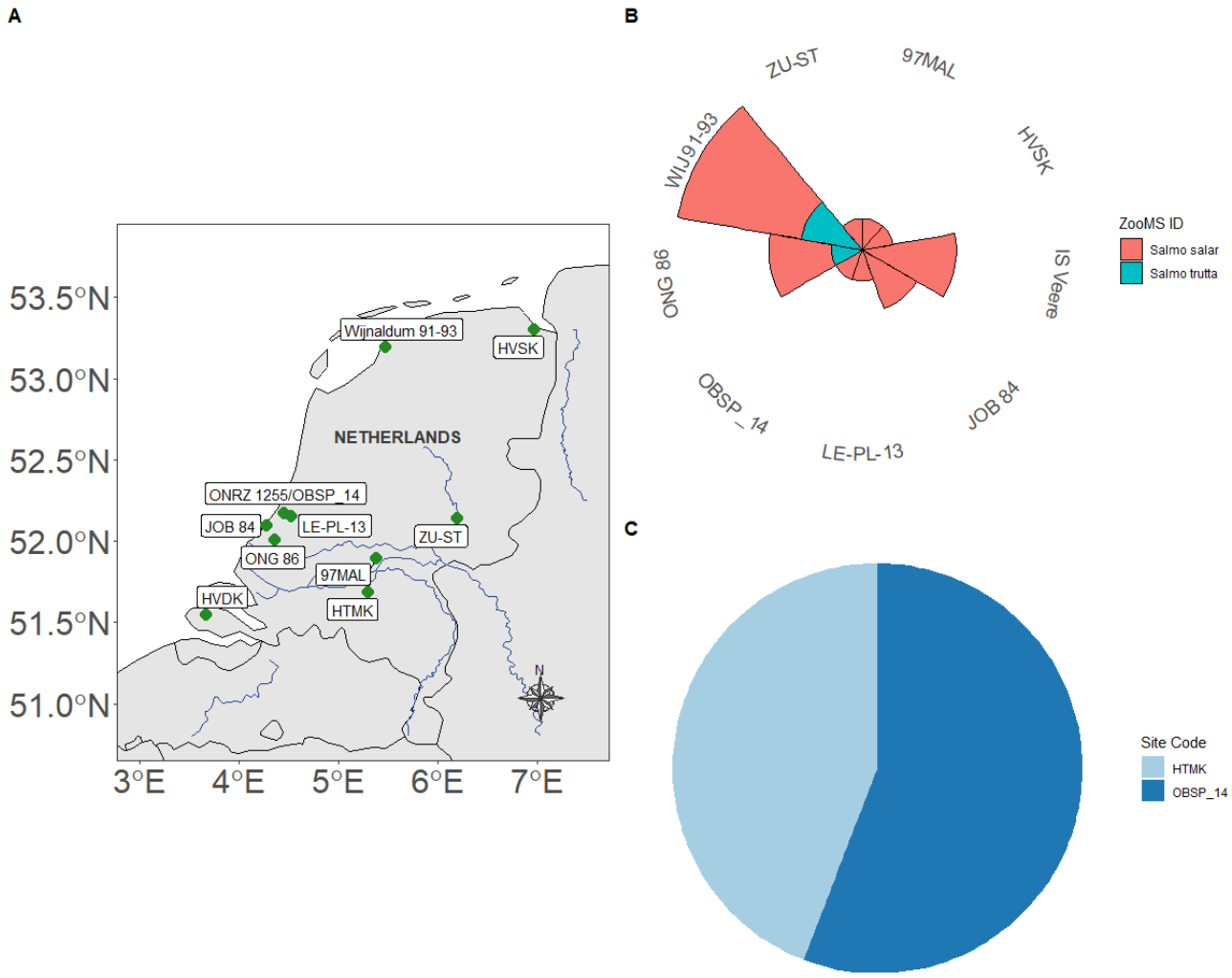


FIGURE 7.14: **A.)** Map of Dutch archaeological site locations that *Salmo* sp. bones were sampled from. **B.)** Polar plot showing the makeup of the small assemblages (all contain N≤3) from the Netherlands. Only two samples (from WIJ and ONG86) were identified using ZooMS as *Salmo trutta*. **C.)** Pie chart representing the proportion of samples identified as *Salmo salar* from each of the two larger sites, Minderbroedersklooster in Den Bosch and Nieuw Rhijngeest-Zuid 2009 2014 in Oegstgeest

7.7 Discussion & Conclusion

The ichthyoarchaeological and ZooMS data reviewed here provides a unique opportunity to investigate the presence and proportions of a single economically-important genus at medieval archaeological sites across the North Sea basin area. Though a far smaller assemblage than may be studied for other important species like cod, herring, or eel, the 2515 bones identified in the ichthyoarchaeological review, 197 of which have been subjected to ZooMS analysis, provide insight into trends in human exploitation of *Salmo* sp. fish over time. Conclusions made from the initial review of archaeological records are supported by the subsequent ZooMS analysis conducted, showing the power of complementary analysis for ichthyoarchaeological study.

Figure 15 displays the changing amounts of *Salmo* sp. bones recovered from all archaeological contexts,

with only the large outlier Belgian site, Chateau La Roche en Ardenne, removed. The justification for removing Chateau La Roche en Ardenne is twofold. First, the NISP for this site (n=598) is 2.33x larger than the next closest assemblage (Coppergate, n=260), making the assemblages hard to compare. Second, as this unusually large assemblage is from a high status site with a comparatively narrow date range (1000-1300CE), it abnormally skews the representation of high status sites among the set of total *Salmo* sp. NISP. With this site removed we are able to examine a more representative visualization of the new total *Salmo* sp. NISP for the review (n=1918), compared with the total fish NISP from the included sites (n=822823).

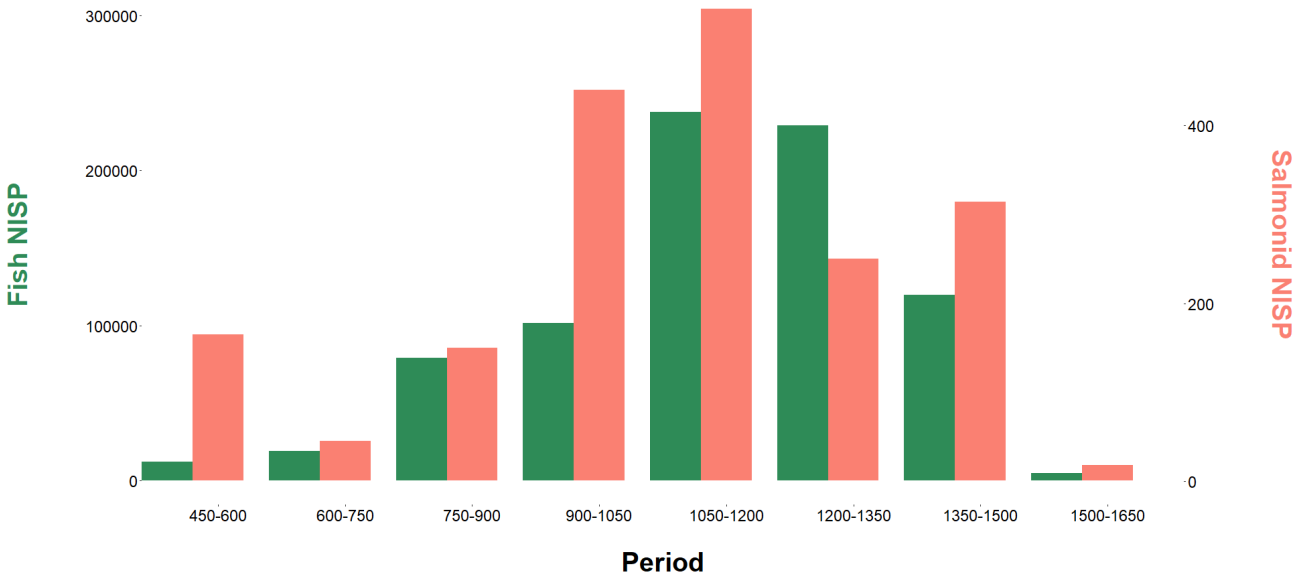


FIGURE 7.15: Multivariate Comparison of *Salmo* sp. NISP and Overall Fish NISP Over Time (Excluding outlier site Chateau La Roche en Ardenne

The general trend visible within the NSAS assemblage is lower NISP values (<200 total) from sites with midpoints that lie between 450-900CE, a drastic jump in NISP value starting around 900CE and continuing to approximately 1200CE (n>400), and then a drop in NISP value post-1200CE (n>200 but <400). Table 6.7 illustrates the changes in overall site numbers over time, with a noticeable increase in excavated archaeological sites with a post-900CE midpoint. In general the number of total sites increases as time goes on, which may indicate a greater interest in "High Medieval" archaeological sites and/or better preservation of artifacts from these time periods. The numbers of both total fish elements (Fish NISP) and *Salmo* sp. elements (Salmo sp. NISP) recovered does not follow this general trend, and varies significantly through time. When viewed together, the change in NISP value at these three site types demonstrates an overall increase in *Salmo* sp. exploitation, concentrated around the described 11th-century fish event horizon (J. H. Barrett, Locker, and C. M. Roberts 2004a). If the majority of the *Salmo* sp. remains reviewed are, in fact, Atlantic salmon, this implies that they were considered more akin to marine fish during the Medieval Period, at least as far as fishing strategy is concerned. This makes sense considering the historical evidence for large weirs that would be used to catch salmon are concentrated in estuarine and coastal areas rather than upstream river environments (Richard Hoffmann 2012; R. C. Hoffmann 1996, 2015). Indeed, contemporary sources like Aelfric's Colloquy, an 11th century monastic text, make specific

note of salmon as marine rather than freshwater fish (Harris 2003).

Time Period	Total Archaeological Sites	Total Fish NISP	Proportion of Total Fish NISP by Period	Total *Salmo* sp. NISP	Period Proportion of Total *Salmo* sp. NISP
450-600 CE	13	12453	1.29%	165	8.6%
600-750 CE	12	18458	1.90%	44	2.29%
750-900 CE	27	79306	8.18%	150	7.82%
900-1050 CE	40	103664	10.70%	431	22.47%
1050-1200 CE	43	402479	41.53%	530	27.63%
1200-1350 CE	63	229290	23.66%	267	13.92%
1350-1500 CE	48	118924	12.27%	314	16.37%
1500-1650 CE	4	4422	0.47%	17	0.89%
TOTALS	**250**	**968996**	**100%**	**1918**	**100%**

TABLE 7.7: Numbers and Proportions of Sites, Fish and *Salmo* sp. NISPs by Period

Interestingly, when the site numbers and *Salmo* sp. NISPs are investigated through the metric of site type (Table 6.8), a clearer pattern of change in exploitation becomes apparent. Seven broad categories of site type were established when cleaning the NSAS dataset, based on the wide variety of site descriptions available from source databases and individual site reports. For example, the "ecclesiastical" category contains all sites described as monasteries, cloisters, abbeys, and any other site primarily occupied and used by clergy of the Christian church. Urban settlements, by far the largest site type (number of Sites=81, NISP=1186), consisted of domestic and commercial sites centered around town or city centres. Some of the largest assemblages in the NSAS review were urban settlements, including centres of trade and cultural exchange in municipalities like Ribe, Oegstgeest, and York.

Site Type	**Total Salmo sp. NISP**	**Total Number of Sites**
Ecclesiastical	191	18
High Status	191	18
Industrial	4	1
Mixed	12	3
Rural Settlement	186	12
Settlement	148	17
Urban Settlement	1186	81
TOTAL	**1918**	**250**

TABLE 7.8: Number of *Salmo* sp. remains and Sites by Site Type
(Excluding outlier site Chateau La Roche en Ardenne)

Looking specifically at the diachronic changes in *Salmo* sp. NISP over time at these urban settlements (Figure 15), there is a clear increase from the earliest periods to the 900-1050CE period, followed by a steady decline

in NISP value until the end of the study period. Comparatively, the diachronic changes in *Salmo* sp. NISP at ecclesiastical and high status sites show fairly steady rates of presence in the present early periods, and then a large increase in NISP value during the 1350-1500CE period.

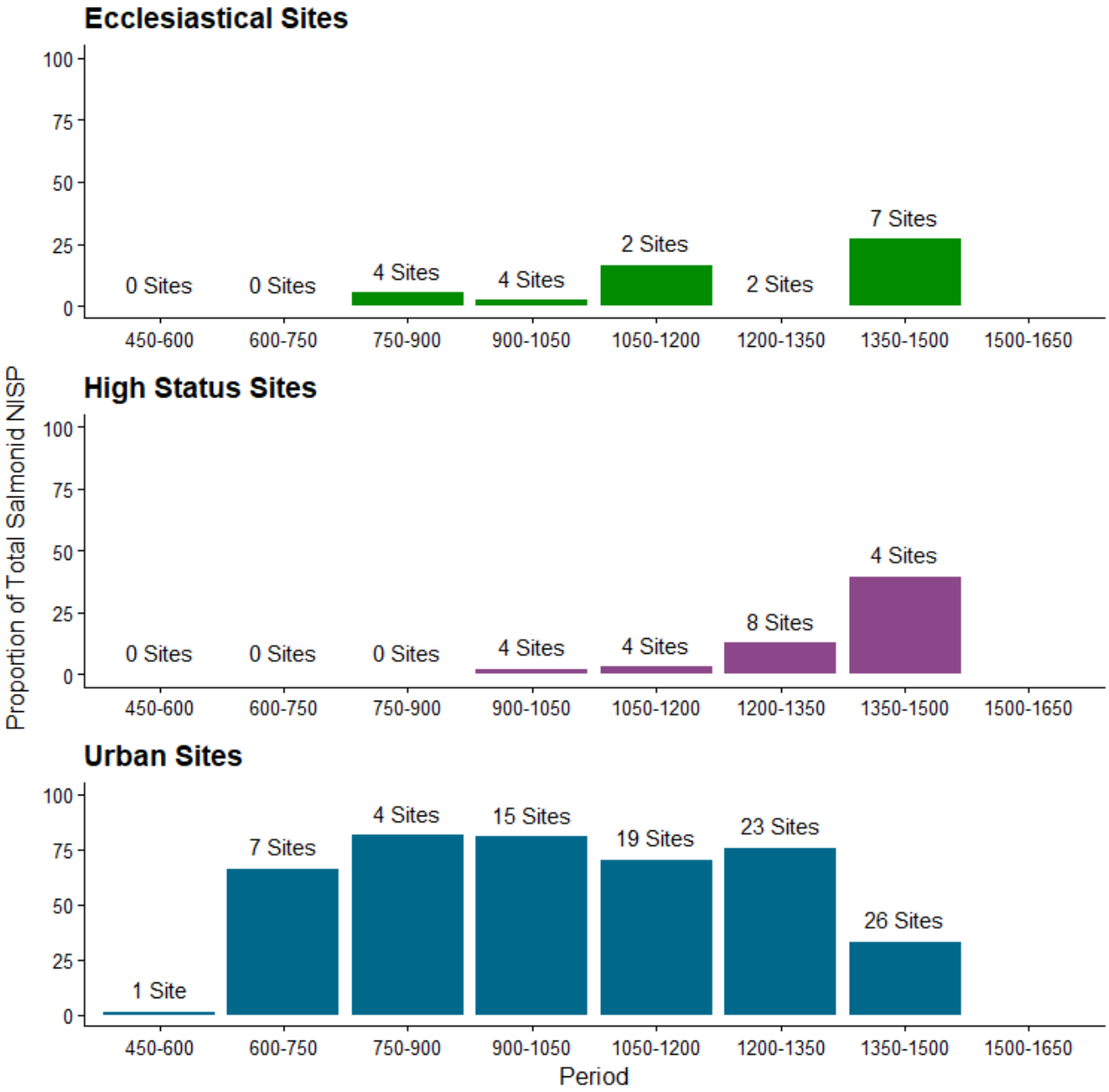


FIGURE 7.16: Comparison of *Salmo* sp. NISP over Time at Ecclesiastial, High status, and Urban Settlements

The jumps in NISP proportion seen at ecclesiastical and high status sites from 1350-1500CE, combined with the decrease seen at urban settlements during the same period, may indicate a shift in ability to procure *Salmo* sp. fishes. While urban settlements may have continued their high demand for salmon, it seems that post-1050 the access to these fish decreased, which is mirrored by a very slight drop in NISP value seen at ecclesiastical sites

during the same period. High status sites show only an increase, which implies that even while other groups had difficulty acquiring salmon, the elite did not. The archaeological record here is supported by historic statues and legislation surrounding salmon weir construction, fish population management, and legality of fishing across the study area. Some of what may be considered the first "conservation" laws regarding limits on salmon catches were enacted in Scotland as early as 1200CE (R. C. Hoffmann 2015), and elite and ecclesiastical control of fishing rights for salmon was tightened as the Late Medieval Period progressed in Germany, the Netherlands, England, and France (J. Galloway 2021; R. C. Hoffmann and Ross 2019; Pickles 2021; The Tweed Foundation 2013).

In addition to the examination of archaeological material itself, one of the benefits of this review is in the analysis of archaeological methods, especially trends in identification and sieving. Figure 17 explores diachronic changes in identification category used by faunal analysts from the earliest reports published in the 1970s to the late 2010s. For this examination, the category Salmon refers to bones which have been confidently identified as *Salmo salar*, Trout refers to those confidently identified as *Salmo trutta*, and *Salmo* sp. is a catch-all category which contains bones of any uncertain identification. As may be expected, the largest category is *Salmo* sp., which reflects the general uncertainty in assigning species identifications to archaeological salmonid bones. Prior to 1980 we see no identifications of Salmon, but these do appear in all other decades. There is a clear, and unsurprising, trend of increasing fish bone identification over time, with the highest NISP value seen in the recent 2010s decade. Interestingly, the highest proportion of confident *Salmo salar* identifications are also from the 2010s– whether this implies a new confidence in identification or is dependent on some other factor is unknown.

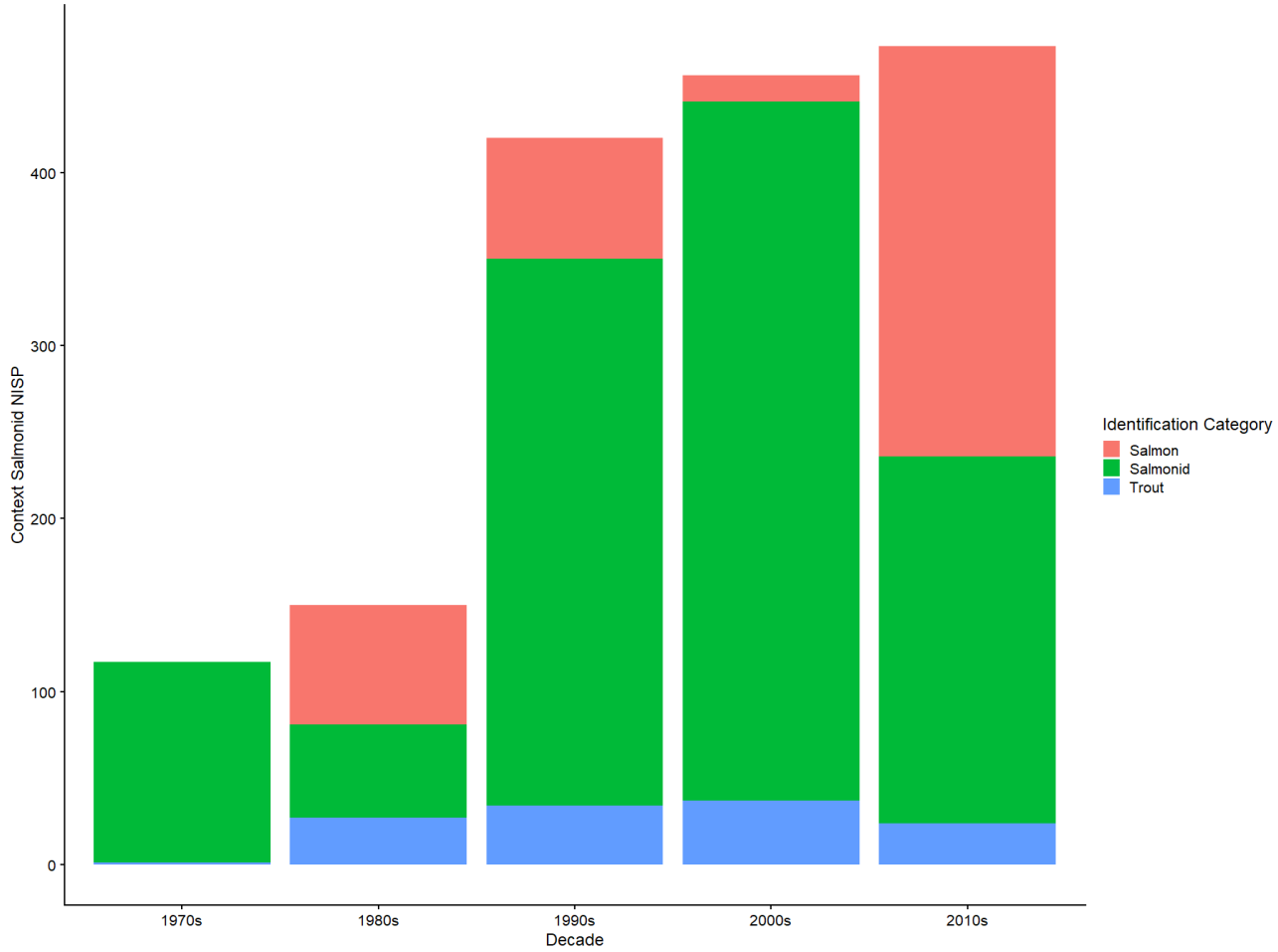


FIGURE 7.17: Identification trends through time for Salmon, Trout, and *Salmo* sp.

As demonstrated by the increase in overall identifications through recent decades, there has been an overall increase in interest in fish remains from archaeological sites during the same period. One of the major factors in the increased ability to identify fish remains is the increase in sieving at archaeological sites across the study area. Figure 18 neatly demonstrates this trend, showing a steady and substantial increase in site sieving over the last 50 years.

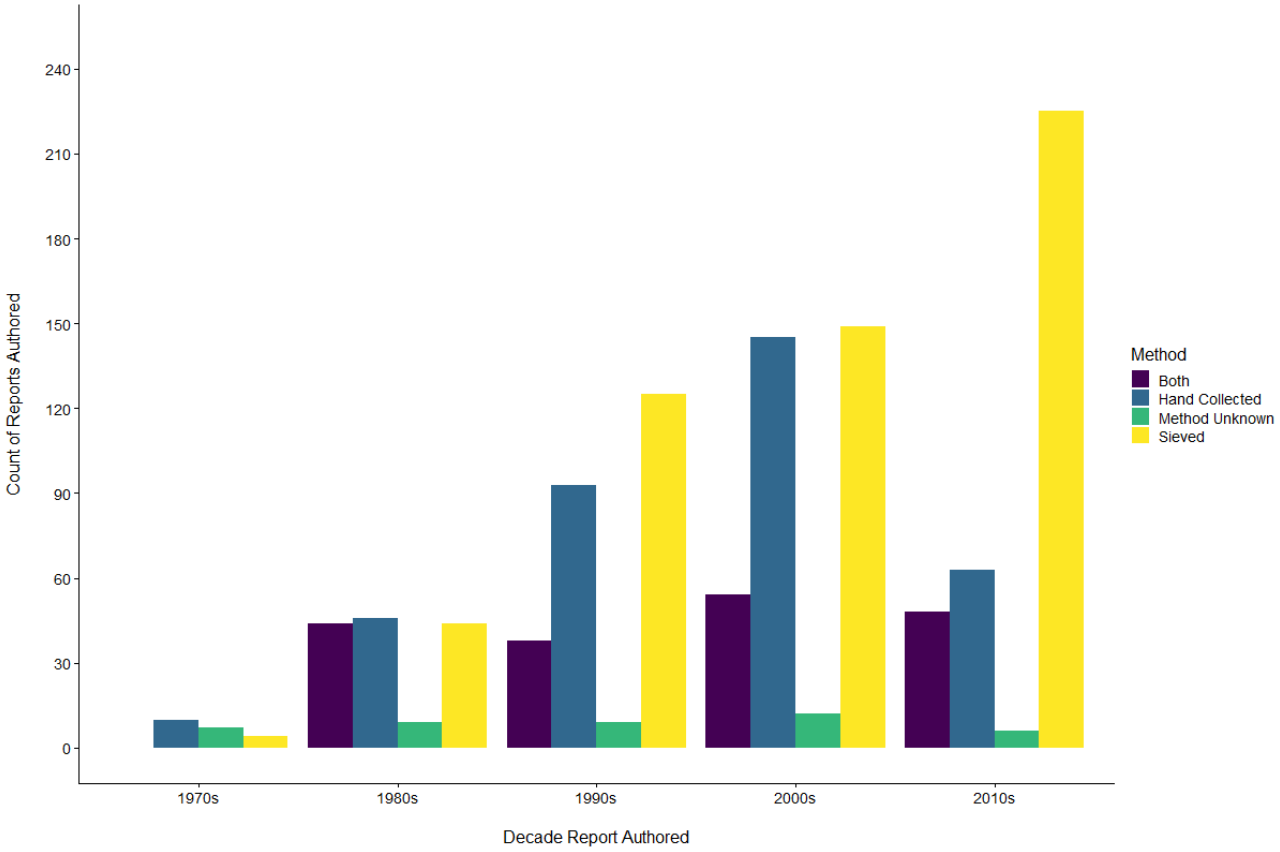


FIGURE 7.18: Collection Methods Outlined in Reports Authored from 1970-2021

This increase in sieving has not only led to an overall increase in fish bone identification, but a much higher recovery rate for *Salmo* sp. (Figure 17). Over 70% (n=1824) of archaeological *Salmo* sp. remains recovered were from contexts which applied some sort of sieving, either on site or during post excavation. Sieve sizes ranged from .3mm to 5mm, and often were used in conjunction with traditional hand collection methods. Its clear that an increase in sieving has led to an increase in recovery of *Salmo* sp. remains, and implies that sites with only hand collected remains may in fact contain remains from these fish which have been missed.

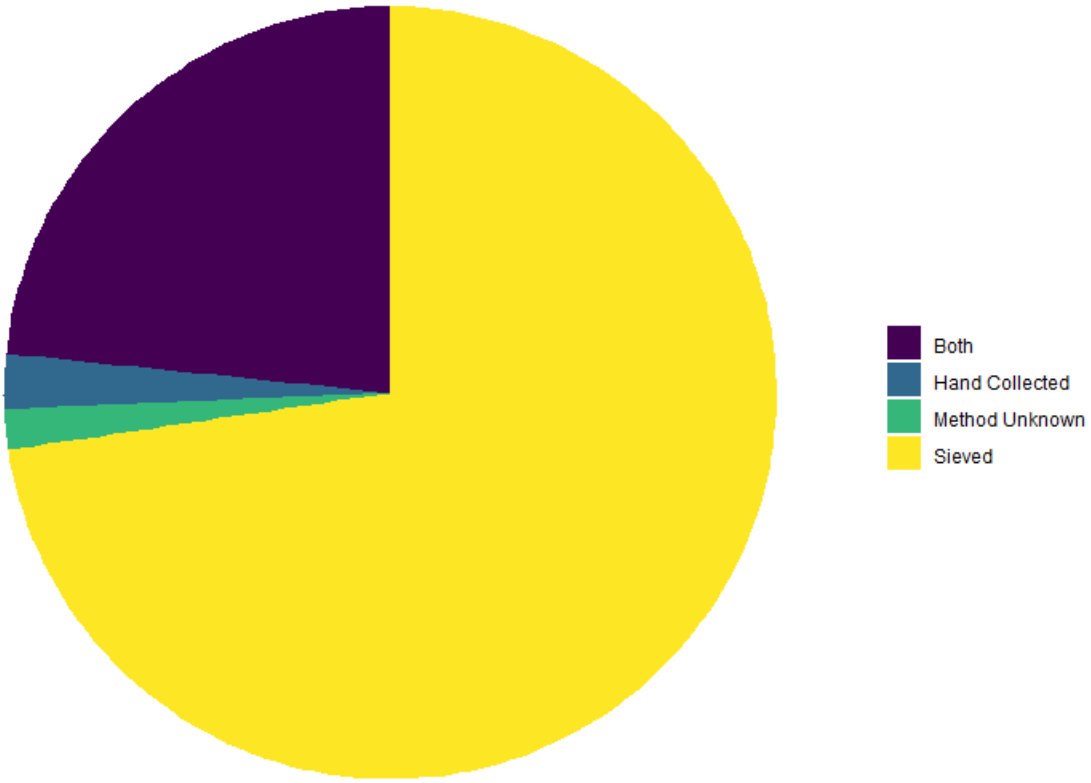


FIGURE 7.19: *Salmo* sp. NISP Proportions by Collection Method

In order to take proper advantage of these drastically increased proportions of sieve-recovered fish bones, alternative identification methods to traditional osteological analysis must be considered. If we want to refine our understanding of the impact and exploitation of Atlantic salmon during the Medieval Period, we must first understand how many of these *Salmo* sp. remains are trout and how many are salmon. There remain several barriers to a more complete understanding of the role Atlantic salmon played in the medieval North Sea Basin area, not the least of which being the question of accurate species identification. Differentiating between Atlantic salmon and brown/sea trout is key to properly interpreting the wide variety of archaeological sites found in northwestern Europe. While osteological identification is possible for some elements, the issues of poor preservation complicate the use of traditional zooarchaeological methods. We have proposed three additional methods to aid in bridging the gap, and Table 6.9 below presents benefits and costs of these methods in more detail. Implementing these methods into interdisciplinary studies of archaeological *Salmo* sp. will not only strengthen our knowledge of this particular species, but our overall interpretation of medieval fisheries across a wide geographical area. The results of the pilot study of *Salmo sp.* remains identified using collagen peptide fingerprinting reported here demonstrate the practicality of high-throughput ZooMS analysis for single-genus reviews like this one. With 185 identifications to species made within the genus *Salmo*, these results indicate geographic variability in proportions of Atlantic salmon vs. Brown/sea trout at archaeological sites around the North Sea basin area. With lower

overall costs and destructive sampling requirements than aDNA analysis, along with the ability to rapidly process hundreds of samples in a relatively short period of time, it's clear that high-throughput applications of ZooMS can greatly improve archaeological abundance knowledge on both a site and regional level.

After conducting this expansive review of *Salmo* sp. remains through time and across the North Sea Basin it has become clear that the archaeological record contains less salmon remains than would be expected based on the perceived importance of these fish during the Medieval Period. While documentary and literary records, artistic representations, and recipe books all refer to the prestige and ubiquity of salmon on the medieval dinner table, the total *Salmo* sp. NISP (n=2515) from this review falls far short. The question of "missing" animal remains in the archaeological record is not a new one, however, with observed discrepancies between the perceived importance of a given species sometimes evident when viewing archaeological and documentary data together (Albarella 1999). One of the most famous examples of these "missing" animal remains are domestic goats in the European medieval period, which have, like *Salmo* sp. fishes, historically been over-represented in the documentary record and relatively scarce in zooarchaeological assemblages (Albarella 1999, 2003). As demonstrated in this chapter with *Salmo* sp. fishes, ZooMS identifications have clarified some aspects of the "missing" goat representation in the archaeological record, but both groups of animals still remain more common within the documentary record than the physical one (Salvagno and Albarella 2019). This being said, we do see a general increase in *Salmo* sp. exploitation based on archaeological remains surrounding the 11th-century fish event horizon, followed by a dramatic drop in *Salmo* sp. NISP values immediately after. Despite the overall drop in *Salmo* sp. numbers, there is a visible increase in the proportion of *Salmo* sp. remains seen at Ecclesiastical and High Status sites, suggesting a great degree of influence on *Salmo* sp. exploitation by those occupying elite and religious sites.

Method	Positives	Negatives	Costs
Traditional comparative zooarchaeology	Cheap and relatively quick	Difficulties with preservation, requires specialist training and reference collection, some elements indistinguishable, accuracy not guaranteed.	Dependant on post-excavation freelance market rates and budget
Geometric morphometrics	Cheap and accurate, even for elements which cannot usually be distinguished	Time consuming photography, requires specialist software, equipment and training. Identification protocol not standardized.	Camera and labor
Bulk stable isotope analysis	D13C and D15N values can aid in identification of salmon and trout. Provides additional environmental data. Relatively cheap.	Specialist training and equipment required. Destructive process, which requires minimum 200mg samples.	Dependent on lab, can be as little as £15 per sample. In-house costs may vary.
Incremental stable isotope analysis	Provides time-series of environmental data for a single individual.	Requires large samples, fully destructive. Sampling protocol requires specialized equipment and is not standardized.	Dependent on lab and availability of experienced personnel.
Zooarchaeology by Mass Spectrometry	Provides identification to species. Less material required for sampling. Can be applied to collagen extracted for SI analysis.	Hybrids possibly complicate IDs. Specialist lab, training and equipment required. Destructive process.	Dependent on lab and availability of experienced personnel.

TABLE 7.9: Cost-Benefit Table of Methods for Identification of archaeological *Salmo* sp. remains.

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Chapter 8

A Combined Biomolecular Method for the Identification of *Salmo* sp. Ecotypes within Ichthyoarchaeological Assemblages

8.1 Abstract

Sea trout, the behaviorally anadromous morph of brown trout (*Salmo trutta*), are an economically and culturally important fish across the North Sea basin area. While not as popular as Atlantic salmon, references to these migratory trout occur throughout the documentary record. Their presence in the archaeological record, however, has remained more obscure, due to the limited potential for morphological differentiation between skeletal elements of Atlantic salmon, brown trout and sea trout. To investigate the true significance of sea trout in the Medieval Period,we apply a novel, combined biomolecular approach to identify sea trout in the archaeological record, investigating case studies from two UK sites in the North Sea basin. Bulk carbon (δ^{13}C) and nitrogen (δ^{15}N) stable isotope analysis and collagen peptide sequencing (ZooMS) are used to differentiate clearly between potamodromous brown trout, anadromous sea trout, and anadromous Atlantic salmon.

8.2 Introduction

Brown trout, *Salmo trutta*, have been exploited by humans living in Europe for at least 40,000 years (Turrero, García-Vázquez, and Leaniz 2014). Brown trout can be found in river systems originating from the Mediterranean in the south, the White Sea to the north, and the North Atlantic to the west, and reached their maximum distribution just after the end of the Younger Dryas, approximately 11,700 years ago (Hynes, Ferguson, and McCann 1996; Rasmussen et al. 2006; Turrero, García-Vázquez, and Leaniz 2014). Their impressive geographic range has led to a wide variety of ecotypes which fill riverine, lacustrine, estuarine, and anadromous environmental niches (B. Jonsson and N. Jonsson 2007). While these fish never attained the widespread cultural and economic influence of the closely related Atlantic salmon (*Salmo salar*), brown trout (*Salmo trutta*) have played a key role in the fishing activity of Northwestern Europe through time, and especially during the Medieval Period c. 500-1500 CE (Coenen 1580). While Atlantic salmon have historically been considered both marine and freshwater fish, depending on the source and life cycle position in question (Coenen 1580; Harris 2003), brown trout are generally thought of as strictly potamodromous, or freshwater, fish– with most occupying river and lake environments across their range. There are, however, a large proportion of *Salmo trutta* individuals which undergo a similar *smolting* process to that of the Atlantic salmon and become behaviorally anadromous– travelling from their natal streams or lakes out to the open ocean, and returning in order to spawn after an intensive period of feeding (B. Jonsson and N. Jonsson 2007). This anadromous ecotype is known as sea-run trout, sea trout, or peel/peal in English, and variously as finnock (Scots), sewin (Welsh), zeeforel (Dutch), Meerforelle (Danish, German, Norwegian, and Swedish), truite saumonée (French) across its range.

8.2.1 *Salmo* ecotypes

Sea trout, sometimes differentiated from brown trout with the Latin name *Salmo trutta* morpha *trutta*, grow far larger than their freshwater-resident cousins, often rivalling Atlantic salmon in size and coloration (B. Jonsson and N. Jonsson 2007). All anadromous Atlantic salmon and most anadromous sea trout undergo a series of physical, behavioural and morphological changes, known as smolting, that allow the fish to transition from their juvenile freshwater environments to their adult ocean environment (McCormick et al. 1998). Smolts of both species develop a tolerance for saltwater, shift to their "pelagic camouflage" silver, white and dark grey coloration, and increase both their buoyancy and scope for growth (B. Jonsson and N. Jonsson 2007; McCormick et al. 1998). Sea trout develop several physical features that allow them to be differentiated from salmon, (Figure 1) including characteristic dark spots which extend below the lateral line, a triangular rather than forked tail, and a more

rounded head. Despite these physical differences, the skeletal structure of both species remains the same, with differentiation between them generally based only on overall size (Figure 2).



FIGURE 8.1: Illustration of Atlantic salmon (top) and sea trout (bottom) showing physical features characteristic of each fish. Image ©Sveriges Sportfiske- och Fiskevårdsförbund.



FIGURE 8.2: Caudal vertebrae of adult *Salmo salar* (top) and *Salmo trutta* (bottom).

Despite following the same general anadromous pattern, there remains some variability in foraging ecology between salmon and sea trout, resulting in detectable differences in bulk carbon and nitrogen isotope ratios in both modern and archaeological specimens. Modern ecological data shows that bulk stable isotope signatures of adult anadromous Atlantic salmon should result in typically "marine" signatures, with high δ^{13}C values and moderately high δ^{15}N values. Modern salmon of European origin have a reported δ^{13}C range of -18.7‰ to -13.8‰ (Almodóvar et al. 2020; Dempson et al. 2010; MacKenzie et al. 2011; O'Toole et al. 2020; Trueman 2022). δ^{15}N values for adult anadromous European Atlantic salmon have a reported range of 6.9‰ to 14.8‰ (Almodóvar et al. 2020; Dempson et al. 2010; MacKenzie et al. 2011; O'Toole et al. 2020; Trueman 2022). The mean δ^{15}N values for brown trout and Atlantic salmon are fairly comparable, with adult salmon of European origin having a reported mean of 10.6 ± 0.7‰, and adult potamodromous trout having a reported mean δ^{15}N value of 9.2 ± 1.5‰ (Almodóvar et al. 2020; Dempson et al. 2010; MacKenzie et al. 2011; McCarthy and Waldron 2000; O'Toole et al. 2020; Trueman 2022).

Critically, anadromous sea trout show enriched δ^{15}N values, with a mean value of 14.7 ± 1.3‰ (McCarthy and Waldron 2000; Poiesz et al. 2021), resulting in an average difference of 4.1‰ – on the scale of a trophic level increase (3.0-5.0‰) from values seen in Atlantic salmon (Schoeninger and DeNiro 1984). These differences are attributed to the increased access to fish-derived protein by anadromous sea trout which migrate to estuarine and marine environments, which result in a faster growth rate, overall increased body size, and increased access to nitrogen-rich foraging habitats (McCarthy and Waldron 2000). Identifying the mechanisms behind the observed isotopic differences between Atlantic salmon and anadromous sea trout is slightly more complex, due to

their surface-level similarities in size, feeding strategy, and life cycle (B. Jonsson and N. Jonsson 2007; Kristensen et al. 2019). While both fish are anadromous, and leave freshwater environments around the same point in their life cycle, their patterns of foraging ecology remain fairly distinct, with a great deal of regional variation seen in both species (B. Jonsson and N. Jonsson 2007; Kristensen et al. 2019; McCormick et al. 1998; Strøm et al. 2018). Sea trout and salmon both begin feeding on fish larvae, copepods, and amphipods around the same time, however the overall productivity of foraging environments preferred by sea trout may be higher than those of salmon (Aas et al. 2010; B. Jonsson and N. Jonsson 2007; Strøm et al. 2018). While most Atlantic salmon populations tend to directly migrate out to their open ocean feeding grounds, and spend most of their marine phase within the first 10m of the pelagic zone, sea trout appear to show greater variation in their migration patterns (Kristensen et al. 2019; Strøm et al. 2018). One comprehensive tagging study of sea trout from Denmark showed that, while some individuals travelled up to 500km away from their natal river outlet, all fish stayed within 100km of the coastline (Kristensen et al. 2019). This suggests that most anadromous sea trout are foraging in exclusively nearshore and estuarine environments. Estuarine and nearshore nitrogen cycling is a complex field of study, however higher overall nitrogen values from both anthropogenic impacts and natural riverine runoff is known to impact the base nitrogen levels of primary producers in these environments, thereby increasing the nitrogen values of the entire local trophic web (European Environment Agency 2019; E. Guiry 2019; Woodland et al. 2015).

Though salmon and sea trout can be identified easily in life, this becomes harder after deposition into the archaeological record, where only bone and scales are likely to survive in most environments. Both *Salmo salar* and *Salmo trutta* display a characteristic 'honeycomb' bone texture, especially in vertebral elements, which allow them to be easily differentiated from morphologically similar species like Northern pike (*Esox lucius*) (Watt, Pierce, and Boyle 1997). The presence of this honeycomb structural feature was one of the key factors in confirming previous IDs as belonging to the *Salmo* genus, which resulted in a sample of 94 elements that were confidently identified as being either salmon or trout (*Salmo* sp.) and included in this study. While there are some skeletal elements which can be used to identify archaeological salmonid remains to species, they are primarily cranial elements, which very rarely survive the taphonomic processes fish bones are subjected to post-deposition (Kacem and Meunier 2009; Kirczuk and Domagała 2011; Locke 1929; Norden 1961; Tchernavin 1938; Watt, Pierce, and Boyle 1997). The survival of salmon elements within ichthyoarchaeological assemblages is often heavily biassed towards vertebrae, which are more robust and dense than cranial elements and can better withstand diagenetic processes (Lubinski 1996). This limits the potential identification of archaeological salmonid bones even further, as almost all vertebrae (with the exception of the atlas, or first vertebra) in *Salmo salar* and *Salmo trutta* are morphologically indistinguishable using traditional osteological identification methods (Feltham and Marquiss 1989; Watt, Pierce, and Boyle 1997). While the vertebrae of adult potamodromous brown trout and anadromous Atlantic salmon can be provisionally separated based on size reconstructions (Table 1), and research suggests that geometric morphometrics analysis can be used to identify the species more closely (Guillaud, Cornette, and Béarez 2016)), these methods do not fully account for crossover in the lower size ranges of potamodromous brown trout and salmon, nor does it allow anadromous sea trout to be seen clearly within the archaeological record.

Common Name	Species	Adult length range (CM)	Mean adult length (CM)	Regression formula
Atlantic salmon	*Salmo salar*	30-150	73.1	Watts et al., 1997
Sea trout	*Salmo trutta m. trutta*	20-140	40.9	None - Watts et al., 1997 may be substituted for estimates
Brown trout	*Salmo trutta m. fario*	15.2-97.9	56.6	None

TABLE 8.1: Table of relevant osteological measures for anadromous Atlantic salmon, potamodromous brown trout, and anadromous sea trout. Measurements sourced from the following references: (Burkhead 2021; B. Jonsson and N. Jonsson 2007; Muus and Dahlström 1967; Robins and Ray 1986)

8.2.2 Medieval exploitation of salmonid fishes

The previously discussed identification issue creates a significant gap in our understanding of how past humans exploited Atlantic salmon, potamodromous brown trout, and anadromous sea trout. When it is assumed that all larger vertebrae represent the presence of Atlantic salmon and all smaller vertebrae represent potamodromous brown trout, the true extent of past fishery exploitation, local preference, and cultural importance is obscured. Additionally, the past biogeography of the species in question may be artificially expanded or contracted leading to an inaccurate understanding of the historical ecology of salmon, trout, and sea trout. In order to clarify the importance of anadromous sea trout to the past human exploitation of salmonid fish we present a combined biomolecular method applied to North Sea archaeological sites dating between 700-1500 CE. Given the importance of these salmonid species to medieval populations in the North Sea basin, this geographical area is an ideal case study for our approach. The North Sea played a key role in social, economic and cultural exchange during the Medieval Period, with its harbours and tributaries vital components of the development of early urban trade centres (Ayers 2016). The spread of Scandinavian economic power across the North Sea, in the form of early "Viking" raids and later Danish and Norse colonisation, resulted in exchange networks that were capable of transporting large amounts of fish across great distances (Ayers 2016; J. H. Barrett 1997). The "fish event horizon", centred around the 10th-11th centuries CE, saw a rise in exploitation of marine fish that coincided with periods of colonial expansion, religio-social reliance on fish in an increasingly Christian society, and the development of new fishing technologies that drastically improved catch capacities (J. H. Barrett, A. M. Locker, and Roberts 2004; J. H. Barrett and Orton 2016; Galloway and Murphy 1991; R. Hoffmann 2000; Orton, Morris, et al. 2014). Throughout the study area, Atlantic salmon were "ubiquitous features of conspicuous consumption", retaining a position as prestige fish throughout the Medieval Period (R. C. Hoffmann 2015) while potamodromous trout appear to have been more accessible, being fished by hand, with fly tackle and, later in the Medieval Period, stocked in ponds (Bonow et al. 2016; R. C. Hoffmann 1985; Svanberg and A. Locker 2020).

8.3 Methods

8.3.1 Biomolecular Identification

ZooMS utilises collagen peptide sequencing to identify and match unique sequences of amino acid peptides found in bone collagen (Buckley, Collins, et al. 2009; Kristine Korzow Richter et al. 2022). Molecular barcodes, developed using a modern reference set of identified bone material, can be used for taxa-specific identification

of archaeological remains (Buckley, Collins, et al. 2009; Collins et al. 2010; Kristine Korzow Richter et al. 2022). Teleost fish remains are uniquely suited to identification to genus and species due to their distinct third COL1 alpha chain, which creates a larger number of collagen sequence variants (Collins et al. 2010; Kristine K. Richter et al. 2011; Kristine Korzow Richter et al. 2022). ZooMS identification markers for Atlantic salmon and brown trout were first published in 2011 (Kristine K. Richter et al. 2011), with updates to some markers for each species published in 2018 and 2022 as well (Buckley, Harvey, et al. 2022; Harvey, Daugnora, and Buckley 2018). The published data provides four sets of unique biomarkers that can be used to differentiate *Salmo salar* specimens from *Salmo trutta* specimens (for all markers see Supplemental Materials). However, three of the markers, at peptide position COL1α2 10 - 42 and COL1α3 746 - 762, have shown considerable variability in presence during the course of this research and, therefore, the primary set of markers used to differentiate the two species for this study are those at peptide positions COL1α3 568-579 (Figure 4). *Salmo salar* collagen should show a m/Z peak of 1026 at peptide position COL1α3 568-579, while *Salmo trutta* collagen should show a m/Z peak of 996 (Buckley, Harvey, et al. 2022; Harvey, Daugnora, and Buckley 2018).

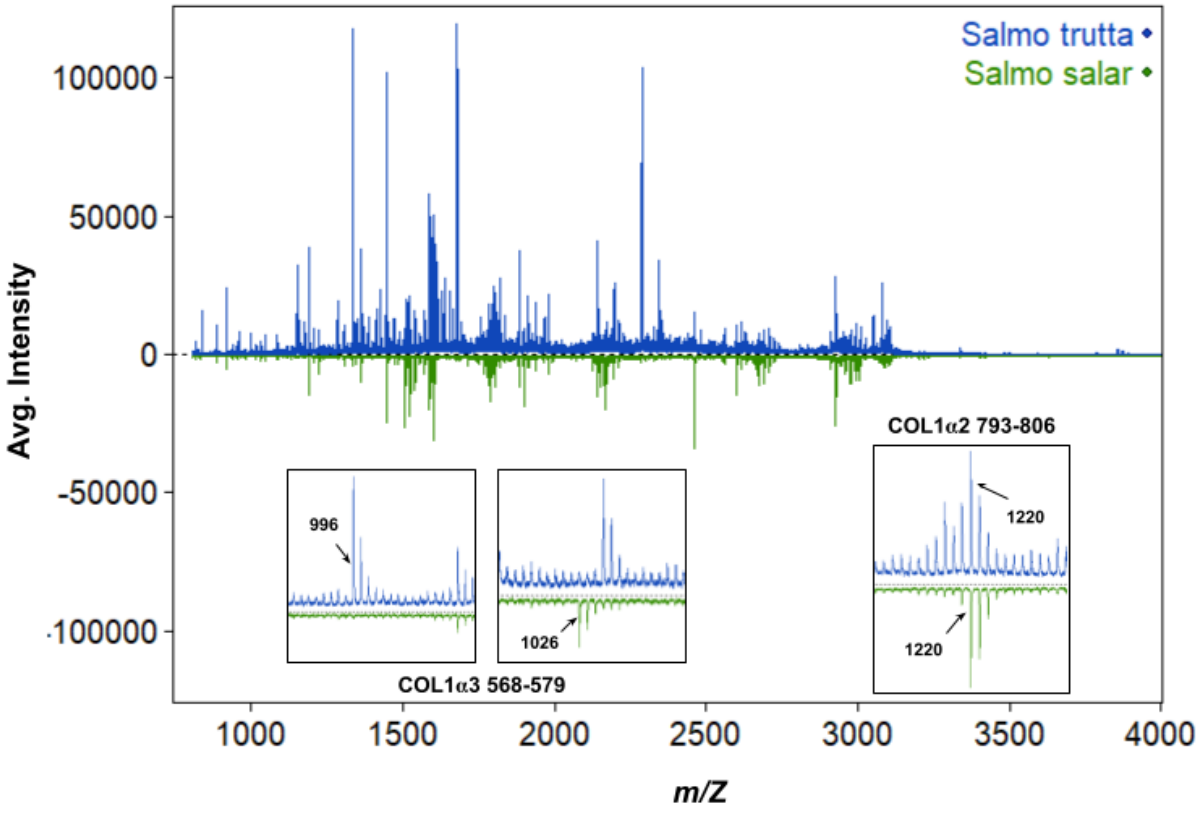


FIGURE 8.3: Spectra of two samples from Earl's Bu (LMQEB_034 and LMQEB_038) which have been identified as *Salmo trutta* (blue, top) and *Salmo salar* (green, bottom) using ZooMS analysis. The far left and middle insets show the presence of a peak at m/Z 996 at peptide position COL1A3T47 for the trout sample, and presence of a peak at m/Z 1026 at the same position for the salmon sample. The far right inset shows a peak at m/Z 1220 at peptide position COL1α2T69 that is present in both samples, as would be expected.

Bulk stable isotope analysis of carbon (δ^{13}C) and nitrogen (δ^{15}N) isotopes is a well established tool for the investigation of ichthyoarchaeological material to investigate the baseline characteristics of past aquatic envi-

ronments, changes in fish biogeography, and even as proxies for anthropogenic climate change (J. Barrett et al. 2008; E. J. Guiry, Needs-Howarth, et al. 2016; E. J. Guiry, Szpak, and Richards 2016; Häberle and Hüster Plogmann 2019; Orton, Makowiecki, et al. 2011; Orton, Morris, et al. 2014; Tsutaya et al. 2022, e.g.). In fish, high δ^{13}C values are generally associated with species that primarily feed in marine environments, while low δ^{13}C values indicate freshwater environments (Schoeninger and DeNiro 1984). While recent research has shown that there can be more variability in isotopic compositions found within freshwater and estuarine environments than previously thought (E. Guiry 2019), the basic assumptions generally hold true– anadromous salmon can be expected to show high δ^{13}C values and potamodromous brown trout can be expected to show low δ^{13}C values. Similarly, anadromous sea trout would be expected to show typically marine high δ^{13}C values, with the major difference between their isotopic profile and that of Atlantic salmon being the overall higher mean δ^{15}N values seen in sea trout. This difference is the basis for the approach to identifying anadromous sea trout within the archaeological record presented in this study. ZooMS analysis of archaeologically derived collagen can assign species, but behavioural ecotypes of *Salmo trutta* are not proteomically or genetically distinct from their freshwater-resident fellows (B. Jonsson and N. Jonsson 2007). Therefore it is necessary to use the known differences in δ^{15}N values of anadromous sea trout to apply a combined biomolecular method which can confidently identify anadromous Atlantic salmon, potamodromous brown trout and anadromous sea trout.

8.4 Archaeological Materials and Background

This study focuses on a selected assemblage (n=94) of archaeological fish bones recovered from two medieval sites located in the northern and southern regions of the North Sea in the UK (Fig 2.; Table 2), in modern-day Scotland and England. The total assemblage includes several smaller subsamples– *Salmo* sp. bones which have both ZooMS identification and bulk stable isotope data (n=68), *Salmo* sp. bones with ZooMS identifications only (n=13), *Salmo* sp. bones with bulk stable isotope data only (n=5), fish remains which were misidentified as *Salmo* sp. (n=3) and subsequently excluded, and samples which were excluded due to quality control criteria (n=4). In general,*Salmo* sp. remains from European medieval archaeological sites remain elusive, with most published sites containing fewer than 20 bones, with most assemblages comprised primarily of of vertebrae (Galtie 1995; Grimm 2011; A. Jones 2011; A. Locker 1988). Two exceptionally large assemblages of archaeological salmonid remains can be found at the high status Norse Scottish site of Earl's Bu (n = 104) and the urban settlement at 16-22 Coppergate (n = 260). The two case study sites were selected based on their numbers of previously identified salmonid remains, location around the North Sea, and period of occupation.

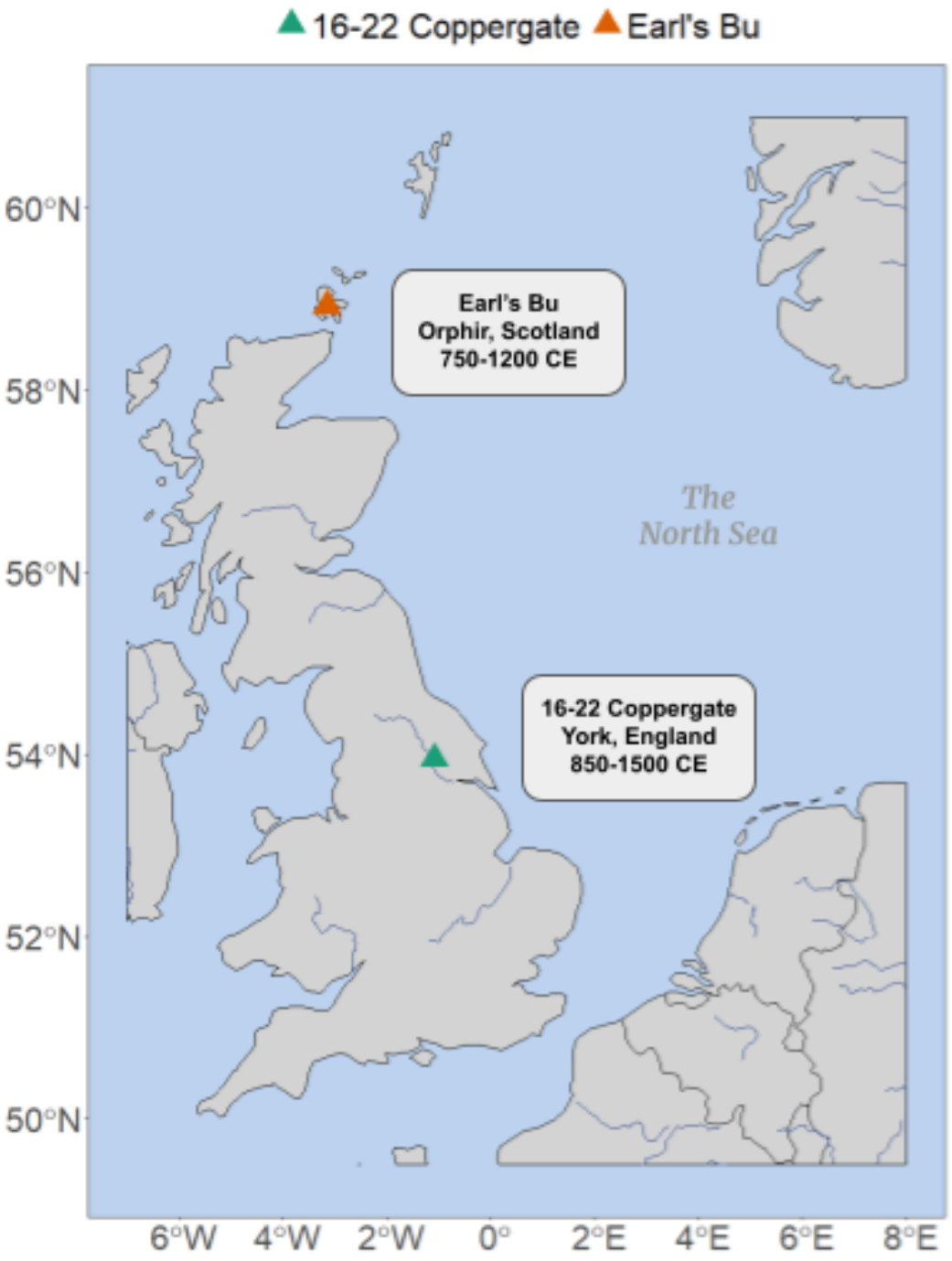


FIGURE 8.4: Map indicating locations of the two case studies.

Site Name	Location	Date Range	Site Type	Total Salmo sp. NISP	No. of Samples	Publications
Earl's Bu	Orphir, Orkney Scotland	881-1164 CE	High status residence	84	29	Harland, 2006
16-22 Coppergate	York, North Yorkshire England	850-1700 CE	Urban settlement	260	69	Jones c. 1988 (unpublished dataset); Harland et al. 2016

TABLE 8.2: Characteristics of the archaeological sites included within this study

8.4.1 Earl's Bu - Orphir, Scotland

Located approximately 14 kilometres southwest of Kirkwall, the largest town in the Orkney archipelago, the site of Earl's Bu at Orphir has a complex settlement history spanning the Norse occupation of these northern islands of Scotland. The past and present structures at the site include a Norse mill, several Norse domestic and agricultural structures, the remains of a 12th-century round church (*kirk*), a small graveyard, and a modern farm (J. Harland 2006). The Norse period of occupation in the Orkney archipelago began in the early 9th-century CE, and the islands were reportedly annexed and placed under Norwegian rule by Harald Fairhair in the late 9th-century (Anonymous 2018; J. H. Barrett, Beukens, et al. 2000; J. Harland 2006). Mentioned in the 12th-century Orkneyinga Saga, the *bu*, or large farm with associated church, originally belonged to Earl Paul Haakonsson and was reportedly the site of several political meetings and feasts over the 11th-12th centuries (Anonymous 2018; J. Harland 2006). The site was first investigated by antiquarians in the mid-18th and 19th centuries, and later again in the 1930s and 40s– with little official recording done of the excavations completed during any of these periods (J. Harland 2006). Academic excavations led by Colleen Batey and the University of Durham began in 1979, and continued off and on until 1993, with large amounts of environmental material recovered, including one of the largest assemblages of fish bones from any Scottish medieval site (J. H. Barrett, Beukens, et al. 2000; J. Harland 2006). The fish bone assemblage from Earl's Bu has a total NISP of 18,957, with 104 *Salmo* sp. bones identified by three different faunal analysts. A total of 29 bones were sampled from this assemblage for biomolecular analysis (Table 3), and the samples were from two primary depositional contexts, the first being a series of middens dated to between 881-1164CE, and the second being features contemporary with the Norse mill dated to between 1032-1155CE. While most of the samples were clearly identifiable as salmonids based on morphological features described in section 3.1, one indeterminate, but suspected cranial element, was included as it displayed the distinctive honeycomb texture associated with *Salmo* sp. elements.

Element	Count
caudal vertebra	18
cranial bone	1
first vertebra	3
opercular	1
posttemporal	1
precaudal vertebra	3
preopercular	1
vertebral centrum	1
TOTAL	**29**

TABLE 8.3: Element breakdown of Earl's Bu *Salmo* sp. Sample

8.4.2 16-22 Coppergate - York, England

Excavated between 1976-1981, the archaeological site located at 16-22 Coppergate in York, England has become one of the most iconic urban excavations in UK archaeology. The site consists of several intensive occupation periods spanning multiple socio-cultural and economic power shifts, with domestic tenements, industrial workshops, and trade spaces all uncovered during the excavations (R. A. Hall 2014). York was variously controlled by Angle and Saxon kings, Scandinavian forces, and Norman invaders throughout its long history, with the Coppergate site showing the influence of Anglo-Scandinavian and Anglo-Norman identity (R. A. Hall 2014). The chronology of the Coppergate site runs from the mid-5th to early-16th century CE, with the densest periods of occupation in the late-9th and early-10th centuries (R. A. Hall 2014). An impressive amount of zooarchaeological material was recovered from the site, including a fish bone NISP of 20,463, with 260 salmonid bones recorded (J. F. Harland, A. K. Jones, and Orton 2016). From this assemblage a total of 69 bones were sampled for biomolecular analysis (Table 4). The majority of fish remains from the site were recovered from the "Anglo-Scandinavian" (circa 850-950 CE) and "Medieval" (circa 950-1250 CE) periods, and therefore the majority of salmonid remains included in this study were from periods dated to between 850-1220 CE. As with the sample from Earl's Bu, most of the Coppergate samples were clearly identified using morphological identification methods, however there were 4 indeterminate bone fragments and three ribs that were included because they either displayed features consistent with *Salmo* sp. elements, or because they were the only present specimens that could reasonably be matched with previous identifications of salmonid bones from a given context.

Element	Count
articular	1
caudal vertebra	30
ceratohyal	2
cranial bone	1
dentary	1
indeterminate	3
precaudal vertebra	26
rib	3
vertebral centrum	2
TOTAL	**69**

TABLE 8.4: Element Breakdown of 16-22 Coppergate *Salmo* sp. Sample

8.5 Methods

8.5.1 Zooarchaeological Identification

The identification of *Salmo* sp. bones for this study followed commonly employed zooarchaeological methods, involving the use of comparative specimens, literature references, and digitised resources to make genus or species level determinations. Both archaeological assemblages were previously studied by ichthyoarchaeologists James H. Barrett, Andrew K.G. Jones and Jennifer F. Harland and the identifications made by these analysts formed the basis of the sampling strategy employed herein. Sampling and morphological identification confirmation was conducted using facilities and materials housed at the Orkney Museum and University of York from 2020-2021. Provisional identification to *Salmo* sp. was possible using these morphological identification methods, and, but further analysis using collagen peptide fingerprinting (ZooMS) was required to correctly identify them to species.

8.5.2 Biomolecular Methods

Collagen extraction for stable isotope analysis and ZooMS followed a modified Longin method (1971). All salmonid samples had lipids extracted using a 2:1 dichloromethane/methanol (DCM/MeOH) solution (Colonese et al. 2015), in order to remove 13C-depleted lipids commonly present in fish bone, particularly salmon (E. J. Guiry, Szpak, and Richards 2016; Szpak 2011). Samples were submerged in the DCM/MeOH solution and sonicated for 15 minutes, the waste decanted, solution refreshed, and the process repeated a minimum of 2 times, or until the solution remained clear after sonication. After de-lipidification, all samples were demineralized in 0.4M hydrochloric acid at 4°C, gelatinised with weak (pH3) acid for approximately 48 hours, and filtered using an Ezee-Filter™ prior to lyophilization. For bulk stable isotope analysis, collagen samples of 0.5mg were weighed out in duplicate and analysed using a Sercon 20-22 continuous flow isotope ratio mass spectrometer (IRMS) coupled to a Sercon GSL elemental analyzer. Raw data was assessed and quality control measures applied in order to ensure the accuracy of the data reported– in order to control for possible contaminants, samples with a C:N ratio outside of a certain range were excluded. While the generally accepted C:N ratio range for bulk stable isotope analysis may be either 2.9-3.6 or 3.1-3.5, depending on the source referred to (DeNiro 1985; Klinken 1999), the range for

fish from both cold and warm water environments are restricted to a much narrower range of 3.0-3.33 (E. J. Guiry and Szpak 2021). However, while a high C:N ratio may indicate contamination with non-collagenous carbon and affect δ^{13}C values, for studies which are primarily focused on δ^{15}N values, a wider range of 3.0-3.6 can be used as the humic contaminants has very minimal effect on δ^{15}N values (E. J. Guiry and Szpak 2021). All samples with associated bulk isotope values that are included in this study (n=73) fall within this suggested 3.0-3.6 C:N range. For ZooMS analysis, a portion of the lyophilized samples were resuspended in ammonium bicarbonate and digested for approximately 24 hours after the addition of a 1μL trypsin solution. Digested peptides were extracted and filtered using a C18S ZipTip, and spotted onto a 384 ground steel well plate with a αcyano-4-hydroxycinnamic acid matrix solution, and analysed using a Bruker UltrafleXtreme MALDI-TOF/TOF instrument. The resulting spectra were analysed using a combined programmatic and manual approach, with peaks identified for each sample, a table of *m/Z* values compared to known biomarkers for *Salmo salar* and *Salmo trutta* in Python, and the resulting dataset manually checked for outliers and problematic identifications. Where required, spectra were reviewed using the MMass spectra viewer (Niedermeyer and Strohalm 2012; Strohalm 2013; Strohalm, Hassman, et al. 2008; Strohalm, Kavan, et al. 2010) to confirm peak identification, and all samples were able to be assigned an identification to the species level.

Accuracy of the bulk stable carbon and nitrogen isotopic compositions were determined by measurements of international standard reference materials within each analytical run. These were IAEA 600 (δ^{13}C raw = -27.70±0.14‰, δ^{13}C true = -27.77±0.00‰, δ^{15}N raw = 0.79±0.26‰, δ^{15}N true = 1±0.2‰); IAEA N2 (δ^{15}N raw = 20.33±0.25‰, δ^{15}N true = 20.3±0.0‰); and IA Cane (δ^{13}C raw = -11.74±0.09‰; δ^{13}C true = -11.64±0.00‰). Overall uncertainties on these measurements were calculated based on Kragten 1994 by combining uncertainties in the values of the international reference materials with those determined from repeated measurements of samples and reference materials. They are reported here as one standard deviation, and the maximum uncertainty for all samples across all runs was <0.3‰ for both δ^{15}N (0.23‰) and δ^{13}C (0.25‰). In addition to these standard references, a sample of homogenised bovine bone was used as a control. Control bovine collagen was extracted and six samples were analysed within the sample runs, producing a mean δ^{15}N value of 6.12 ± 0.17‰ and δ^{13}C value of -23.11 ± 0.14‰. These values were within the overall mean from 50 separate extracts of this bone sample, which produced values of δ^{13}C = -23.27‰ and δ^{15}N = 6.40‰.

8.6 Results

8.6.1 Zooarchaeological Analysis

In order to identify a suitable sample for biomolecular analysis, a targeted review of each site's fish remains was undertaken by the lead author. While the recovered fish material from both sites had undergone zooarchaeological analysis by several ichthyoarchaeologists in the past, it was decided that a secondary review by an analyst focusing specifically on salmonid bones might result in new identifications. Additionally, the Coppergate assemblage has some discrepancies between the original unpublished ichthyoarchaeological assessment, and the definitive record published in 2016 (J. F. Harland, A. K. Jones, and Orton 2016). Records from the original assessment in 1998 indicated that 394 salmonid bones were present within the fish material recovered from Coppergate, while the 2016 assessment recorded only 116 salmonid bones (J. F. Harland, A. K. Jones, and Orton 2016; A. Jones 1988). A third review of all available fish bone material from Coppergate resulted in a total salmonid NISP of 260, however 45 of those identifications were from contexts which had not been previously recorded by either Jones

or Harland (Table 5).

16-22 COPPERGATE		
Analyst	**Assessment and/or Publication Date**	**Reported Salmo sp. NISP**
Andrew K.G. Jones	1988	394
Jennifer F. Harland	2008/2016	116
Liz M. Quinlan	2020	260
EARL'S BU		
Analyst	**Assessment and/or Publication Date**	**Reported Salmo sp. NISP**
James H. Barrett	1995	27
Jennifer F. Harland	2003	99
Liz M. Quinlan	2021	104

TABLE 8.5: Zooarchaeological Data from Successive Reviews of Material from Coppergate and Earl's Bu

It must be noted that the discrepancy in salmonid identifications from Coppergate is likely due to availability of material and inconsistencies in collection management over the years, rather than a major loss of material or large scale analyst error. The fish material from Earl's Bu was also the subject of several successive reviews, the earliest being a preliminary review of early material by James Barrett in 1995, with a full review completed by Jennifer Harland in 2003. A third review of the Earl's Bu fish material resulted in an additional five salmonid bones being identified within the remains.

8.6.2 ZooMS Analysis

A total of 84 fish bones were included in the dataset of samples subjected to ZooMS analysis from the two site assemblages, 60 from 16-22 Coppergate and 24 from Earl's Bu, representing 23.1% and 28.6% of the site salmonid NISPs, respectively. Of these samples, 63 were identified as *Salmo salar*, 18 as *Salmo trutta*, 2 as Gadus morhua (Atlantic cod), and 1 as Esox lucius (Northern pike). The three samples that were initially misidentified as *Salmo* sp. were a Northern pike dentary and Atlantic cod rib from Coppergate, and an Atlantic cod preopercular from Earl's Bu. The pike dentary was misidentified as a possible salmonid bone due to morphological similarity and the fragmentary nature of the individual element. Both the cod bones had been previously identified as salmonid bones by initial analysts, but were selected for identification confirmation during the tertiary review due to suspected misidentification. The three misidentified bones had initially been included in the bulk stable isotope subsample, but were subsequently removed from the study dataset so only bulk isotope values from known salmon and trout were analysed. While *Salmo salar* were predominant at the Coppergate site, with only four *Salmo trutta* identifications, the opposite was true at Earl's Bu, with the majority (n=14, or 60.9%) of identifications being *Salmo trutta*.

8.6.3 Bulk Stable Isotope Analysis

A total of 94 samples were initially selected for both bulk stable isotope and ZooMS analysis from the two sites, however 3 samples were incorrectly identified as *Salmo* sp., and a further 5 were not included in the isotope dataset due to issues ranging from poor collagen yield, unacceptable C:N ratios, and sample loss during demineralisation. This resulted in a total usable dataset of 86 samples, 73 of which have associated bulk stable isotope values (Table 6). Of those 73 samples, 68 have both associated ZooMS identifications and isotope data which allows them to be identified to *Salmo* ecotype using the combined biomolecular approach. Collagen yield for all 73 samples ranged from a low of 0.44% to a maximum of 19.36%, and the ranges of both %C (33.17-46.53) and %N (12.11-16.90) were unremarkable. In addition to the fish bone, six bovine control samples were analysed and resulted in an average δ^{13}C value of 23.12 ± 0.14‰ and average δ^{15}N value of 6.12 ± 0.17‰.

Quality Criteria	**Min**	**Max**	**Range**	**Mean**	**Standard Deviation**
C:N Ratio	3.05	3.5	0.45	3.20	0.09
Collagen % yield	1.3	19.48	18.18	6.98	3.24
%C	33.17	46.53	13.36	40.55	2.42
%N	12.11	16.9	4.79	14.78	1.02

TABLE 8.6: Bulk stable isotope collagen quality descriptive statistics for 68 combined biomolecular samples

Figure 5 is an isotope bi-plot of δ^{13}C and δ^{15}N values for all samples from the study sites which have been identified as *Salmo salar* and *Salmo trutta* using ZooMS analysis (n=68) (See SI for full dataset). The δ^{13}C values for salmon samples range from -16.31‰ to -13.44‰ (mean: -14.70 ± 0.62‰) and δ^{15}N ranging from 7.88‰ to 11.75‰ (mean: 9.67 ± 0.82‰). The δ^{13}C values for trout samples range from -17.19‰ to -11.41‰ (mean ± SD; -13.51 ± 1.61‰) and δ^{15}N ranging from 10.51‰ to 14.87‰ (mean± SD; 13.32 ± 1.31‰). Table 7 reports the full descriptive statistics for the *Salmo salar* and *Salmo trutta* subsets, as well as the five samples without associated ZooMS identifications (due to poor spectra quality), all separated by archaeological site.

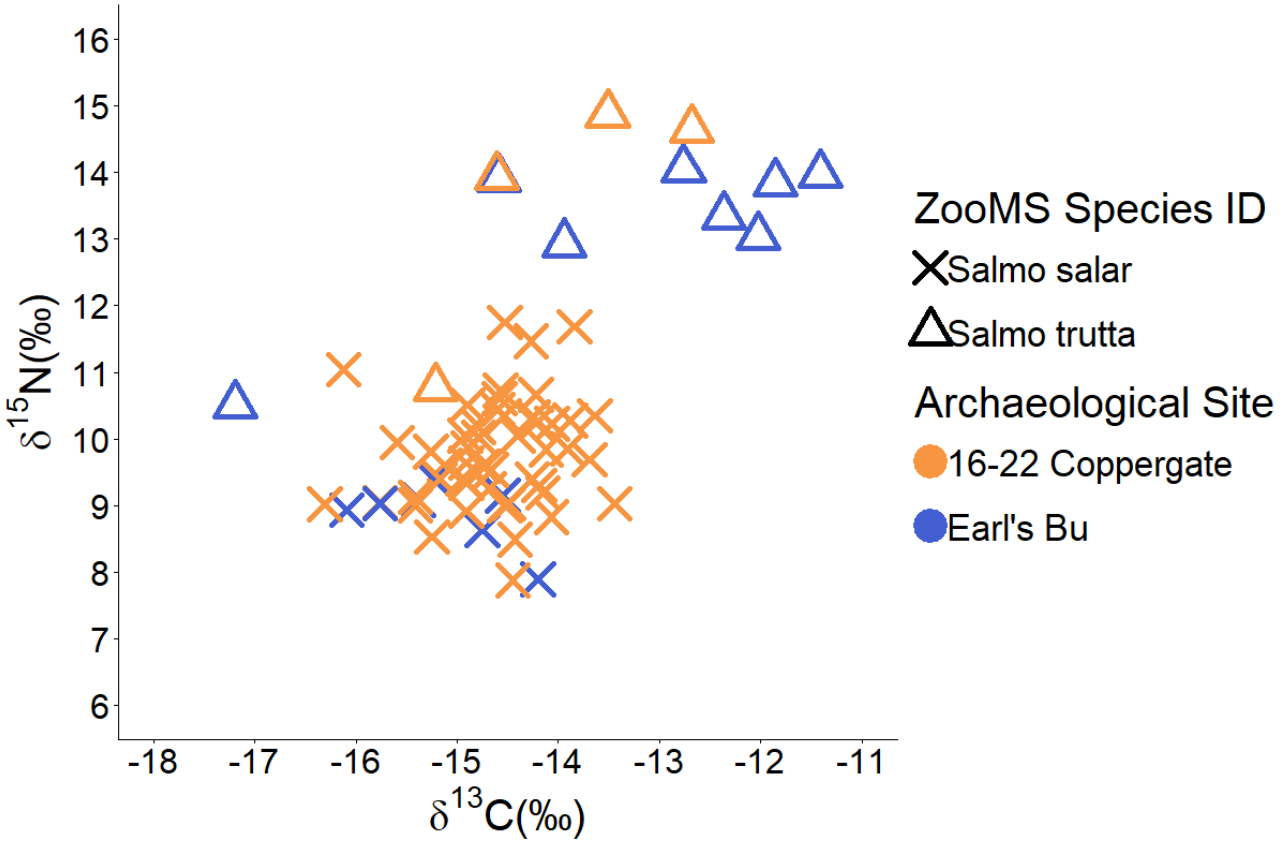


FIGURE 8.5: Isotope bi-plot showing the δ^{13}C and δ^{15}N values for all *Salmo salar* and *Salmo trutta* samples included in the study.

SALMO SALAR

Site	No. Samples	δ^{13}C				δ^{15}N			
		Min.	Max.	Range	Mean	Min.	Max.	Range	Mean
16-22 Coppergate	49	-16.31	-13.44	2.87	-14.64 ± 0.60	7.88	11.75	3.87	9.78 ± 0.80
Earl's Bu	7	-16.09	-14.2	1.89	-15.14 ± 0.63	7.9	9.38	1.48	8.87 ± 0.45
TOTAL	56	-16.31	-13.44	2.87	-14.70 ± 0.62	7.88	11.75	3.87	9.67 ± 0.82

SALMO TRUTTA

Site	No. Samples	δ^{13}C				δ^{15}N			
		Min.	Max.	Range	Mean	Min.	Max.	Range	Mean
16-22 Coppergate	4	-15.21	-12.68	2.53	-14.00 ± 0.98	10.51	14.05	3.54	13.20 ± 1.09
Earl's Bu	8	-17.19	-11.41	5.78	-13.27 ± 1.79	10.77	14.87	4.1	13.55 ± 1.64
TOTAL	12	-17.19	-11.41	5.78	-13.51 ± 1.61	10.51	14.87	4.36	13.32 ± 1.31

SALMO sp.

Site	No. Samples	δ^{13}C				δ^{15}N			
		Min.	Max.	Range	Mean	Min.	Max.	Range	Mean
16-22 Coppergate	3	-14.81	-13.91	0.9	-14.44 ± 0.38	9.11	10.11	1	9.77 ± 0.47
Earl's Bu	2	-14.39	-12.49	1.9	-13.44 ± 0.95	9.15	12.9	3.75	11.03 ± 1.88
TOTAL	5	-14.81	-12.49	2.32	-14.04 ± 0.83	9.11	12.9	3.79	10.27 ± 1.38

TABLE 8.7: δ^{13}C and δ^{15}N value reporting for *Salmo salar*, *Salmo trutta*, and *Salmo* sp. samples by study site

8.7 Discussion

8.7.1 *Salmo* sp. Isotopes and Ecotype Identification

The results from this study of 68 *Salmo* sp. samples indicate clear differences in the isotopic characteristics of *Salmo salar* and *Salmo trutta* samples, and allow us to identify ecotypes of these fish, namely anadromous salmon, anadromous sea trout, and potamodromous brown trout. The range of δ^{15}N and δ^{13}C values for the 56 *Salmo salar* samples fall comfortably within the range of values for modern anadromous Atlantic salmon from the Northeast coast of the UK, as reported in the literature (Table 8) (Almodóvar et al. 2020; MacKenzie et al. 2011; Trueman 2022). While these published values come from 309 scale-derived collagen samples rather than bone-derived samples like our archaeological material, they can be compared as they both represent long-term averages of nutrient intake and feeding which should reflect the most intense periods of feeding which, in anadromous salmon, occurs in the marine environment (E. J. Guiry, Szpak, and Richards 2016). These values indicate that all *Salmo salar* samples from both Coppergate and Earl's Bu represent migratory Atlantic salmon, which follow an anadromous life cycle, with typically marine carbon signatures reflecting their extensive feeding period in the North Atlantic.

SALMON					
Study	**Ecotype**	**Fish Age**	**Sample Size**	**δ^{13}C Mean**	**δ^{15}N Mean**
Almodovar et al., 2020	Anadromous Salmon	1SW	150	-15.90 ± 0.80	9.70 ± 1.10
Almodovar et al., 2020	Anadromous Salmon	MSW	139	-15.90 ± 0.80	10.50 ± 0.80
MacKenzie et al., 2011; Trueman, 2022	Anadromous Salmon	1SW	10	-15.90 ± 1.05	10.00 ± 1.96
MacKenzie et al., 2011; Trueman, 2022	Anadromous Salmon	2SW	10	-16.00 ± 1.13	10.4 ± 1.74
Present study	Anadromous Salmon	Adult	56	-14.70 ± 0.62	9.67 ± 0.82
TROUT					
Study	**Ecotype**	**Fish Age**	**Sample Size**	**δ^{13}C Mean**	**δ^{15}N Mean**
McCarthy and Waldron, 2000	Brown trout	Adult	38	-22.50 ± 1.30	9.20 ± 1.50
McCarthy and Waldron, 2000	Anadromous Sea trout	Adult	30	-16.50 ± 1.20	13.40 ± 1.00
Poiesz et al. 2021	Anadromous Sea trout	Adult	80	-19.54 ± 0.29	16.00 ± 0.19
Present study	Anadromous Sea trout	Adult	10	-12.97 ± 0.29	13.85 ± 0.59
Present study	Undefined trout	Adult	2	-16.20 ± 0.99	10.64 ± 0.13

TABLE 8.8: Comparison of modern and archaeological average δ^{13}C and δ^{15}N values

The mean δ^{15}N values (13.9 ± 0.6‰) from 10 of the 12 archaeological *Salmo trutta* samples are directly comparable to reported mean values of modern anadromous trout (14.7 ± 1.3‰) (McCarthy and Waldron 2000; Poiesz et al. 2021). The remaining two samples, LMQ_037 and LMQEB_038, are less clearly identifiable; both display the lowest δ^{15}N values within the *Salmo trutta* subset (10.77‰ and 10.77‰, respectively), and lowest δ^{13}C values (-15.21‰ and -17.19‰, respectively). The δ^{15}N values of these two samples align more closely with those reported for potamodromous Brown trout (9.2 ± 1.5‰), but display more intermediate δ^{13}C values, especially when compared to the averages seen within their respective site assemblages. These two samples likely represent individuals which inhabited either estuarine or nearshore environments that were less productive than those inhabited by the anadromous individuals, resulting in an intermediate marine δ^{13}C but without a corresponding high δ^{15}N value. The isotopic characteristics of such nearshore and estuarine habitats have been shown to be much more flexible than previously thought, with some areas showing δ^{13}C ranges of 30‰ or more, depending on local environmental conditions (E. Guiry 2019).

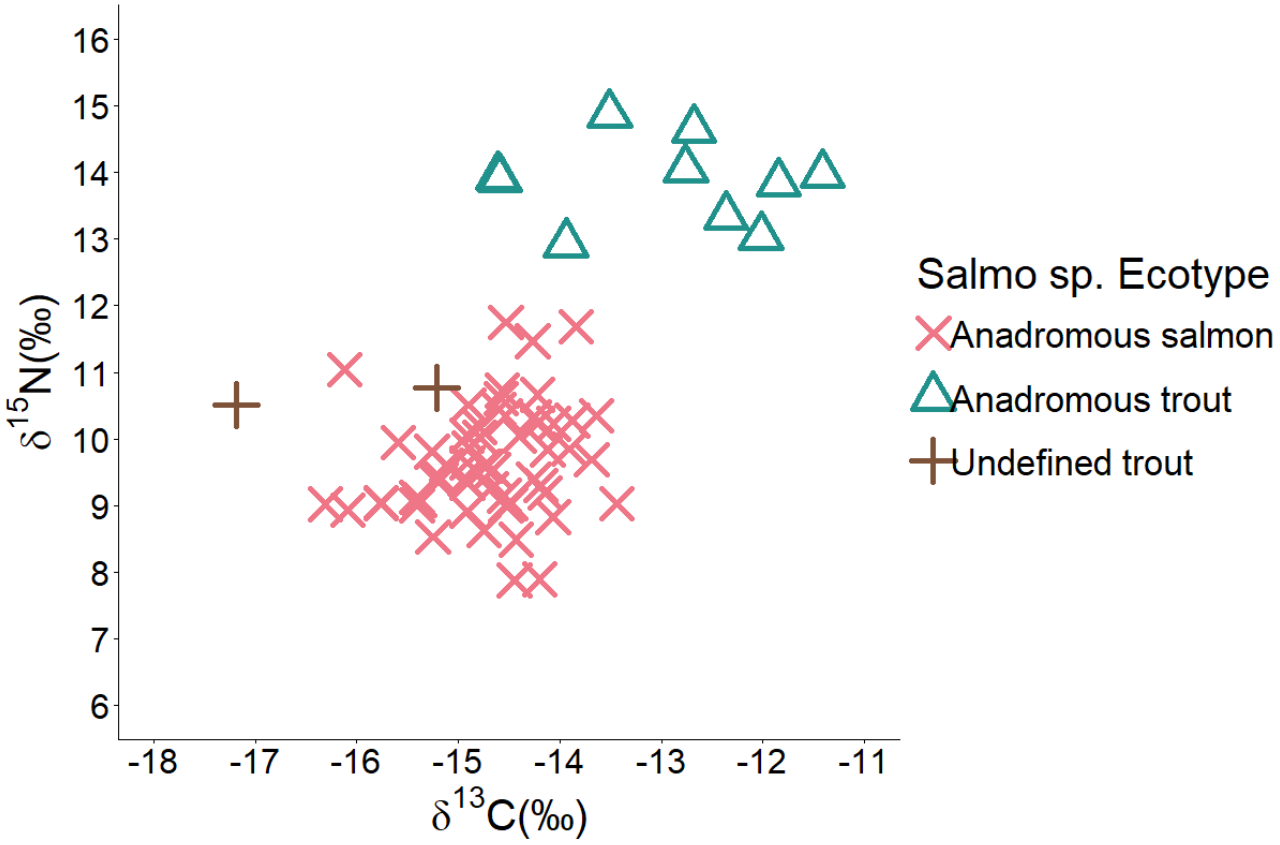


FIGURE 8.6: Isotope bi-plot showing the δ^{13}C and δ^{15}N values for samples included in the study and their corresponding ecotype classifications.

The δ^{15}N sample averages of 13.90 ± 0.6‰ for anadromous sea trout and 9.67 ± 0.82‰ for anadromous salmon strongly reflect the expected δ^{15}N difference between these species, with a mean difference of 4.23‰ between the two species. The results of both a Mann-Whitney U-test and a Welch two-sample t-test indicate that the species groups are non-normatively distributed, and that the mean and median values are significantly different (p-value= 0.001 and 0.007, respectively). This observed difference holds true for both the Coppergate and Earl's Bu sites– with a 4.70‰ difference between mean salmon and sea trout δ^{15}N values for Coppergate and a 4.68‰ difference between salmon and trout δ^{15}N values at Earl's Bu. Fig 4 below illustrates these ecotype-level differences observed in δ^{15}N value ranges from anadromous salmon and anadromous trout samples, and demonstrates the consistently higher *Salmo trutta* δ^{15}N values.



FIGURE 8.7: Box and violin plots showing the range of δ^{15}N values seen across the species included in the study.

8.7.2 Site Specific *Salmo* sp. Characteristics

These combined ZooMS and bulk stable isotope results are not only useful to identify anadromous sea trout in the archaeological record, but inform us about the composition of *Salmo* sp. assemblages from the case study sites. The characteristics of each subassemblage may reflect not only fish preference at these sites, but environmental features of local salmon and trout populations at that period in time. The subassemblage of *Salmo* sp. fish from the 16-22 Coppergate site (n=58) represents 22.3% of all identified *Salmo* sp. remains from the site, however the majority of these samples (n=53) come from a relatively narrow period of time (c. 850-1280 CE) when compared to the full site chronology of circa 400-1720 CE. This being said, the contexts at Coppergate dated to between 850-1280 CE represent successive intensive use periods at the site, and contain the most dense deposits of fish bones found at the site (Bond and T. P. O'Connor 1999; R. A. Hall 2014; R. A. Hall and Hunter-Mann 2002; R. Hall 2011; T. O'Connor 1989). The Coppergate subassemblage is dominated by *Salmo salar* bones, with 49 anadromous salmon, 3 anadromous sea trout and 1 undefined trout identified using bulk stable isotope and ZooMS analysis, as well as a further 5 *Salmo salar* samples identified using ZooMS only. The anadromous salmon from Coppergate are especially homogenous in their δ^{15}N and δ^{13}C values, displaying a tightly clustered sample of re-

sults, and when the samples are assessed based on the period they originate from, there is no significant pattern of difference seen across either δ^{15}N or δ^{13}C values (Figure 8). This, when coupled with the overall homogeneity of the subassemblage, may imply fishing from isotopically similar populations of Atlantic salmon throughout the temporal breadth of the site. This may mean that all salmon from Coppergate was sourced locally, either directly from the River Ouse which runs just east of the site, or perhaps the Humber and its tributaries. If salmon was being imported to Coppergate, then they were likely individuals which belonged to the Southern North Sea population of Atlantic salmon, based on their homogenous δ^{13}C values (MacKenzie et al. 2011) (see Chapter 9).

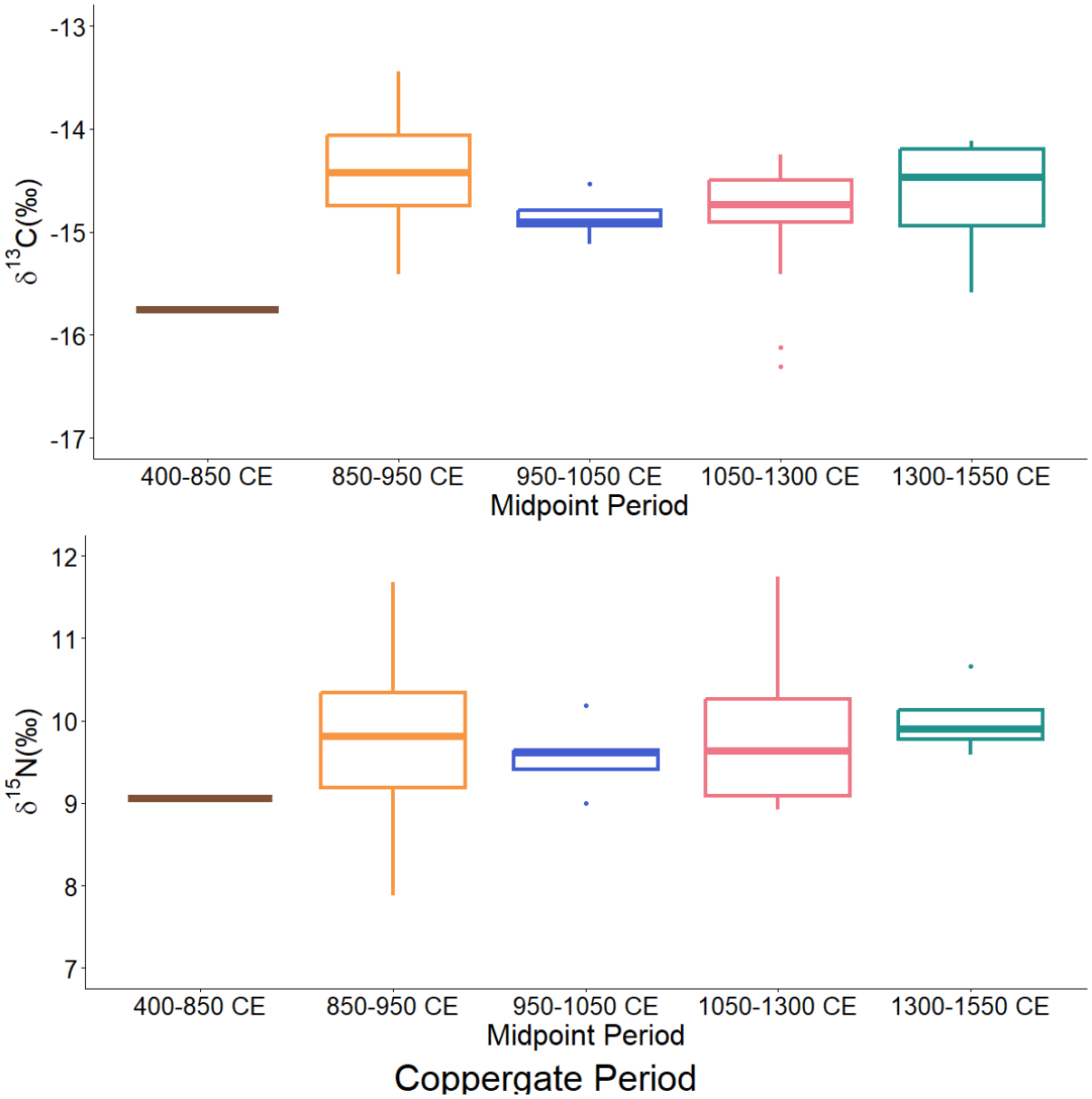


FIGURE 8.8: Box δ^{15}N and δ^{13}C values seen across the anadromous salmon samples recovered and identified from the 16-22 Coppergate site.

The subassemblage from the Earl's Bu site in Orkney, on the other hand, indicates a more complex local fishing strategy during the Norse Orcadian period ranging from 750-1200 CE. The sample of 23 bones has a majority

of *Salmo trutta* (n=14) compared to *Salmo salar* (n=9), and the presence of salmon at this site in particular is interesting. Trout from the Orkney island of Mainland, both anadromous sea trout and potamodromous brown trout, generally originate from one of its freshwater lochs or, more often, it's small *burns* (streams) which empty directly into saltwater lagoons and the sea (Thomson 2015). The Orkney archipelago has no recent or historic Atlantic salmon population, owing to its lack of suitable rivers (Thomson 2015)– therefore if the Norse settlers at Earl's Bu were only exploiting locally caught fish species, we would expect to find only anadromous sea trout or freshwater brown trout. The total *Salmo* sp. assemblage from Earl's Bu constitutes one of the largest found in all of Scotland, and is certainly the largest from a Norse-period site (J. F. Harland, A. K. Jones, and Orton 2016). With 29.1% of that assemblage sampled and identified using ZooMS analysis, we can infer a pattern of *Salmo* sp. exploitation that made use of the locally available trout ecotypes (primarily anadromous sea trout), but also must have involved the import of Atlantic salmon from mainland Scotland or even locations further afield. Earl Paul Haakonsson, the builder of Earl's Bu and joint-Earl of Orkney from 1122-1137 CE, maintained close ties with Norway and greater Scandinavia (Anonymous 2018), and export of cod and other stockfish was likely well established from both Scandinavia and the Earldom of Caithness in northern mainland Scotland by the 12th-centuries (J. H. Barrett 1997). Whether the imported salmon at Earl's Bu were tied to the feasting events noted within the Orkneyinga Saga or not, it is clear that preserved, or even fresh, salmon were being imported alongside the more common Norse staples of cod and stockfish.

8.8 Conclusions

It is clear from the case studies presented here that the combination of bulk stable isotope analysis and zooarchaeology by mass spectrometry is a powerful tool for identifying anadromous sea trout (*Salmo trutta*) in the archaeological record. We have demonstrated a consistent and observable difference in δ^{15}N values obtained from archaeological fish bones identified as *Salmo trutta* and those identified as *Salmo salar* using established ZooMS biomarkers, on the order of a trophic level increase from the former to the latter (Schoeninger and DeNiro 1984). This is consistent with reported differences not only between modern anadromous salmon and modern anadromous sea trout, but also between modern potamodromous brown trout and modern anadromous sea trout (McCarthy and Waldron 2000; Poiesz et al. 2021). When seen in samples that are identified using ZooMS as *Salmo trutta*, and which have typically marine high δ^{13}C values, this difference in δ^{15}N indicates that the individuals likely followed an anadromous migration pattern and were members of the sea trout ecotype. The applications for this combination of analytical methods on archaeological materials are multifold. At its most basic, the described combined biomolecular approach is a reliable way to differentiate between skeletal elements from economically and culturally important salmonids that otherwise cannot be morphologically distinguished. ZooMS analysis is a reliable and cost-effective alternative to ancient DNA (aDNA) analysis, and bulk stable isotope analysis provides environmental data that is beneficial to holistic understandings of fish bone assemblages from archaeological sites as a whole. Using these methods in tandem improves our understanding of use patterns for the species and ecotypes in question– namely, anadromous Atlantic salmon, potamodromous brown trout, and anadromous sea trout.

Finally, assessments of species diversity on archaeological sites provide an increased resolution of historic biogeography of these fish, extending the time depth of knowledge beyond the historic record. The integration of isotopic data from archaeological sources modern and historic isotopic data is essential to developing "deep-time retrospectives" (E. J. Guiry and Hunt 2020) which not only shed light on how past environments have changed over time, but can provide useful data that may impact modern conservation approaches. The data gen-

erated by archaeological isotopic research, like that presented here, provides information on past environmental conditions, foraging strategy and fish origins that can be integrated into modern conservation models. There are lingering questions about the biogeographic variations in salmon and sea trout populations across the species' range, and identifying pre-industrial and pre-agricultural populations of these fish ecotypes is a key step towards understanding the true scale of anthropogenic impacts throughout time. Palaeoecological data has been cited as a key metric for understanding the successes and failures of modern conservation efforts (Grace et al. 2019), and the combined biomolecular method described here provides both environmental and behavioral data for *Salmo* sp. ecotypes that are currently threatened, and, in some cases, regionally extinct.

ZooMS analysis has been used to confidently identify the two species, *Salmo salar* and *Salmo trutta* since the development of peptide biomarkers for each species in 2018, however this method alone cannot inform on ecotype and foraging strategy; factors which can vary greatly between regions and habitats. Bulk stable isotope analysis is essential to clarify the isotopic characteristics of an archaeological salmonid sample, and when combined with ZooMS identification it allows archaeologists to move beyond simple categorical species descriptions like "salmon" and "trout", and recognize the presence of ecotypes like anadromous salmon, potamodromous brown trout, anadromous sea trout. While other researchers have demonstrated the ability to combine genetic and bulk stable isotope data to determine migratory patterns of Atlantic salmon, brown trout, or sea trout alone (E. J. Guiry, Needs-Howarth, et al. 2016; McCarthy and Waldron 2000), this study constitutes a unique application of collagen peptide fingerprinting identification in combination with isotope data to demonstrate both the ability and importance of identifying ecotypes of both *Salmo salar* and *Salmo trutta* fishes. We reccomend this combined approach for future investigations of archaeological *Salmo* sp. remains as a minimally-destructive and cost-efficient way of improving understanding of archaeological site-specific ecotype abundance and cultural use patterns, and providing environmentally rich data for modern conservation efforts.

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Chapter 9

Regional Variation in Isotope Characteristics of Archaeological *Salmo* sp. Remains and Comparative Taxa from the North Sea Basin

9.1 Abstract

This study represents the first targeted research on archaeological *Salmo* sp. remains from the Medieval Period, combining biomolecular and zooarchaeological methods. We explore trends in the exploitation of Atlantic salmon, freshwater brown trout, and anadromous sea trout using remains from key medieval sites from around the North Sea basin. Bulk carbon (δ^{13}C) and nitrogen (δ^{15}N) results from archaeological *Salmo* sp. remains from sites in modern day England, Scotland, Denmark and the Netherlands are compared to understand more about *Salmo* sp. palaeoecology and biogeography. In order to contextualise the isotope results of these *Salmo* sp. remains, δ^{13}C and δ^{15}N values from marine and freshwater fish from the five largest sites are provided for comparison. We discuss the extent to which commercial fisheries for salmon and cultural preferences become visible using biomolecular analysis from these areas, as well as general patterns in identification from these sites. Additionally, isotope niche space analysis is applied to archaeological *Salmo* sp. bones to investigate regional differences in bulk carbon and nitrogen values.

9.2 Introduction

The two primary species of the *Salmo* genus, *Salmo salar* (Atlantic salmon) and *Salmo trutta* (brown/sea trout) have been part of human diets for at least 40,000 years (Turrero, García-Vázquez, and Leaniz 2014), and remain key commercial species to this day. Throughout the Medieval Period (approximately 500-1500 CE) in northwestern Europe these species were not only fished for local consumption, but preserved and traded across long distances, used to fulfil tax obligations, and, eventually strictly controlled as luxury goods reserved for the nobility and ecclesiastical elite (R. C. Hoffmann 2005, 2015; A. M. Locker 2000; Serjeantson and Woolgar 2006). Additionally, these fish, especially the Atlantic salmon, were culturally important to a variety of groups throughout the Medieval Period and across a wide geographic area, with these fish represented in the art, heraldry, place names, and folklore of people settled across northwestern Europe from Glasgow to Gdańsk.

9.2.1 Atlantic salmon (*Salmo salar*) and trout (*Salmo trutta*

)

Atlantic salmon are large piscivorous ray-finned fish with a primarily anadromous migration strategy (Aas et al. 2010; McCormick et al. 1998). The majority of Atlantic salmon begin their lives in fast-flowing, well-oxygenated rivers located in basins that drain into either side of the North Atlantic, historically found as far north as the Barents Sea and far south as the Delaware Bay (Aas et al. 2010; McCarthy and Waldron 2000; Thorstad et al. 2010). Most Atlantic salmon undergo a *smolting* process as they reach the end of their juvenile period, gaining the ability to tolerate saltwater and triggering a migration to the open ocean where they will feed and grow to sexual maturity before returning to their natal stream to spawn (Aas et al. 2010; McCormick et al. 1998; Thorstad et al. 2010). While most Atlantic salmon complete this ocean migration during their life cycles, there are some isolated populations which migrate from rivers to large lakes, or, in some rare cases, spend the entirety of their lives within a single river system (Aas et al. 2010; Guiry, Needs-Howarth, et al. 2016; McCormick et al. 1998).

Brown trout (*Salmo trutta*), on the other hand, are a primarily freshwater species which inhabit much of the same European range as Atlantic salmon, and extend beyond this as far as West Asia and North Africa (B. Jonsson and N. Jonsson 2007). This large geographic range is a key factor in the behavioral plasticity of the species, with lacustrine (lake-dwelling), potamodramous (internally freshwater migratory), and anadromous populations commonly found (B. Jonsson and N. Jonsson 2007; Nina Jonsson and Bror Jonsson 2002). There are significant size

differences between these different populations, or ecotypes, with anadromous *Salmo trutta* individuals, commonly referred to as sea trout, growing as large as Atlantic salmon while freshwater-resident brown trout remain much smaller (Burkhead 2021; B. Jonsson and N. Jonsson 2007; Muus and Dahlström 1967; Robins and Ray 1986).

In life these three ecotypes of *Salmo* fish– sea trout, brown trout, and anadromous salmon– are easily distinguished from each other based on physical characteristics like fin shape, coloration and patterning, body structure, and overall size. While *Salmo salar* and *Salmo trutta* are genetically distinct, there is no genetic determinant for migratory behavior within what geneticists often refer to as the "*Salmo trutta* complex"– a collective term for the often-regionally distinct species and subspecies of *Salmo trutta* found across Europe and Western Asia (D'Agaro et al. 2022; Dysin et al. 2022; Hindar et al. 1991). Despite phylogenetic differences, in archaeological contexts identification to species is more difficult, with very few skeletal differences between the two species other than overall size and inconsistently reported morphological variations in a few rarely-preserved cranial elements including the premaxilla, maxilla dentary, supraethmoid, and vomer (Kacem and Meunier 2009; Norden 1961; Tchernavin 1938; Watt, Pierce, and Boyle 1997). Identification of *Salmo* sp. bones to species is further complicated by the well-documented preservation issues seen in assemblages of *Salmo* sp. remains from European archaeological sites, with the vast majority of sites having fewer than 10 bones identified as *Salmo* sp., even when general preservation of other fish remains is excellent (See Chapters 3 and 7). Most researchers cite the relatively high fat content of *Salmo* sp. bones as the reason for this lack of preservation within archaeological assemblages e.g. J. H. Barrett, Nicholson, and Cerón-Carrasco 1999; Inge Bødker Enghoff 1986; Kerklaan 2016; Lepiksaar and Heinrich 1977; Lepiksaar and Larsson 1982; Lubinski 1996. However this line of reasoning is often contradicted by the presence of large amounts herring, mackerel and other oily fish bones at many archaeological sites that lack *Salmo* sp. remains, as well as much higher ubiquity amongst the Pacific salmon and trout within the *Oncorhynchus* genus, which have similar morphology and life history constraints (Campbell and Butler 2010; Efford et al. 2023; Esteve and McLennan 2007; Orchard and Szpak 2011). This suggests a more complex set of reasons behind these preservation issues based in part on local soil chemistry and species-specific spawning effects on bone density/composition (Szpak 2011).

9.2.2 Medieval *Salmo* sp. Exploitation

The end of Roman influence in northwestern Europe was a period of great political, economic, and social fluctuation, with an observed contraction in population and productive output across many previous Roman centres in modern-day England and the Netherlands (Bavel 2010; Frere 1998; Koning 2003; Loseby 2000; Magendans and Waasdorp 1989). Cultural and economic shifts seen in this post-Roman period included changes in fishing strategy, technology, and preferences. When the legions withdrew established trade networks, including large scale fishing and processing operations, were interrupted and most North Sea basin area settlements show a return to localised, seasonal small-scale fishing with a higher prevalence of freshwater and nearshore taxa represented (J. H. Barrett 2019; J. H. Barrett, A. M. Locker, and Roberts 2004a; J. H. Barrett and D. C. Orton 2016; J. A. Galloway 2017; Marzano 2018). Patterns in fish consumption and exploitation did shift, however, as the Medieval Period moved forward, culminating in what has been referred to as a "Fish Event Horizon", characterized by a shift from primarily freshwater and nearshore fish exploitation to primarily deep water marine species, and an overall intensification of marine fishing efforts (J. H. Barrett, A. M. Locker, and Roberts 2004b). This change does not occur uniformly across northern Europe– nor did they affect all "freshwater", "marine, and "estuarine" taxa in the same way– but for the most part these changes in fishing strategy began somewhere between the years 900-1100 CE (J. H. Barrett, A. M. Locker, and Roberts 2004b; J. H. Barrett, D. Orton, et al. 2011; J. H. Barrett and D. C. Orton 2016; Inge Bodker Enghoff 1999, 2000; J. F. Harland, A. K. Jones, and D. C. Orton 2016; Oueslati 2019; Sick-

ing and Abreu-Ferreira 2009). It is suggested that this shift in fishing trends was primarily demand-driven, with an observable decline in freshwater fish exploitation coinciding with increased pressure from Christian dietary restrictions, rapidly growing urban centres, "globalisation" of trade routes, and changes in fishing technology for gadids and herring (J. H. Barrett, D. Orton, et al. 2011).

The position of *Salmo* sp. fishes within these concepts of "marine", "freshwater" or "nearshore" fisheries of the Early and Late Medieval Period is complex. At least one 10th-century writer, Aelfric of Eynsham, referred explicitly to salmon as being ocean-going fish caught in the sea (Garmonsway 1938; Harris 2003). However, the majority of archaeological and historical evidence for salmon fishing across the Medieval Period indicates that most salmon were caught either in riverine or estuarine environments via the use of fixed weirs, seine nets, traps, line angling, and, occasionally, spearing (Bennema and Rijnsdorp 2015; J. Galloway 2021; R. C. Hoffmann 1985, 1996; Kowaleski 2016; Svanberg and A. Locker 2020; Wolter 2015). Unlike the marine gadid and herring fisheries, which saw consistent innovations in fishing technology and rapid growth of long-distance commercial processing and trade industries, the fisheries for *Salmo* sp. fish were more varied in their development, management, and, in some cases, collapse (J. H. Barrett, D. Orton, et al. 2011; R. C. Hoffmann 2005). Though various species of salmon, trout, char, grayling, and whitefish were generally preferred above many other freshwater fish in the Medieval Period (Bennema and Rijnsdorp 2015; R. C. Hoffmann 1996; Maccarinelli 2020; Svanberg and A. Locker 2020), historical references illustrate a hierarchy of preference within the *Salmo* genus. Anadromous Atlantic salmon are the largest of the western European salmonids, closely followed by anadromous sea trout, and due to their fatty flesh, higher meat yield, and more robust flavor, both fish have long been preferred for consumption over the smaller and less flavorful– but generally more abundant– freshwater Brown trout (R. C. Hoffmann 2015). Across the North Sea basin area Atlantic salmon, and, to a lesser degree, brown and sea trout, were taxed at higher rates and more economically valuable than other fish species, reserved in times of scarcity for exclusively high status or ecclesiastical use, and subject to some of the first "conservation" minded legislative efforts (B. Beerenhout 2016; Bob Beerenhout 2011; R. Hoffmann 2012; R. C. Hoffmann 1996, 2005; Frits Laarman and Lauwerier 1996; Svanberg and A. Locker 2020).

The historical record is fairly clear on the status of salmon and sea trout as preferred, and even luxury, fish at various points throughout the Medieval Period, and their presence at archaeological sites of varying kinds is expected. However, though *Salmo* sp. fish are certainly present at many North Sea basin sites, they are by no means abundant, with most published datasets having fewer than 20 individual *Salmo* sp. bones recorded (92.3% of sites reviewed in Chapter 7). This lack of ubiquity prompts questions about regional preferences, potential declines in population due to factors like overfishing, human environmental modification, and climactic fluctuations. In order to enrich our understanding of the *Salmo* sp. populations exploited by medieval groups around the North Sea Basin area, we have applied a combined biomolecular approach aimed at both identifying these taxa to species as well as providing a comparative isotopic baseline analysis of North Sea basin fishing throughout the period from approximately 500-1500 CE.

9.2.3 Medieval Archaeology of the North Sea Basin

A highly productive marine environment spanning approximately 750,000 square kilometers, the North Sea geological basin connects the coastal regions of the modern day nations of England, Scotland, France, Belgium, the Netherlands, Germany, Denmark, Norway and Sweden (Milner et al. 2008). There is evidence for marine resource use across the coastal margins of this area from as early as circa 8000 BCE, and the Medieval Period from approximately 500-1500CE saw some of the most intensive use of the basin area's marine, estuarine, and riverine environments (Milner et al. 2008). The North Sea acted as not only a source of subsistence resources, but

a nucleus of social and political connection, economic growth, and cultural transmission during the Medieval Period (Ayers 2016; Milner et al. 2008). This importance to a wide variety of human cultural groups, combined with it's historically robust populations of Atlantic salmon, sea trout and brown trout, makes the North Sea basin area an ideal locale for the study of archaeological *Salmo* sp. fishes. A combined biomolecular approach using zooarchaeology by mass spectrometry (ZooMS) and bulk carbon and nitrogen analysis (SIA) allows for the identification of fish to species, the differentiation of ecotypes, and study of regional changes in *Salmo* sp. isotope ecology.

To this end, fish bone material from a total of 14 medieval North Sea archaeological sites located in modern day England, Scotland, Denmark and the Netherlands (Figure 1) was selected for bulk stable carbon and nitrogen analysis, with the majority of the *Salmo* sp. remains having their species identifications confirmed using zooarchaeology by mass spectrometry (ZooMS). Additional sites of interest across the southern portions of England, France, mainland Scotland and Belgium were initially identified but issues of *Salmo* sp. bone survival, general sample availability, and logistical barriers resulting from the ongoing COVID-19 pandemic prevented more comprehensive sampling. Despite this, the sites included represent cover several key areas of the North Sea itself, including the Northern North Sea (Earl's Bu), the Wadden Sea (the three Danish sites, plus Tjitsma Wijnaldum in the Netherlands), and the Southern North Sea (eight remaining Dutch sites, plus 16-22 Coppergate). These sites were selected based on the presence of *Salmo* sp. remains within the fish bone assemblages recovered during excavations and identified by zooarchaeologists. Seven of these sites had large enough fish bone assemblages to allow for sampling of both *Salmo* sp. bones and bones from comparative freshwater, marine and estuarine fish taxa. The following subsections offer brief descriptions of the phasing and interpretations for each of these sites, including those sites which have a full comparative sample set of freshwater, marine, and migratory fish bone isotopic data available.

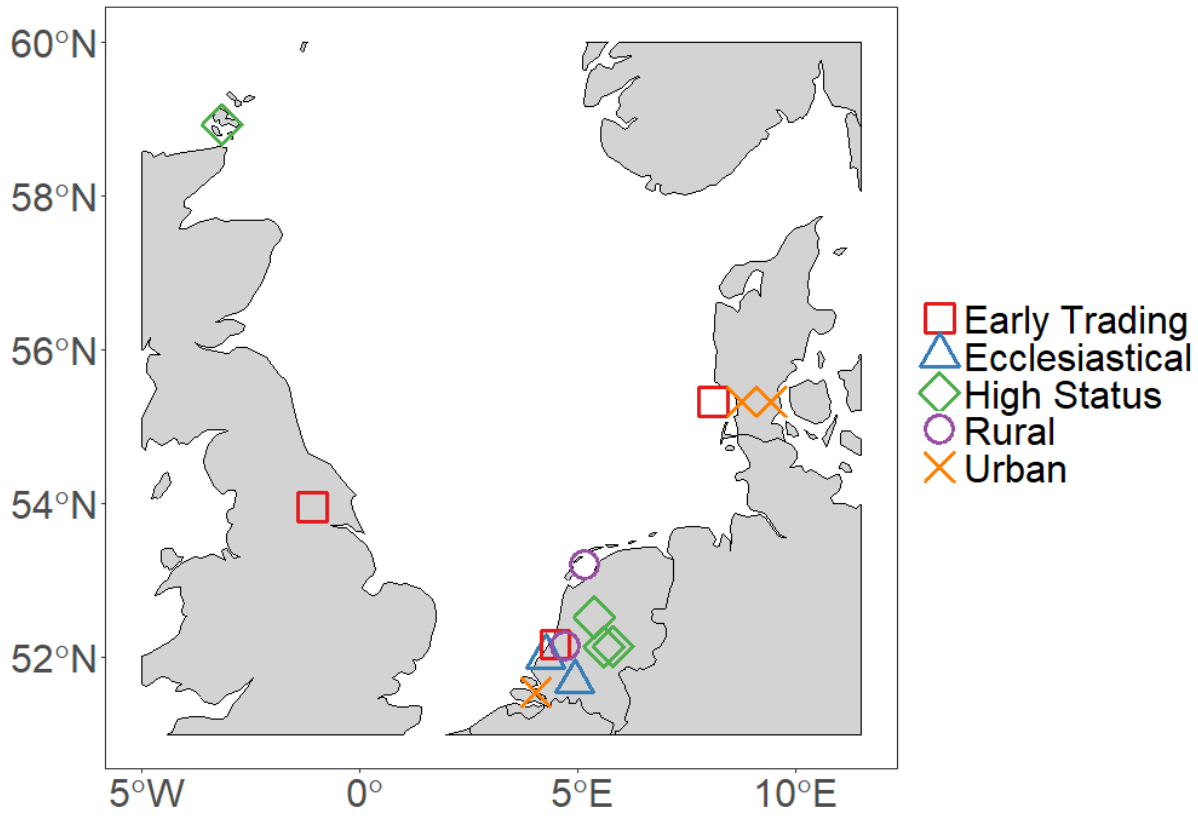


FIGURE 9.1: Locations of archaeological sites included within this study, differentiated by site type

16-22 Coppergate - York, England

York, situated on the banks of the River Ouse, has long been a crossroads of complex trade networks due to it's direct connections to North Sea ports, southern cities like London, and highly productive agricultural land across Yorkshire. Located in the city centre, the site uncovered at 16-22 Coppergate in 1976 is to this day one of the most archaeologically productive, and publicly impactful Early Medieval urban sites excavated in England (R. A. Hall 2014). Thanks to an intensive bulk soil sampling regime at the site, a fish bone assemblage with a NISP of nearly 32,000 was recovered that spans a period from the 5th-century CE to approximately 1500 CE (Bond and O'Connor 1999; R. A. Hall 2014; R. A. Hall and Hunter-Mann 2002).The two periods of greatest interest are those designated as "Anglo-Scandinavian" and "Medieval" by the original excavators, and the contexts associated with these periods have the richest deposits of cultural, osteological, architectural and faunal material at the site (Bond and O'Connor 1999; R. A. Hall 2014; R. A. Hall and Hunter-Mann 2002; MacGregor, Mainman, and Rogers 1999; Mainman 1990). This urban site is mostly comprised of domestic tenements, artisan workshops, and mixed-use structures that supported a craft-based commercial sector in the city with evidence for long-term occupation throughout shifts in the political and social fabric of the site from a post-Roman Anglian *wic*, Anglo-Scandinavian capital, and Anglo-Norman city (R. A. Hall 2014; R. A. Hall and Hunter-Mann 2002; Mainman 1990).

Earl's Bu - Orkney, Scotland

The Earl's Bu site located in the parish of Orphir on Orkney's Mainland island, approximately 14km southwest of Kirkwall and associated with a partially standing Norse round church, or *kirk*. The *bu*, or landed estate was built by Earl Paul Haakonsson in the early 12th-century (Anderson 1873; J. Harland 2006) and excavations from 1979-1993 uncovered several pre-Norse occupation phases, a Norse horizontal mill, Norse domestic and agricultural structures, a small graveyard, and Early Modern farm deposits (J. Harland 2006). Faunal material, including one of the largest medieval fish bone assemblages found in Scotland, has been excavated from deposits dating from approximately 881-1164 CE (J. Harland 2006). The Norse period in Orkney spanned from the 9th-13th centuries, and the archipelago was ideally placed to act as an important trade stop between Scandinavia, mainland Scotland, Ireland, Iceland and the Faroes (J. H. Barrett, Beukens, et al. 2000; J. Harland 2006). Sites across this region show direct evidence for long-distance trade in Norse-produced goods as well as local agricultural, terrestrial and marine resources (J. H. Barrett, Beukens, et al. 2000; J. Harland 2006).

ASR 9, ASR 13, and ASR 2090 - Ribe, Denmark

While dozens of medieval archaeological sites have been uncovered in the modern day Southern Jutland town of Ribe, one of the most important remains the early-8th to mid-9th century marketplace first discovered in 1973, and fully excavated from 1990-1991 (Feveile 2006; Søvsø 2006). The marketplace itself was likely the site of a small earlier agrarian settlement, but beginning around the year 700 CE a seasonal, and later permanent, collection of artisan workshops and domestic dwellings were constructed just north of the Ribe Å river (Feveile 2006; Søvsø 2006). Within a decade of it's founding the marketplace was organized in systematic plots along a main road, and the 1990-1991 ASR 9 "Posthuset" excavation uncovered waste pits, middens, workshop debris, and remains one of the most important Germanic Iron Age-Viking Period transition sites in southern Scandinavia (Feveile 2006; Søvsø 2006). The materials from the ASR 9 site indicate varied artisan craft production, including glass making, metalworking, and boneworking as well as evidence for long-distance and local trade in animal products and other finished goods across northwestern Europe including direct connections to the Northern Netherlands and England (Feveile 2006). The later medieval sites designated ASR 13 "Lindegården" and ASR 2090 "von Støckens Plads" were part of the relocated Ribe settlement, which moved from the marketplace area north of the Ribe Å river to the modern day town centre to the south in the 11th century (Feveile 2006; Sovso and Jensen 2016). ASR 2090 is a loosely affiliated group of medieval cesspits and a "bone road", made from compressed kitchen refuse, with animal bone material dating from approximately 1000-1200 CE (Slippe, Sogn, and Sovso 2006). ASR 13 is a slightly more complex site, located directly adjacent to the Ribe *Domkirke* cathedral and interpreted as a series of timbered buildings associated with the early church, with faunal material recovered that dates to between 1200-1300 CE (Sovso and Jensen 2016). After the 11th-century relocation Ribe continued to be an important ecclesiastical centre in the united Danish kingdom, but never regained it's position as a key trading and manufacturing emporium after the abandonment of the marketplace (Sovso 2022; Sovso and Jensen 2016).

Minderbroedersklooster - Den Bosch, Netherlands

Excavated between 1997-1999, the Minderbroedersklooster site in 's-Hertogenbosch contains several phases of occupation from approximately 1175-1500 CE (Genabeek 2016). First utilized as the manor house of the namesake duke of the city, Hertog Hendrik van Brabant, the site was later incorporated into the holdings of the first Franciscan friary in the Netherlands (Genabeek 2016). The pre-monastic residence yielded cultural and organic

material dating to between 1145-1250 CE, with the monastic occupation beginning around 1250 and seeing a large expansion of buildings and use in the late 14th-early 15th centuries CE (Genabeek 2016). Both occupations benefited from the city's location within the prosperous Duchy of Brabant, which enjoyed excellent trade connections to the North Sea via river and land routes during it's 13th-14th century "golden age" (Genabeek 2016).

Nieuw Rhijngeest-zuid 2014 - Oegstgeest, Netherlands

The Nieuw Rhijngeest-zuid excavations in the Dutch town of Oegstgeest took place from 2009-2014 and were one of several series of excavations focused on a suspected Early Medieval emporium site in the from the late 1990s to 2010s (Bruin, Bakels, and Theuws 2021). An incredibly rich assemblage of cultural, architectural, and biological material was uncovered from waste pits, flood management structures, dwellings, and wells all dating to between 400-800 CE (Bruin, Bakels, and Theuws 2021). With it's most intensive use period between 550-725 CE, this site's 26 Early Medieval houses, 73 outbuildings, and 100-plus wells indicates the presence of a complex fishing, trading, and farming community that was under the control of both Frisian and Frankish dynastic kings at various points (Bruin, Bakels, and Theuws 2021). This site rivals similar Early Medieval trading emporia found at Dorestad in the Netherlands and is even comparable to the later marketplace at Ribe. In close proximity to the North Sea drainage of the Old Rhine (Oude Rijn), this site was ideally placed to operate within the sphere of influence of Anglian, Frisian, Frankish, Germanic, and Scandinavian trading networks active in northwestern Europe from the post-Roman period onward (Bruin, Bakels, and Theuws 2021).

Remaining Dutch Sites

Archaeological *Salmo* sp. fish remains were sampled from an additional seven archaeological sites located across the Netherlands, and spanning a combined date range from approximately 550-1425 CE (Table 1). The oldest of these sites, the constructed dwelling mound, or *terp*, at Tjitsma Wijnaldum, is fairly isolated from the other Dutch sites included within this study. It underwent several periods of occupation, ranging from a late Roman outpost in the 2nd century CE, a Migration Period phase from approximately 425-550 CE and later Frankish and Germanic periods from 550-950 CE (Prummel, K. Esser, and Zeiler 2013). Roughly contemporary with this *terp* site as well as the Nieuw Rhijngeest-zuid site from Oegstgeest, the Plantage site– located in Leiderdorp, South Holland– is primarily a Merovingian and Carolingian settlement with intensive use periods dating from 650-850 CE (Dijkstra, Verhoeven, and Straten 2016). This site was likely part of the same Early Medieval North Sea trading networks as Nieuw Rhijngeest-zuid, Ribe ASR 9, and Dorestad, with mixed Frisian, Frankish, Germanic and Scandinavian influences seen at this small fishing settlement located on the banks of the Old Rhine (Dijkstra, Verhoeven, and Straten 2016). Moving forward in time, the closely associated sites of Huize van den Kasteele and Stadhuis Zutphen are part of the early 11th-12th century palatial complex associated with the Counts of Zutphen and Guelders (Bob Beerenhout 2011; Nijsten 2004). These explicitly high status contexts provide an interesting point of comparison to the contemporary Orcadian Norse high status settlement at Earl's Bu, as well as the later 13th-century Kasteel Voorst site located in Zwolle. This site, directly associated with the Van Voorst tot Voorst family, is an example of a wealthy estate occupied during the height of power of the County of Guelders– a time when key North Sea basin tributaries of the Maas, Waal, Lek and Ijssel rivers were all controlled by the Count or vassal nobles, like the Van Voorst tot Voorst family (Hove 2005; Nijsten 2004). Moving into the final century of the study period, we see two distinctly different archaeological sites with sampled *Salmo* sp. remains, the first of which was a Norbertine priory-run hospital complex located in Delft. This hospital, called the Oude en Nieuwe Gasthuis, was founded by 1252 CE and continued operations in some form until 1968 (Onisto, Maat, and Bult

1998). The material studied from this site is from a much narrower date range, focused on a cesspit and beer cellar which were filled with mixed hospital and monastic food waste between 1400-1450 CE (E. Esser 1992). Finally, the In den Struys site in Veere, Zeeland inhabits a critical location where the Scheldt, Rhine and Meuse rivers empty into the North Sea. This single feature site consists of a cesspit likely used by a family of wealthy Dutch merchants operating independently from the collapsing Burgundian ruling family (Frits Laarman and Lauwerier 1996; Schepper 1994).

Site	Location	Date Range	Site Type
Tjitsma Wijnaldum	Foarryp, Friesland	550-950 CE	Terp settlement
Plantage Leiderdorp	Leiderdorp, South Holland	650-850 CE	Small fishing settlement
Huize van den Kasteele	Zutphen, Gelderland	1000-1100 CE	Palatial complex
Stadhuis Zutphen	Zutphen, Gelderland	1125-1175 CE	Palatial complex
Kasteel Voorst	Zwolle, Overjissel	1280-1360 CE	High status castle site
Oude en nieuwe Gasthuis	Delft, South Holland	1400-1450 CE	Monastic hospital
In den Struys	Veere, Zeeland	1425-1500 CE	Merchant house

TABLE 9.1: Site descriptions and dating for Dutch archaeological *Salmo* sp. remains included in this study

9.3 Materials

A sample (n=196, Table 2) of archaeological fish bones has been analysed from 14 medieval sites located around the North Sea basin. In total, 104 of the sampled bones were initially categorised as *Salmo* sp.– defined here as fish bones which can be positively identified as belonging to the *Salmo* genus, but which cannot be assigned to species or ecotype using morphological features alone. The majority of these *Salmo* sp. samples were vertebral elements (n=89), with the remainder including cranial elements like articulars, ceratohyals, and preoperculars, as well as indeterminate cranial elements.

These comparative taxa included fish from the broad carp (Cyprinidae), cod (Gadidae), flatfish (Pleuronectiformes), and whitefish (Coregonidae) taxonomic groups, as well as individual specimens identified morphologically as belonging to the following species; *Gadus morhua, Melanogrammus aeglefinus, Liza ramada, Raja clavata, Perca fluviatilis, Anguilla anguilla, Esox lucius, Abramis brama* and *Alosa fallax.* These taxa were categorized according to their expected habitat into one of four groups– marine, freshwater, migratory and flatfish. Flatfish are categorized separately, as the Pleuronectiformes order shows a particularly high degree of behavioral plasticity across the North Sea basin area (Van Der Reijden et al. 2018) and ZooMS markers had not been developed at the time of this study. Within the subset of comparative specimens, 25.7% (n=25) were freshwater, 37.1% (n=36) were marine, 32% (n=31) were migratory, and 5.2% (n=5) were flatfish.

Site	Cod Family	Atlantic Cod	Haddock	Carp Family	Common Bream	European eel	European Perch	Flatfish Families	Northern Pike	Salmo sp.	Thinlip Grey Mullet	Thornback Ray	Twait Shad	Whitefish	TOTAL
England															
16-22 Coppergate	1	4	1	1		7			1	53					68
Denmark															
ASR 13 Lindegården			1							2					3
ASR 2090 von Støckens Plads			3	1	2					4					10
ASR 9 Posthuset			2	1	5	1	1	4	1	8	6				29
Scotland															
Earl's Bu	3	1	10			3		1		17		1			36
The Netherlands															
Huize van den Kasteele										1					1
In den Struys' Veere										4					4
Kasteel Voorst Zwolle										1					1
Minderbroedersklooster	1		10	2					6	2				5	26
Nieuw Rhijngeest-zuid (2009-10, 2014)					1	1	2			4			1	1	10
Oude en nieuwe Gasthuis										2					2
Plantage Leiderdorp										2					2
Stadhuis Zutphen										1					1
Tjitsma Wijnaldum										3					3
TOTAL	5	6	27	5	8	12	3	5	8	104	6	1	1	6	196

TABLE 9.2: Materials sampled for bulk carbon and nitrogen stable isotope analysis

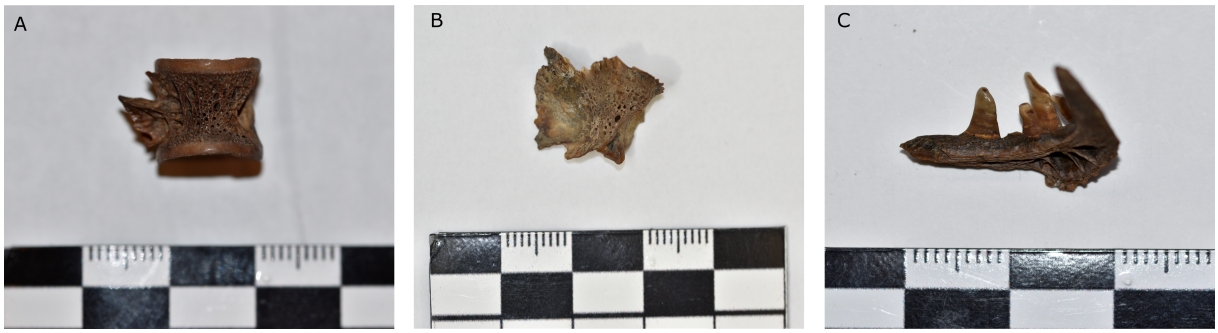


FIGURE 9.2: Three archaeological fish bone samples included in this study– A. NL_salmo_002, a salmon caudal vertebra; B. NL_salmo_047, a trout basioccipital fragment; C. NL_comp_014, a cyprinid pharyngeal.

9.4 Methods

9.4.1 Zooarchaeology

The identification of *Salmo* sp. bones for this study followed commonly employed zooarchaeological methods, involving the use of comparative specimens, literature references, and digitised resources to make genus or species level determinations (Sykes and Saddler 2017; Watt, Pierce, and Boyle 1997; A. C. Wheeler, A. K. G.

Jones, and R. Wheeler 2009). All archaeological assemblages were previously recorded by zooarchaeologists associated with either original excavations or post-excavation commercial or academic archaeology units, and the identifications made by these analysts formed the basis of the sampling strategy employed herein (Besteman and Nieuwhof 1999; Cavallo 2011; Dijkstra, Verhoeven, and Straten 2016; Inge B. Enghoff 2006; E. Esser 1992; Genabeek 2016; J. Harland 2006; J. F. Harland, A. K. Jones, and D. C. Orton 2016; IJzereef 1983; Jagt and F.J. Laarman 2018; A. Jones 1988; Kerklaan 2016; Slippe, Sogn, and Sovso 2006; Sovso 2022; Sovso and Jensen 2016; Vreenegoor and Kuipers 1996). Sampling and morphological identification confirmation was conducted using facilities and materials housed at the Orkney Museum, York Archaeological Trust, Copenhagen Zoologisk Museum, the Dutch Rijksdienst voor het Cultureel Erfgoed and affiliated storage depots, the Sydvestjyske Museer, Universiteit Leiden, and the University of York between October 2020 and November 2021. Provisional identification of salmonidae vertebral and cranial elements to *Salmo* sp. was possible using morphological identification methods, but further analysis using collagen peptide fingerprinting (ZooMS) was required to correctly identify them to species. The comparative specimens were generally assumed to have been correctly identified by the original analysts, and so only cursory confirmation checks were made in the field.

9.4.2 Biomolecular Methods

Collagen extraction for stable isotope analysis and ZooMS followed a modified Longin method (1971). All fish bone samples underwent lipid extraction using a 2:1 dichloromethane/methanol (DCM/MeOH) solution (Colonese et al. 2015), in order to remove 13^C depleted lipids commonly present in fish bone, particularly salmon (Guiry, Hepburn, and Richards 2016; Szpak 2011). Samples were submerged in the DCM/MeOH solution and sonicated for 15 minutes, the waste decanted, solution refreshed, and the process repeated a minimum of 2 times, or until the solution remained clear after sonication. After de-lipidification, all samples were demineralized in 0.4M hydrochloric acid at 4°C, gelatinised with weak (pH3) acid for approximately 48 hours, and filtered using an Ezee-Filter™ prior to lyophilization.

For bulk stable isotope analysis, collagen samples of 0.5mg were weighed out in duplicate and analysed using a Sercon 20-22 continuous flow isotope ratio mass spectrometer (IRMS) coupled to a Sercon GSL elemental analyzer. Raw data was assessed and quality control measures applied in order to ensure the accuracy of the data reported– in order to control for possible contaminants, samples with a C:N ratio outside of a certain range were excluded. While the generally accepted C:N ratio range for bulk stable isotope analysis may be either 2.9-3.6 or 3.1-3.5, depending on the source referred to (Michael J DeNiro 1985; Klinken 1999), the range for fish from both cold and warm water environments are restricted to a much narrower range of 3.0-3.33 (Guiry and Szpak 2021). Subsequently, all samples (n=196) included in this study had C:N ratios within the 3.0-3.33 range, indicating %C and %N ranges within normal limits.

For ZooMS analysis, a portion of the lyophilized samples were re-suspended in ammonium bicarbonate and digested for approximately 24 hours after the addition of a 1μ L trypsin solution. Digested peptides were extracted and filtered using a C18S ZipTip, and spotted onto a 384 ground steel well plate with a α cyano-4-hydroxycinnamic acid matrix solution, and analysed using a Bruker UltrafleXtreme MALDI-TOF/TOF instrument. The resulting spectra were analysed using a combined programmatic and manual approach, with peaks identified for each sample, a table of m/Z values compared to known biomarkers and biomarker combinations for *Salmo salar* and *Salmo trutta* in Python, and the resulting dataset manually checked for outliers and problematic identifications. Where required, spectra were reviewed using the MMass spectra viewer (Strohalm 2013; Strohalm, Hassman, et al. 2008; Strohalm, Kavan, et al. 2010; Strøm et al. 2018) to confirm peak identification, and all samples were able to be assigned an identification to the species level.

Accuracy and precision of the bulk stable carbon and nitrogen isotopic compositions were determined by measurements of international standard reference materials within each analytical run. The averages of these across this runs affiliated with this dataset were IAEA 600 (δ^{13}C raw = -27.70±0.14‰, δ^{13}C true = -27.77‰, δ^{15}N raw = 0.79±0.26‰, δ^{15}N true = 1.00‰); IAEA N2 (δ^{15}N raw = 20.33±0.25‰, δ^{15}N true = 20.31±0.03‰); IA Cane (δ^{13}C raw = -11.74±0.09‰; δ^{13}C true = -11.64‰); and sigma fish gel δ^{13}C raw = -15.35±0.09‰, δ^{13}C true = -15.29±0.05‰, δ^{15}N raw = 15.15±0.10‰, δ^{15}N true = 15.19±0.24‰). Overall uncertainties on these measurements were calculated based on Kragten (1994), combining uncertainties in the values of the international reference materials with those determined from repeated measurements of samples and reference materials. They are reported here as one standard deviation, and the maximum uncertainty for all samples across all runs was 0.17‰ for δ^{13}C and 0.22‰ for δ^{15}N. In addition to these standard references, a sample of homogenised bovine bone was used as a control in 6 out of 12 total runs. Control bovine collagen was extracted and analysed within the sample batches, and produced a mean δ^{15}N value of 6.12 ± 0.17‰ and δ^{13}C value of -23.12 ± 0.14‰. These values were within the overall accepted mean range from 50 previous separate extracts of this bone sample completed at the BioArCh lab at the University of York, which produced average values of δ^{13}C = -23.27‰ and δ^{15}N = 6.40‰.

9.4.3 Statistical Methods

A key component of the overall analysis of bulk stable isotope data produced for this study was the calculation of isotope niche space estimates and overlaps, utilizing the rKIN programming package (Albeke 2017; Eckrich et al. 2020). Isotope niche space analysis is based on the ecological concept of estimating an organism or population's ecological niche, and has been used in archaeological contexts to investigate taxonomic and regional variations in isotopic niche spaces of several hominin species (Hermes et al. 2018; Robinson 2022, 2023). The rKIN programming package combines three methods of isotope niche width estimations; kernel utilization density (KUD), standard ellipse area (SEA), and minimum convex polygon (MCP) estimates. The rKIN package output provides visualisations of the calculated kernels, ellipses, and polygons as well as isotope niche width estimates and ecological niche overlap estimates for each method (Albeke 2017; Eckrich et al. 2020). The three methods together allow the researcher to view the data and directly compare how sample sizes, outliers, and uncertainties are dealt with– providing a more comprehensive understanding of the isotope niche space (Eckrich et al. 2020; Robinson 2022). As with most statistical methods, isotope niche space calculations are often limited by sample size, and a minimum of 10 samples is generally required for taxonomic comparisons to produce reliable niche space and overlap estimates (Albeke 2017; Eckrich et al. 2020; Robinson 2022). This being said, the rKIN package does allow for this minimum to be overridden using a smallSamp() argument, and as little as five samples to be used for analysis (Eckrich et al. 2020). For this study a minimum of 10 samples was used for taxonomic comparisons between comparative marine (haddock), freshwater (Northern pike), and *Salmo* sp., but the smallSamp() argument was used for comparisons between hypothetical regional populations of *Salmo* sp. fish (see Section 5.2).

9.5 Results

9.5.1 ZooMS

The combined biomolecular approach used here focused primarily on the correct identification of the 104 *Salmo* sp. remains included in this study. The final ZooMS dataset (Appendix C) consists of 96 samples with ZooMS identifications; 63 identified as *Salmo salar*, 27 as *Salmo trutta*, three as *Esox lucius*, two as *Gadus morhua*, and 1

as Scopthalmidae (Figure 3). Eight samples of the initial 104 do not have associated ZooMS identifications due to a combination of inconclusive results and machine error; the first two runs of ZooMS analysis were analyzed using an older Bruker Ultraflex III which had known mechanical errors due to it's age, and subsequent re-runs were performed using a newer UltrafleXtreme instrument which provided more consistent spectra results. Several of the bones initially identified as *Salmo* sp. by original faunal analysts proved to be misidentified, with six samples actually belonging to species other than *Salmo salar* or *Salmo trutta* according to ZooMS analysis. Figures 3B shows a ceratohyal from the Huize van den Kasteele site, which was originally recorded as *Salmo* sp. during original post-excavation analysis, but subsequently identified via ZooMS analysis as *Esox lucius*, or Northern pike. Figure 3C shows a caudal vertebra from the Oude en Niuewe Gasthuis site, which was originally recorded as a *Gadus* sp. bone, but which is clearly a salmonid and was subsequently identified via ZooMS as *Salmo salar*.

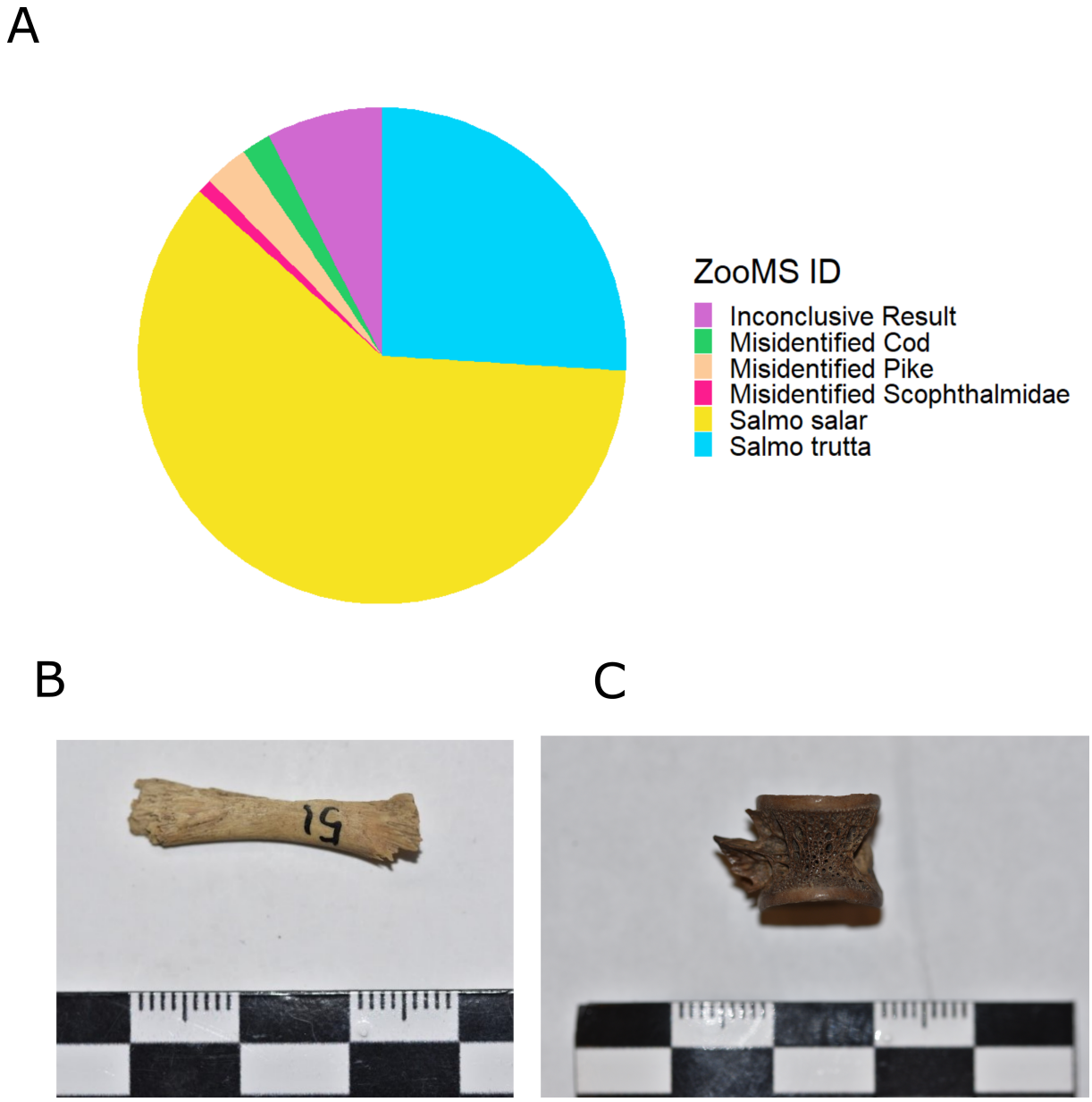


FIGURE 9.3: A). Proportions of ZooMS identification results for 91 samples initially identified as *Salmo* sp., B). misidentified pike ceratohyal (lmq_NL_salmo_112) from Huize van den Kasteele, C.) salmon caudal vertebra (lmq_NL_salmo_002) from Oude en Nieuwe Gasthuis, initially identified as a Gadidae vertebra

9.5.2 Bulk Stable Isotope Analysis

The final isotope dataset (see Supplementary Materials) for this study consists of 190 samples, out of a total 248 analyzed, which provided both a.) enough collagen for analysis and b.) results within the acceptable 3.0-3.33 C:N ratio range (Guiry and Szpak 2021). The ZooMS identifications discussed above shift the proportions of isotope data by species slightly, resulting in a final count of 90 samples identified as either *Salmo salar* or *Salmo trutta*, 8

Salmo sp. samples with inconclusive ZooMS results, and 95 comparative taxa samples (Figure 4). Table 3 below presents the summary statistics for each taxonomic group included within this thesis, and the overall range of of δ^{13}C values was between -26.3‰ and -7.6‰, with δ^{15}N values ranging between 5.2‰ to 18.7‰.

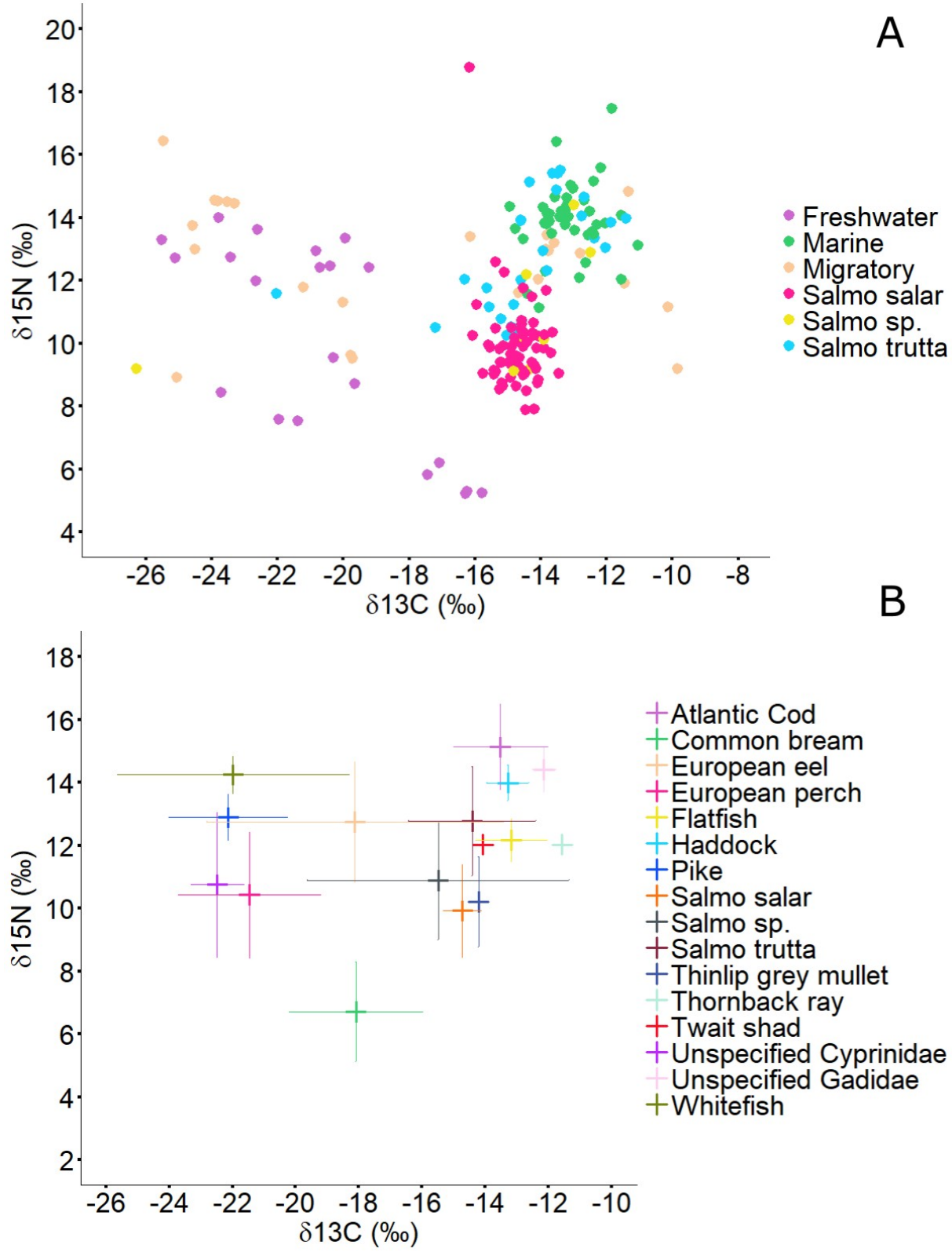


FIGURE 9.4: Plot A is an isotope bi-plot displaying all 190 sample values, with the comparative samples categorized by their environmental group and *Salmo* sp. by identification. Plot B represents mean δ^{13}C and δ^{15}N values reported for each of sixteen taxonomic groups included in the study.

		D13C			D15N		
TAXA	**No.**	*Min.*	*Max.*	*Mean*	*Min.*	*Max.*	*Mean*
Unspecified Gadidae	4	-12.5	-11.6	-12.1 ± 0.4	13.8	15.6	14.4 ± 0.7
Atlantic Cod	6	-15.8	-11.8	-13.5 ± 1.5	13.5	17.5	15.1 ± 1.4
Haddock	26	-14.8	-12.0	-13.3 ± 0.7	12.6	15.1	14.0 ± 0.6
Unspecified Cyprinidae	3	-23.4	-21.4	-22.5 ± 0.8	7.5	12.7	10.8 ± 2.3
Common Bream	8	-22.0	-15.8	-18.1 ± 2.1	5.2	9.6	6.7 ± 1.6
European Eel	12	-25.5	-11.3	-18.1 ± 4.7	9.5	16.4	12.8 ± 1.9
European Perch	1	-23.7	-19.2	-21.5 ± 2.3	8.4	12.4	10.4 ± 2.0
Flatfish	6	-14.4	-11.1	-13.2 ± 1.1	11.1	13.1	12.2 ± 0.7
Northern Pike	11	-25.5	-19.9	-22.1 ± 1.9	11.4	14.0	12.9 ± 0.7
Salmo sp.	8	-26.3	-12.5	-15.5 ± 4.2	9.1	14.4	10.9 ± 1.9
Salmo salar	63	-16.2	-13.4	-14.7 ± 0.6	7.9	18.8	9.9 ± 1.5
Salmo trutta	27	-22.0	-11.4	-14.4 ± 2.0	10.2	15.5	12.8 ± 1.7
Thinlip Grey Mullet	6	-25.1	-7.6	-14.2 ± 6.5	8.3	11.9	10.2 ± 1.4
Thornback Ray	1	-11.6	-11.6	-11.6 ± 0.0	12.0	12.0	12.0 ± 0.0
Twait Shad	1	-14.1	-14.1	-14.1 ± 0.0	12.0	12.0	12.0 ± 0.0
Whitefish	6	-23.9	-13.8	-22.0 ± 3.7	12.9	14.6	14.2 ± 0.6

TABLE 9.3: Summary statistics for all fish bone samples included in this study

The results for comparative freshwater, migratory and marine taxa were all fairly consistent with observed published values within the archaeological literature (e.g. J. Barrett et al. 2008; Fuller, Müldner, et al. 2012; Häberle et al. 2016). Piscivorous freshwater fish like Northern pike (n=11) display higher mean δ^{15}N value of 12.89 ± 0.73‰, characteristic of their high trophic level, and a lower mean δ^{13}C value of -22.13 ± 1.88‰, characteristic of their freshwater environment. Similarly, piscivorous marine fish like haddock (n=26), Atlantic cod (n=6), and unspecified gadids (n=4) show higher means for both δ^{15}N and δ^{13}C values. Migratory or estuarine taxa, such as European eel (n=12), thinlip grey mullet (n=6), whitefish (n=6) and flatfish (n=6) present a more complicated isotopic view, which is to be expected given the behavioral plasticity in foraging ecology and migration seen within these groups (Gibson, Stoner, and Ryer 2014; Hayden et al. 2022; Lebreton et al. 2011; Lundsgaard-Hansen et al. 2013; Pereira et al. 2021). Though thinlip grey mullet demonstrate the widest range of observed δ^{13}C values (-25.07 to -7.57‰), the subset of whitefish samples (n=6) provides a particularly interesting migratory comparative to the available *Salmo* sp., *Salmo salar*, and *Salmo trutta* values (see Section 5).

The following three tables (Tables 4-6) present summary statistics for the three distinct groups of *Salmo* sp. fish remains (total n=96) broken down by site of origin; those identified using ZooMS as *Salmo salar* (n=60), *Salmo trutta* (n=26), and those not identified by ZooMS but morphologically confirmed as *Salmo* sp. (n=10). For *Salmo salar* the range of δ^{13}C values was -16.16‰ to -13.44‰ (mean = -14.72 ± 0.60‰), and the δ^{15}N values ranged from 7.88‰ to 18.78‰ (mean = 9.92 ± 1.47‰). For *Salmo trutta* the range of δ^{13}C values was -22.02‰ to -11.41‰ (mean = -14.72 ± 0.60‰), and the δ^{15}N values ranged from 10.24‰ to 15.50‰ (mean = 12.78 ± 1.74‰). Finally, the range of δ^{13}C values for unspecified *Salmo* sp. was -26.29‰ to -12.49‰ (mean = -15.49 ± 4.15‰),

and the δ^{15}N values ranged from 9.11‰ to 14.39‰ (mean = 10.89 ± 1.89‰).

		δ^{13}C			δ^{15}N		
SITE	**No.**	*Min.*	*Max.*	*Mean*	*Min.*	*Max.*	*Mean*
16-22 Coppergate	44	-15.59	-13.44	-14.53 ± 0.49	7.88	11.75	9.78 ± 0.80
Earl's Bu	6	-15.76	-14.20	-14.98 ± 0.53	7.9	9.38	8.86 ± 0.48
In den Struys' Veere	3	-16.07	-14.10	-15.23 ± 0.83	8.74	10.25	9.62 ± 0.64
Minderbroedersklooster	2	-15.38	-15.19	-15.29 ± 0.10	8.73	10.48	9.61 ± 0.88
Nieuw Rhijngeest-zuid (2009-10, 2014)	3	-15.96	-14.53	-15.20 ± 0.59	10.28	12.25	11.26 ± 0.80
Oude en nieuwe Gasthuis	1	-14.53	-14.53	-14.53 ± 0.00	9.89	9.89	9.89 ± 0.00
Plantage Leiderdorp	1	-15.13	-15.13	-15.13 ± 0.00	9.91	9.91	9.91 ± 0.00
Stadhuis Zutphen	1	-15.37	-15.37	-15.37 ± 0.00	12.58	12.58	12.58 ± 0.00
Tjitsma Foarryp Wijnaldum	2	-16.16	-15.15	-15.66 ± 0.50	8.63	18.78	13.71 ± 5.08
TOTAL	63	-16.16	-13.44	-14.72 ± 0.60	7.88	18.78	9.92 ± 1.47

TABLE 9.4: Intersite comparison of summary statistics for all *Salmo salar* specimens

		δ^{13}C			δ^{15}N		
SITE	**No.**	*Min.*	*Max.*	*Mean*	*Min.*	*Max.*	*Mean*
16-22 Coppergate	4	-15.21	-12.68	-14.00 ± 0.98	10.77	14.87	13.55 ± 1.64
ASR 13 Lindegården	2	-14.88	-14.58	-14.73 ± 0.15	10.52	10.70	10.61 ± 0.09
ASR 2090 von Støckens Plads	4	-13.81	-13.40	-13.58 ± 0.16	12.32	15.50	14.66 ± 1.35
ASR 9 Posthuset	7	-16.31	-14.61	-15.26 ± 0.56	10.24	12.03	11.24 ± 0.69
Earl's Bu	8	-17.19	-11.41	-13.27 ± 1.79	10.51	14.05	13.20 ± 1.09
Oude en nieuwe Gasthuis	1	-22.02	-22.02	-22.02 ± 0.00	11.58	11.58	11.58± 0.00
Tjitsma Foarryp Wijnaldum	1	-14.34	-14.34	-14.34 ± 0.00	15.13	15.13	15.13 ± 0.00
TOTAL	27	-22.02	-11.41	-14.72 ± 0.60	10.24	15.50	12.78 ± 1.74

TABLE 9.5: Intersite comparison of summary statistics for all *Salmo trutta* specimens

		δ^{13}C			δ^{15}N		
SITE	**No.**	*Min.*	*Max.*	*Mean*	*Min.*	*Max.*	*Mean*
16-22 Coppergate	3	-14.81	-13.91	-14.44 ± 0.38	9.11	10.11	9.77 ± 0.47
ASR 9 Posthuset	1	-14.44	-14.44	-14.44 ± 0.00	12.18	12.18	12.18 ± 0.00
Earl's Bu	2	-14.39	-12.49	-13.44 ± 0.95	9.15	12.90	11.03 ± 1.88
Kasteel Voorst	1	-26.29	-26.29	-26.29 ± 0.00	9.2	9.20	9.20 ± 0.00
Nieuw Rhijngeest-zuid (2009-10, 2014)	1	-12.98	-12.98	-12.98 ± 0.00	14.39	14.39	14.39 ± 0.00
TOTAL	8	-26.29	-12.49	-15.49 ± 4.15	9.11	14.39	10.89 ± 1.88

TABLE 9.6: Intersite comparison of summary statistics for all Unspecified *Salmo* sp. specimens

9.6 Discussion

9.6.1 Comparative Isotope Ecology of Medieval North Sea Fishes

The data presented here provides a multi-dimensional look at the comparative isotope ecology of not only *Salmo* sp. ecotypes (see below for further discussion), but a variety of marine, migratory and freshwater taxa which were routinely exploited by humans across the study area during the Medieval Period. Figures 5-7 show the variation in δ^{13}C and δ^{15}N values seen in the 13 comparative taxonomic groups included in this study, ranging from fully marine species like Atlantic cod to fully freshwater species like common bream. As discussed in the results section, the majority of the comparative taxonomic groups conform to expected isotope foraging ecology signatures, with the enriched carbon values typical of marine environments seen in the unspecified Gadidae, Atlantic cod, haddock, and thornback ray groups, and depleted carbon values typical of freshwater environments seen in the European perch, pike, unspecified Cyprinidae, and common bream groups.

Cod samples (Figure 5) were sourced exclusively from Coppergate (n=4) and Earl's Bu (n=2), and in both cases the majority of the samples were from the Norse period of occupation. Interestingly, the mean δ^{13}C values (-13.52 ± 1.49‰) and δ^{15}N values (15.13 ± 1.36‰) for Atlantic cod are consistent with averages reported for medieval Atlantic cod samples originating from the southern North Sea and eastern North Atlantic (δ^{13}C = -13.03 ± 1.08‰ and δ^{15}N = 15.63 ± 1.10‰), likely indicating fairly localized origins for the individual fish rather than imports from the Kattegat, Baltic, or Arctic Norwegian populations of cod (D. C. Orton et al. 2011).

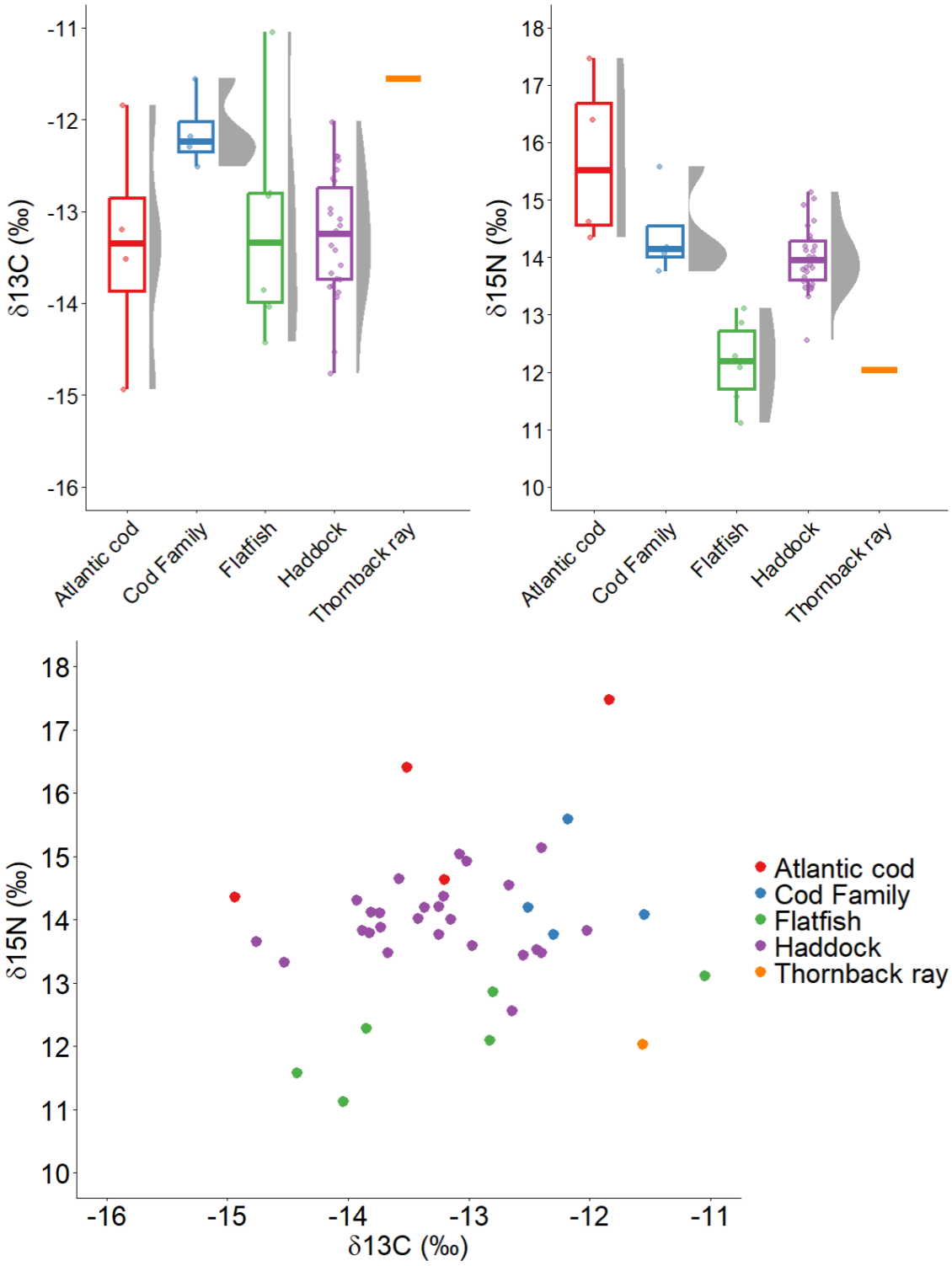


FIGURE 9.5: Mean δ^{13}C (top) and δ^{15}N (bottom) values reported for each of five marine taxonomic groups; Atlantic cod (*Gadus morhua*), Cod Family (Gadidae), Flatfish (Pleuronectiformes), Haddock (*Melanogrammus aeglefinus*), and Thornback ray (*Raja clavata*).

While a similar set of published archaeological data for haddock is not currently available, the mean δ^{13}C values for the haddock specimens in this study (n=26, Figure 5) can be compared to a comprehensive modern dataset from the North Sea (Jennings and Cogan 2015). The archaeological δ^{13}C values (mean -13.28 ± 0.66‰) differ significantly from the modern North Sea δ^{13}C values (mean -17.99 ± 1.22‰)– with an average decrease of 4.71‰ Jennings and Cogan 2015. This likely reflects significant changes over time in regional seawater temperature affecting foraging migration strategy– it has been observed that lower δ^{13}C values in Gadidae fishes correlate positively with lower overall temperatures and regional climate fluctuations (Edvardsson et al. 2022; Ólafsdóttir et al. 2021; Wada, Kabaya, and Kurihara 1993).

Commonly exploited flatfish species in the North Sea include plaice, dab, sole, turbot, brill, and flounder which can all inhabit a wide variety of ecosystems, from the open sea to estuaries, and shift their foraging habits accordingly (Link et al. 2014). This means that archaeological samples from any given flatfish species could potentially fall within a wide range of stable carbon values, depending on their individual life history. Despite this potential variety, all flatfish samples from this study (n=6) fall firmly within a typically marine δ^{13}C range of -11.1 to -14.4‰. Similar to haddock, the mean δ^{13}C value for the broad flatfish group (-13.2 ± 1.1‰) was significantly different from those obtained from modern North Sea plaice (-16.9 ± 0.7‰) and dab (-18.5 ± 0.8‰) (Jennings and Cogan 2015). This may again be a case of long-term climate change affecting the mean stable carbon characteristics of fish in the North Sea, as with cod and haddock (Edvardsson et al. 2022; Ólafsdóttir et al. 2021). The Northern pike samples (n=11, Figure 6) included within this study dataset came from the Netherlands, Denmark and England, but the majority of samples (n=8) were from the Minderbroedersklooster's site in 's-Hertogenbosch and Coppergate in York. The overall range of pike δ^{13}C (-25.51 to -19.93‰) and δ^{15}N (11.37 to 13.99‰) values in the data align closely with expected values for pike – which are large, piscivorous predators ubiquitous in freshwater environments across the North Sea basin area and which were highly valued for food during the Medieval Period (Beaudoin et al. 1999; Ervynck, Boudin, and Van Neer 2018; Maccarinelli 2021). Similarly, the range of δ^{13}C (-21.96 to -15.77‰) and δ^{15}N (5.22 to 9.55‰) values for the common bream samples (n=8, Figure 6) reflect the variable isotopic range expected for this bottom-feeding species that was commonly consumed during the Medieval Period (Ervynck, Boudin, and Van Neer 2018; Maccarinelli 2021).

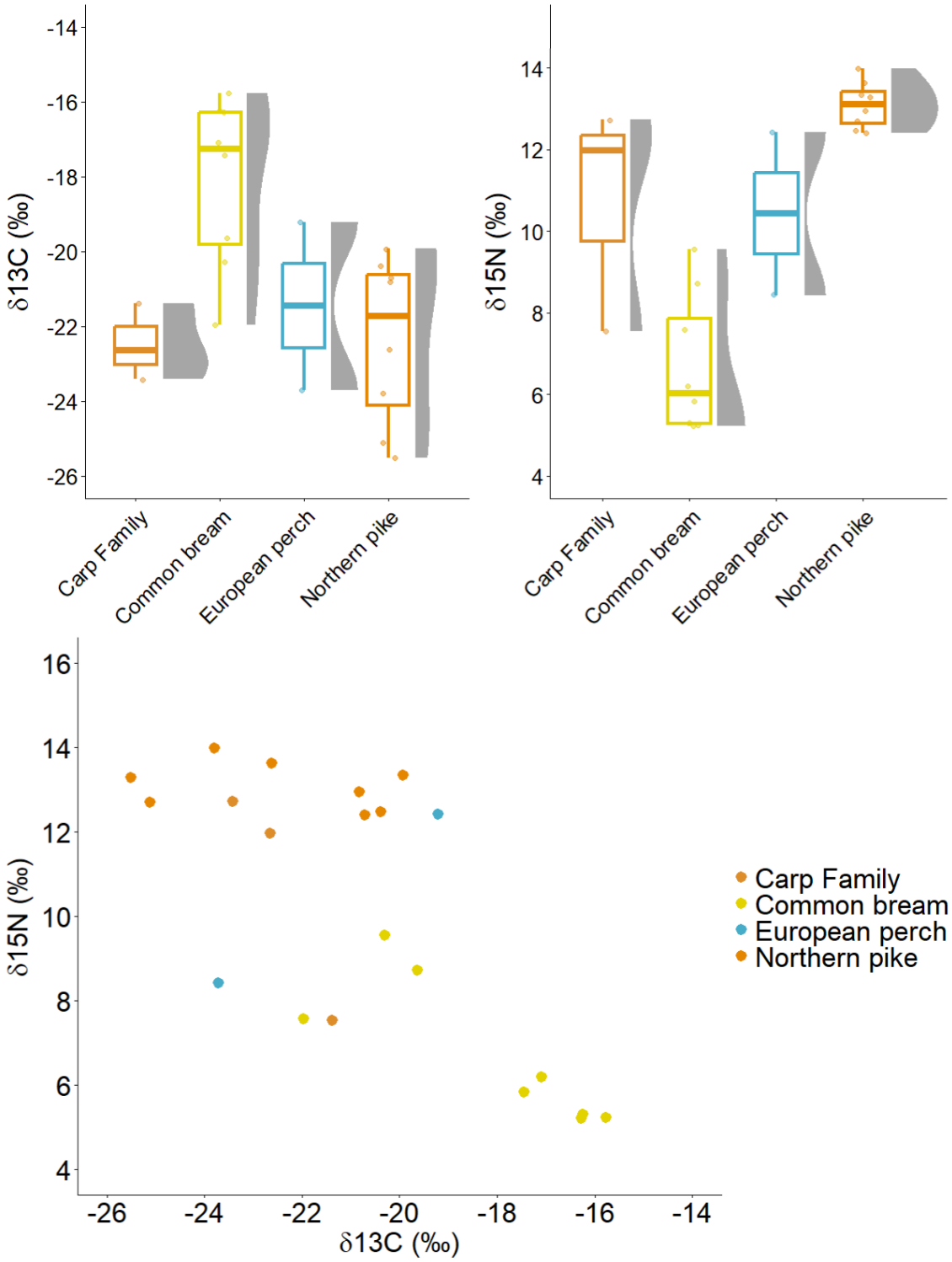


FIGURE 9.6: Mean δ^{13}C (top) and δ^{15}N (bottom) values reported for each of four freshwater taxonomic groups; Carp Family (Cyprinidae), Common bream (*Abramis brama*), European perch (*Perca fluviatilis*), Northern pike (*Esox lucius*).

The fish identified as thinlip grey mullet (*Liza/Chelon ramada*, n=6) are the taxonomic group with both the largest range of δ^{13}C values and the individuals with the highest overall δ^{13}C values of the entire study (Figure 7). The sample contains two individuals that display typically freshwater depleted δ^{13}C values (-25.07‰ and -21.21‰), and four with typically marine enriched δ^{13}C values (ranging from -11.46‰ to -7.57‰)– resulting in a particularly wider split between the two groups. As this species is a highly migratory one which has historically been caught from the Mediterranean to the Skagerrak (Otterstrøm 1912), placing them within a "typical" range of bulk carbon values is difficult. Fish from the Mugilidae family are known to thrive in wildly varying salinity levels, which greatly impacts their δ^{13}C values (Fuller, Van Neer, et al. 2020). Archaeological isotope data from Mugilidae specimens sourced from Mesolithic-Classical period Greece reflect a similar range of δ^{13}C values (-12.99‰ to -7.30‰) as the carbon-enriched samples seen in Ribe (Vika and Theodoropoulou 2012). Meanwhile, samples from the modern Italian Gulf of Gaeta displayed mean δ^{13}C values of 26.54 ± 0.36‰ in the southeastern region of the gulf, and 19.15 ± 1.64‰ in the northwestern region- far more comparable to the carbon-depleted samples seen at Ribe (Cicala et al. 2019). The differences in salinity levels between the Northern Aegean (relatively low salinity) and Gulf of Gaeta (relatively high salinity) suggest a strong impact on the carbon isotopic composition of mullet from these regions, and sheds some light on the salinity of environments the mullet from Ribe must have been feeding in (Cicala et al. 2019; Fry 2002; Vika and Theodoropoulou 2012). Thinlip mullet have historically been known to enter the Ribe Å during spawning periods, and the species has been caught, albeit infrequently, along the various fjords and coastal waters of Denmark from the Wadden Sea to the Skagerrak (Otterstrøm 1912). Interestingly, salinity levels in the Ribe Å estuary are fairly low comparable to other coastal North Sea regions, which may suggest that the carbon-enriched thinlip mullet samples from the Ribe sites were locally sourced, and the carbon-depleted samples were sourced from other locations (Burt et al. 2016).

The whitefish group (n=6, Figure 7) includes fish belonging to the subfamily Coregoninae, within the wider Salmonidae family, which are closely related to Atlantic salmon, with a genomic similarity of approximately 93% (Koop et al. 2008). The range of δ^{13}C values from a lower -23.9‰ to an higher -13.77‰ reflect the observed environmental variability seen within whitefish taxa, which include fully freshwater species like lavaret (*Coregonus lavaretus* and anadromous species like the presumed-extinct houting (*Coregonus oxyrhynchus*), which was native to the North Sea basin area (Freyhof and Schoter 2005; Hansen et al. 2008). There is a slight overlap between the highest δ^{13}C values for whitefish and the lowest seen in unspecified *Salmo* sp. samples, and the highest δ^{15}N values for unspecified *Salmo* sp. samples overlap with the mean whitefish δ^{15}N values. However, for the most part, the multi-isotoptic signature of the whitefish samples remain distinct from unspecified *Salmo sp.*, *Salmo salar* and *Salmo trutta* samples.

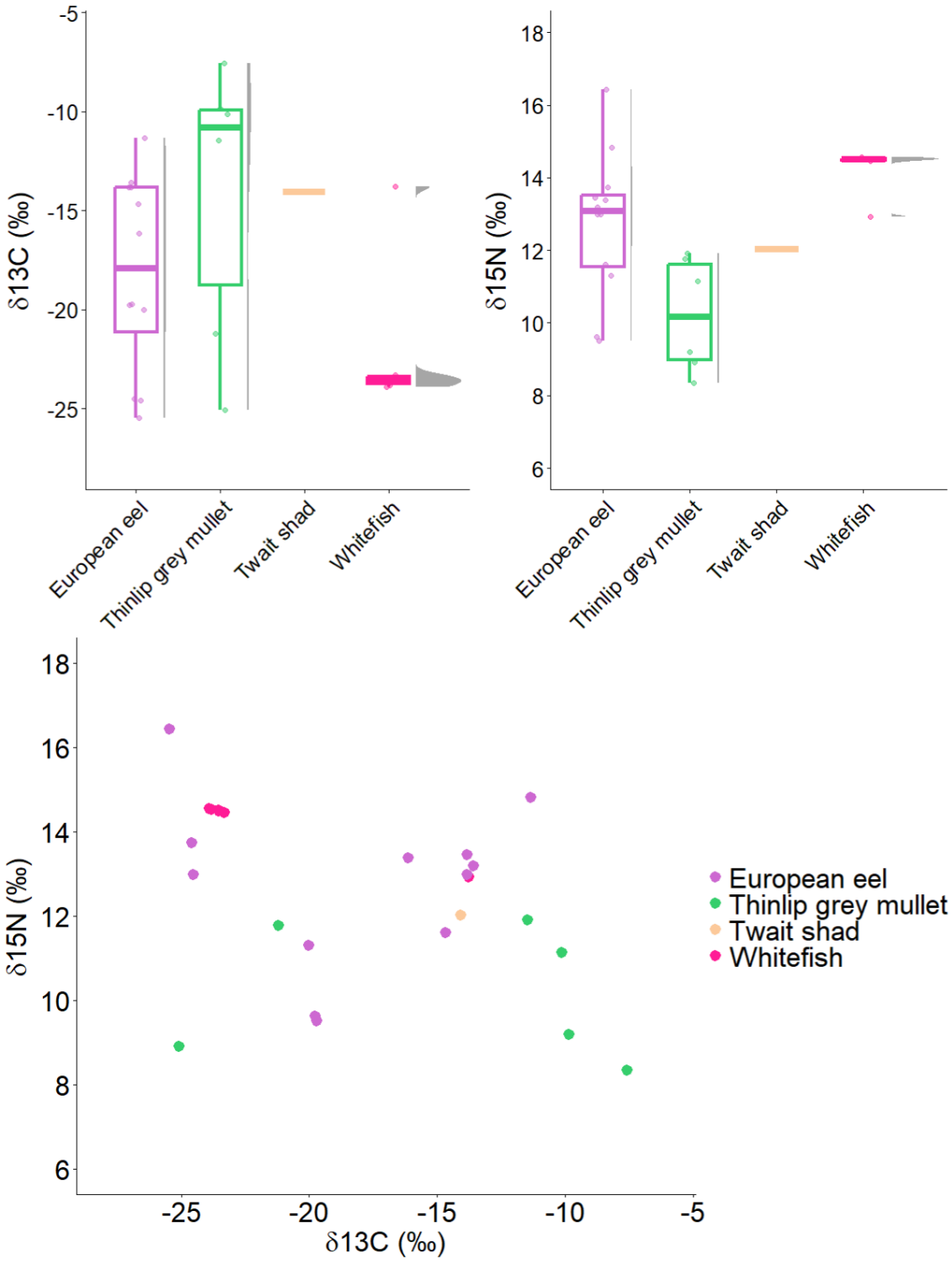


FIGURE 9.7: Mean δ^{13}C (top) and δ^{15}N (bottom) values reported for each of four migratory taxonomic groups; European eel (*Anguilla anguilla*), Thinlip grey mullet (*Chelon ramada*), Twait shad (*Alosa fallax*), and Whitefish (*Coregonus* sp.).

The final significant subgroup of comparative fish are the European eel, with isotope results for twelve specimens from Nieuw Rhijngeest-zuid (n=1), ASR 9 Posthuset (n=1), Earl's Bu (n=3) and Coppergate (n=7). Like the migratory thinlip grey mullet, the eel group demonstrates a particularly wide range of δ^{13}C values (-25.46 to -11.34‰), with five individuals displaying more typically marine δ^{13}C values (< -15.00‰), six individuals displaying more typically freshwater δ^{13}C values (> -19.00‰) and one with an intermediate δ^{13}C value of -16.14‰. This variation in environmental signals is comparable to that seen in Robson et al. (2012), which reported distinctive groupings of eels based on site location for archaeological samples and catch location for modern samples. The δ^{13}C values for the five carbon-enriched eel samples– four from Coppergate and one from ASR 9 Posthuset– are consistent with those seen at coastal archaeological sites in Denmark and Germany (Robson et al. 2012). The carbon-depleted samples from Earl's Bu and Nieuw Rhijngeest-zuid (n=3, mean= -19.83 ± 0.13‰) are comparable to the reported δ^{13}C values (n=2, mean= -18.5 ± 2.6‰) from an inland archaeological site in Northern Germany (Robson et al. 2012). The final three samples from Coppergate display even lower δ^{13}C values than the previous group, and are, on average, more depleted than even the modern freshwater eel samples reported in Robson et al., with a mean of -24.86 ± 0.43‰ (compared to -22.8 ± 0.7‰) (Robson et al. 2012). The split between reported δ^{13}C values for the seven Coppergate individuals is interesting, and may indicate variation in sourcing for eel at the site. There appears to be no temporal component to this observed variation, with most samples (n=6) coming from contexts dated to between 955-1240 CE, and no visible pattern of earlier or later shifts in observed δ^{13}C values. This may indicate that eels were sourced from a variety of locations throughout the occupation of the site, and not solely from the freshwater environment of the nearby River Ouse.

9.6.2 Isotope Ecology of *Salmo* sp. Ecoytpes

One of the most useful aspects of this dataset is the ability to distinguish between *Salmo* sp. ecotype presence at medieval archaeological sites across the study area. When identifications to species are made using ZooMS analysis and combined with bulk multi-isotope analysis of carbon and nitrogen, the foraging strategy, and, therefore, the ecotype of individual fishes becomes visible (see Chapter 8). Figure 8 below visualizes the carbon and nitrogen isotope characteristics of all *Salmo* sp. samples (n=98), with differentiation made based on ZooMS species identification. The vast majority of these samples (n=95) fall within an isotopic carbon range of -16.31‰ to -11.41‰, and an isotopic nitrogen range of 7.88‰ to 15.5‰.

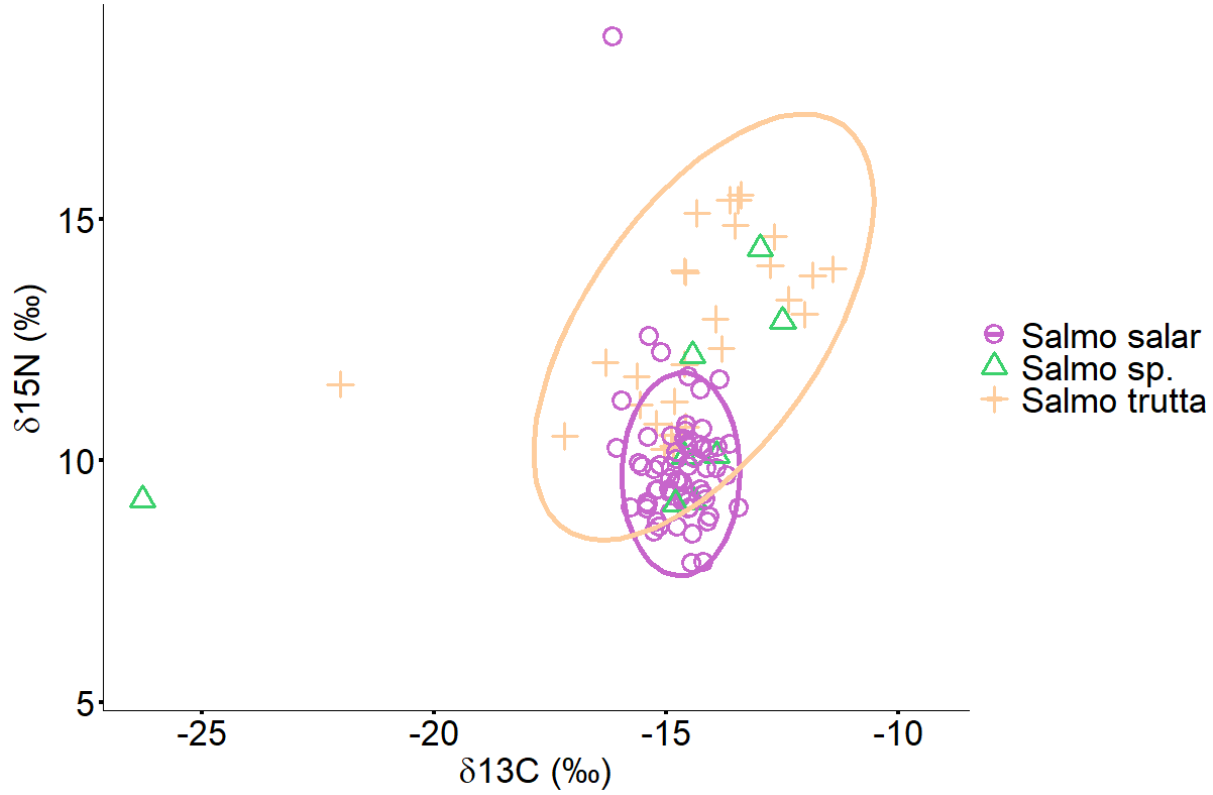


FIGURE 9.8: δ^{13}C and δ^{15}N values reported for each of *Salmo* sp. subgroups included in this study– those identified via ZooMS analysis as *Salmo salar*, as *Salmo trutta*, and those with no associated ZooMS identifications. Ellipse contains 95% of samples in each give species.

Upon first review, the sample of fish remains identified via ZooMS as *Salmo salar* is an exceptionally homogenous one, with a range of only 2.72‰ for δ^{13}C and, after a single exceptional outlier sample (lmq_NL_salmo_102) is removed, 4.7‰ for δ^{15}N. The homogeneity within the sample is particularly interesting considering this is the largest single group included in the study, with 63 individual specimens from 10 archaeological sites across four modern countries. All Atlantic salmon samples within this study have been identified using bulk stable isotope analysis as those which followed a marine feeding foraging strategy, meaning they were anadromous– moving between their natal freshwater streams and various nearshore and open ocean feeding grounds.

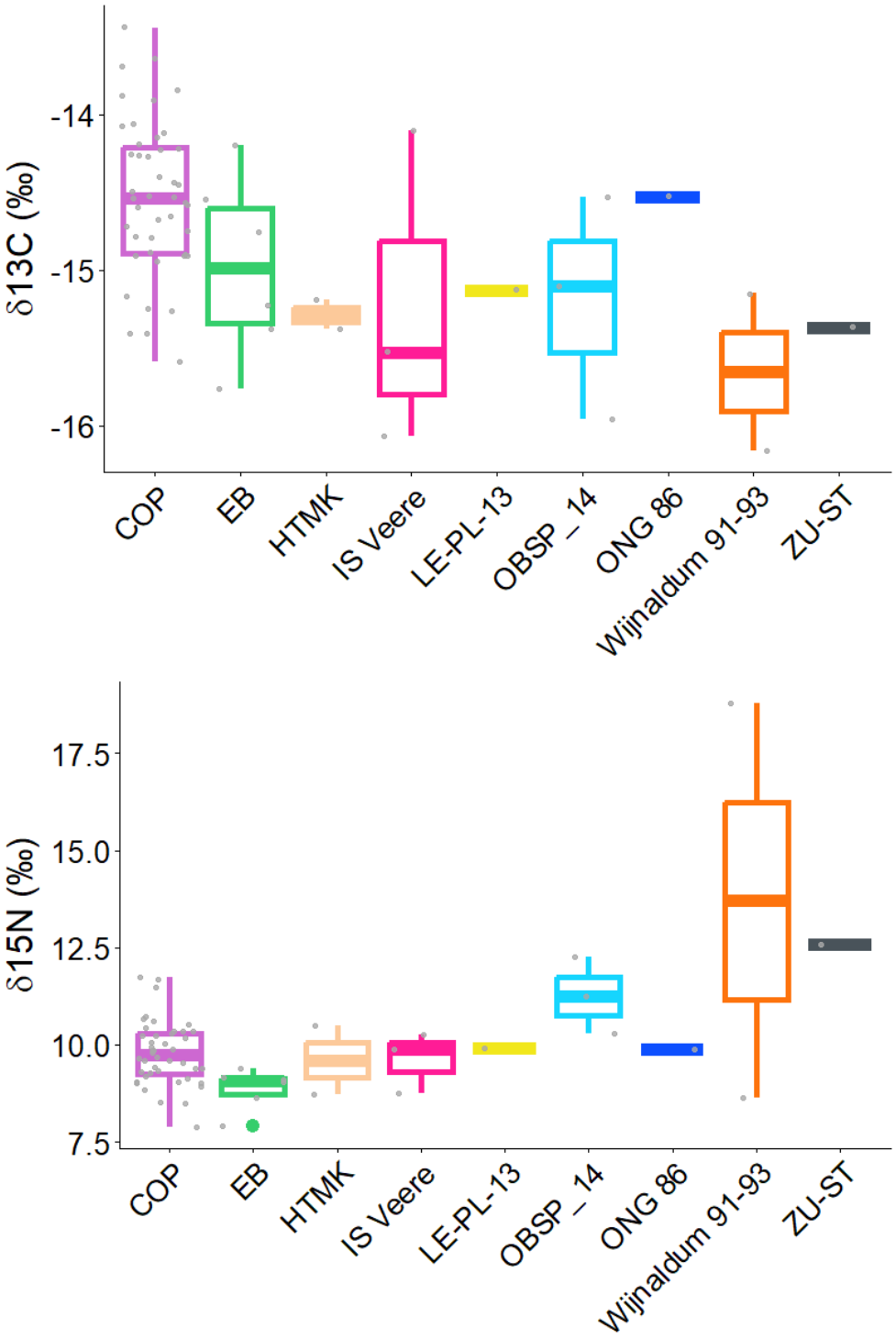


FIGURE 9.9: Box plots reporting δ^{13}C and δ^{15}N values for samples identified as *Salmo salar* via ZooMS analysis, ordered by archaeological site of origin.

Figure 9 demonstrates the ranges of both bulk carbon and nitrogen values seen across the Atlantic salmon

subsample, separated by archaeological site of origin. It's clear that the impact of the 16-22 Coppergate subset of salmon remains is quite significant, comprising 53 of 63 total samples. Thus, for the sites with only a single sample not much can be concluded about the isotopic carbon characteristics of the local environment beyond the life history of the individual fish in question. Both the bulk carbon and nitrogen values from the salmon subset vary in their expression across this geographic study area, but while carbon variation is influenced mostly by foraging strategy and environmental variation in ambient dissolved inorganic carbon, nitrogen values have the added variable of fish age. There is evidence for a demonstrable correlation between fish age/total length and enrichment of δ^{15}N in many species of piscivorous fish– as the individual ages and grows larger, it is able to feed at higher trophic levels, and therefore will experience a bulk enrichment of δ^{15}N values (J. H. Barrett, D. Orton, et al. 2011; Michael J. DeNiro and Epstein 1978; Nakazawa et al. 2010; Riekenberg et al. 2021; Schoeninger and Michael J DeNiro 1984). Total length (TL) reconstructions for salmon are possible using a regression formula adapted from Watt et al. (1997), and calculated using standard measurements of vertebrae according to Wheeler et al. (2009). The relationship between δ^{15}N values and total length (cm) is seen within the set of salmon with associated TL reconstructions (n=48), and is visualized in Figure 10. This moderate correlation (R=0.41, p=0.0037) is even stronger (R=0.5, p=0.002) within the largest subassemblage of salmon bones, all sourced from Coppergate (n= 35). This correlation explains further some of the visible variations in δ^{15}N values both across the study sample of salmon, and within individual sites.

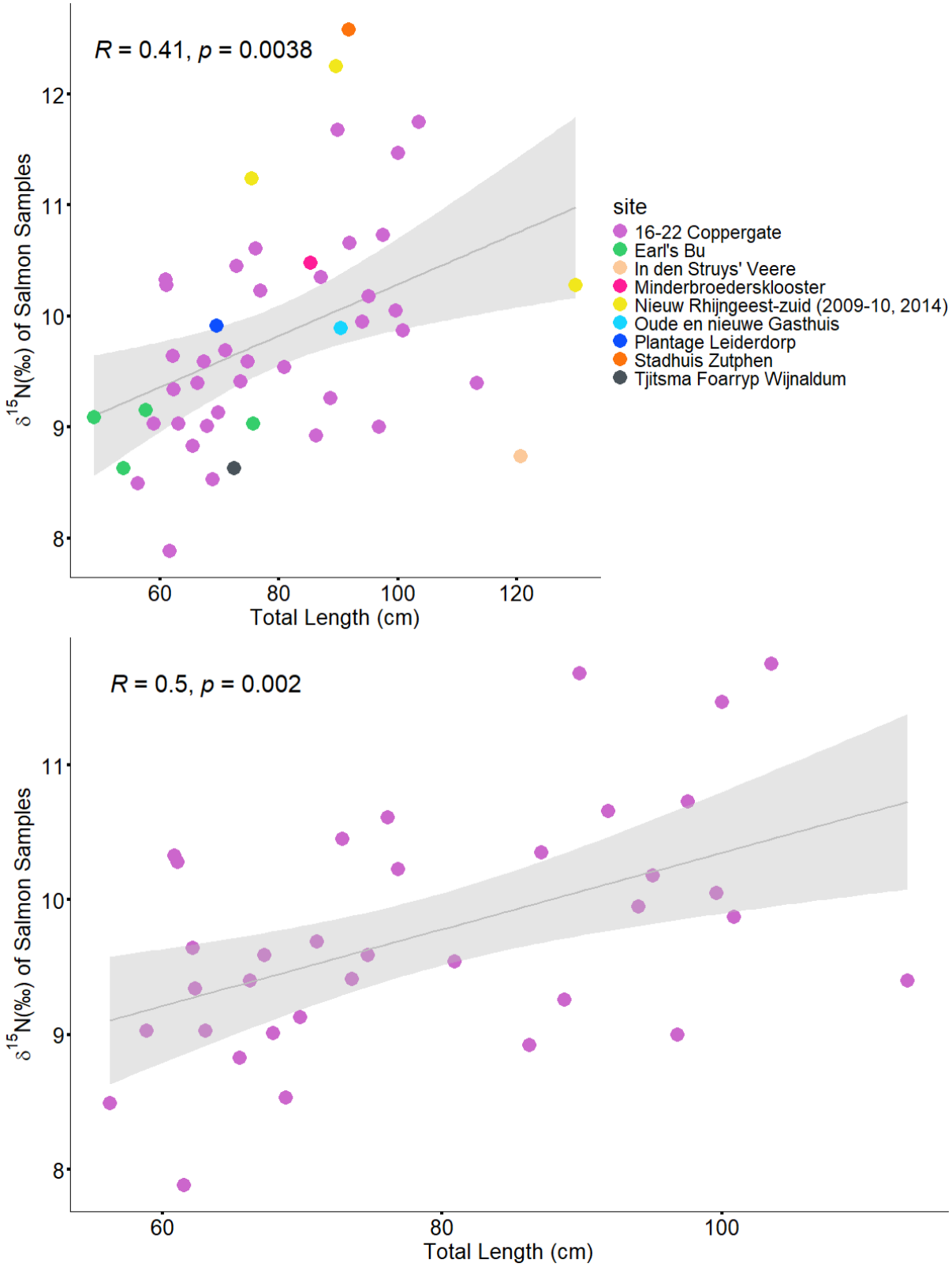


FIGURE 9.10: Top: δ^{15}N values for salmon samples plotted against estimated total length of the individual fish, ordered by archaeological site of origin. Bottom: Coppergate δ^{15}N values plotted against estimated TL of individuals.

As shown in Figure 8, the set of *Salmo trutta* samples can be differentiated from the set of *Salmo salar* samples, though there is less overall homogeneity within the sample set. The vast majority of these samples (n=21) can be assigned to the "sea trout" ecotype based both on their confident ZooMS species identification and their typically marine δ^{13}C values, which range between -11.41 and -16.31‰ (Figure 11). More heterogeneous here are the nitrogen values, which show some distinctions by site– likely reflecting the impact of variables such as feeding location, prey choice, and fish age/size. Interestingly, when the total length of the sea trout samples with available TL estimations (n=20) is plotted against δ^{15}N values there is a weak negative correlation (R= -0.35, p=0.13). However, the total length estimations used for this substituted the available salmon formula, as there is no calculated regression formula available for *Salmo trutta* of any ecotype. Based on differences in foraging ecology, migration timing, and growth patterns it is unlikely that this substitution is a 1-1 equivalency, and the observed weak negative correlation cannot be reliably reported as fact. If and when total length estimation formulas become available for the various *Salmo trutta* ecotypes, it will be interesting to see whether this correlation holds true.

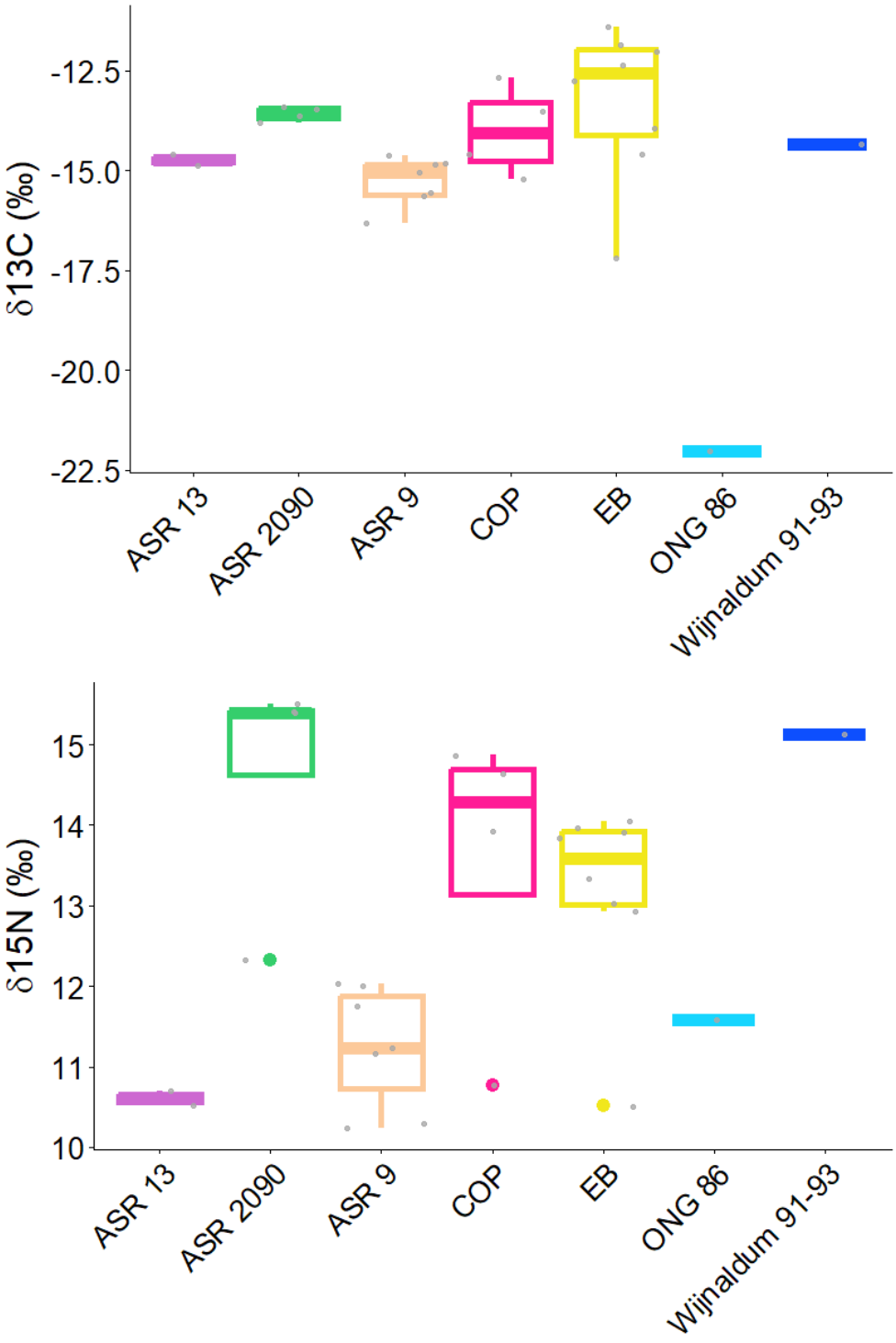


FIGURE 9.11: Box plots reporting δ^{13}C and δ^{15}N values for samples identified as *Salmo trutta* via ZooMS analysis, ordered by archaeological site of origin.

The remaining two samples from the *Salmo trutta* set are considered "marginal" based on their δ^{13}C val-

ues, with one true outlier and the other more borderline. The first of these samples, LMQEB_038, is a precaudal vertebra from Earl's Bu, which returned a δ^{13}C value of -17.19‰ and δ^{15}N value of 10.51‰. It is likely that this individual represents a migratory trout which, if local, must have originated either in one of the small streams on the island of Mainland and migrated to estuarine waters for feeding, or perhaps in the brackish Loch of Stenness. The second of these marginal samples, NL_salmo_001, is an axis vertebra from Oude en nieuwe Gasthuis, identified via ZooMS analysis as *Salmo trutta* and which returned a δ^{13}C value of -22.02‰ and δ^{15}N value of 11.58‰. This individual was likely a fully freshwater Brown trout, and its isotopic characteristics fall well within the observed δ^{13}C (-23.79‰ to -19.21‰) and δ^{15}N (8.43‰ to 12.29‰) values for freshwater piscivorous fish taxa from the Netherlands (n= 10), i.e. Northern pike and European perch. These comparative samples, with the exception of one from Huize van den Kasteele in Zutphen, were all likely sourced from streams or rivers within the massive Rhine-Meuese-Scheldt delta, which includes the Oude Rijn and Oude Maas, which were connected to Delft in the 14th-century via the Vliet and Delftse Schie canals, respectively (Tracy 2018).

The remaining 8 *Salmo* sp. samples (Figure 12) span a comparatively wide range of both δ^{13}C (-26.29‰ to -12.49‰) and δ^{15}N (9.11‰ to 14.39‰) values. There are visible divisions between the samples which display typically marine δ^{13} values (< -16.00‰) and typically freshwater values (> -16.00), as well as those with higher and lower δ^{15}N values. Five of these samples display relatively low δ^{15}N values (9.15‰ to 10.11‰), and three display relatively high δ^{15}N values (12.18‰ to 14.39‰). The difference between the highest value of the first group and the lowest value of the second group is 2.07‰, and the difference between the group means (9.53‰ and 13.16‰, respectively) is 3.63‰, on the order of a trophic level difference between the two groups (Schoeninger and Michael J DeNiro 1984). Due to these visible group separations, the three δ^{15}N enriched samples are hypothesized to be anadromous sea trout (*c.f. Salmo trutta*) while the four δ^{15}N depleted samples are hypothesized to be anadromous salmon (*c.f. Salmo salar*). These hypotheses are also supported by the clear divisions seen within each sample along site of origin– for example, the two Earl's Bu *c.f. Salmo salar* samples differ by 3.75‰ from the single *c.f. Salmo salar* from the same site. The two *c.f. Salmo trutta* samples from ASR 9 Posthuset fall neatly within the observed δ^{15}N range of 12.03‰ to 10.24‰ for the samples identified via ZooMS and isotopes as anadromous sea trout from the same site. Similarly, the Coppergate samples all fall within the established Coppergate *Salmo salar* δ^{15}N range of 7.88‰ to 11.75‰.

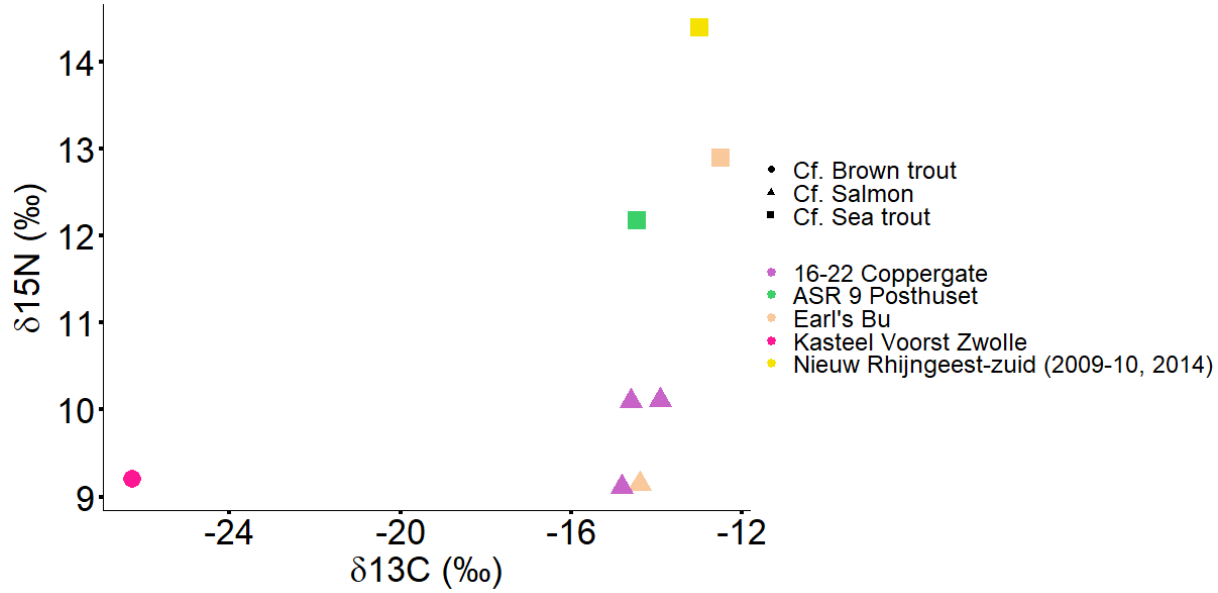


FIGURE 9.12: δ^{13}C and δ^{15}N values for samples without associated ZooMS identification, with point color indicating archaeological site of origin and point shape indicating hypothesized *Salmo* sp. ecotype.

The one visible Salmo sp. outlier, sample NL_salmo_047 from Kasteel Voorst, is a partial basioccipital (Fig.2b) that was originally identified as *Salmo salar* by primary analysts, but which does not have a confirmed ZooMS identification at present due to a spectrometry error. This individual is presumed to be a freshwater Brown trout based on it's depleted δ^{13}C value of -26.29‰, though the chance that it could represent a fully freshwater migratory (potamodromous) Atlantic salmon individual cannot be ignored. However, if that were so then the individual would be the sole recorded potamodromous Atlantic salmon contained within this dataset, and it's unusually depleted δ^{13}C value of -26.29‰ is more consistent with δ^{13}C values observed in modern potamodromous trout from Loch Ness (mean = -25.4 ± 1.7‰) than modern (mean range= -21.63 to -20.52‰) and archaeological (-19.92‰ ± 0.41) potamodromous Atlantic salmon from Canada, respectively (Dempson et al. 2010; Grey et al. 2002; Guiry, Needs-Howarth, et al. 2016) (see section 5.3.3).

9.6.3 Spatial and Temporal Variation in Atlantic salmon and Sea trout Isotopes

Temporal Variation of *Salmo* sp. Samples

In order to ascertain whether there is any observable temporal change in the δ^{13}C and δ^{15}N values seen in both anadromous Atlantic salmon (n=63) and Sea Trout ecoytypes (n=26) a timeseries analysis was applied (Figure 13). Sites included in this study have salmon samples from multiple dated contexts, many of which span anywhere from a handful of years to several dozen. To mitigate the impact of this variation, midpoints were calculated from the available context dates, and each sample's site midpoint is taken to indicate the approximate time period when the sample was deposited into the archaeological record. This creates a very rough, but ultimately useful, average view of salmon abundance over time at sites. Figure 13A shows the bulk carbon and nitrogen data for anadromous salmon across a time period of approximately 900 years, with a midpoint range of 600-1500 CE. The site with both the most samples (n=48) and internal variation in midpoints is 16-22 Coppergate in York,

which is related to the extremely precise and comprehensive dating information available for the site. In general, despite the salmon sample set containing 63 individuals from five geographically distinct locations (York, Ribe, Orkney, the northern and southern Netherlands) there is very little variation over time seen in either bulk carbon or bulk nitrogen values. Bulk carbon values are especially homogeneous over time, only ranging between -13.44‰ and -16.31‰ and showing only the slightest visible fluctuations in carbon values over time– none of which are statistically significant. Nitrogen is slightly more variable, as can be expected due to the known linear relationship between δ^{15}N and fish body TL/age and the presence of individuals within the salmon sample set which range from a fairly small 48.93cm to a truly exceptional 130cm.

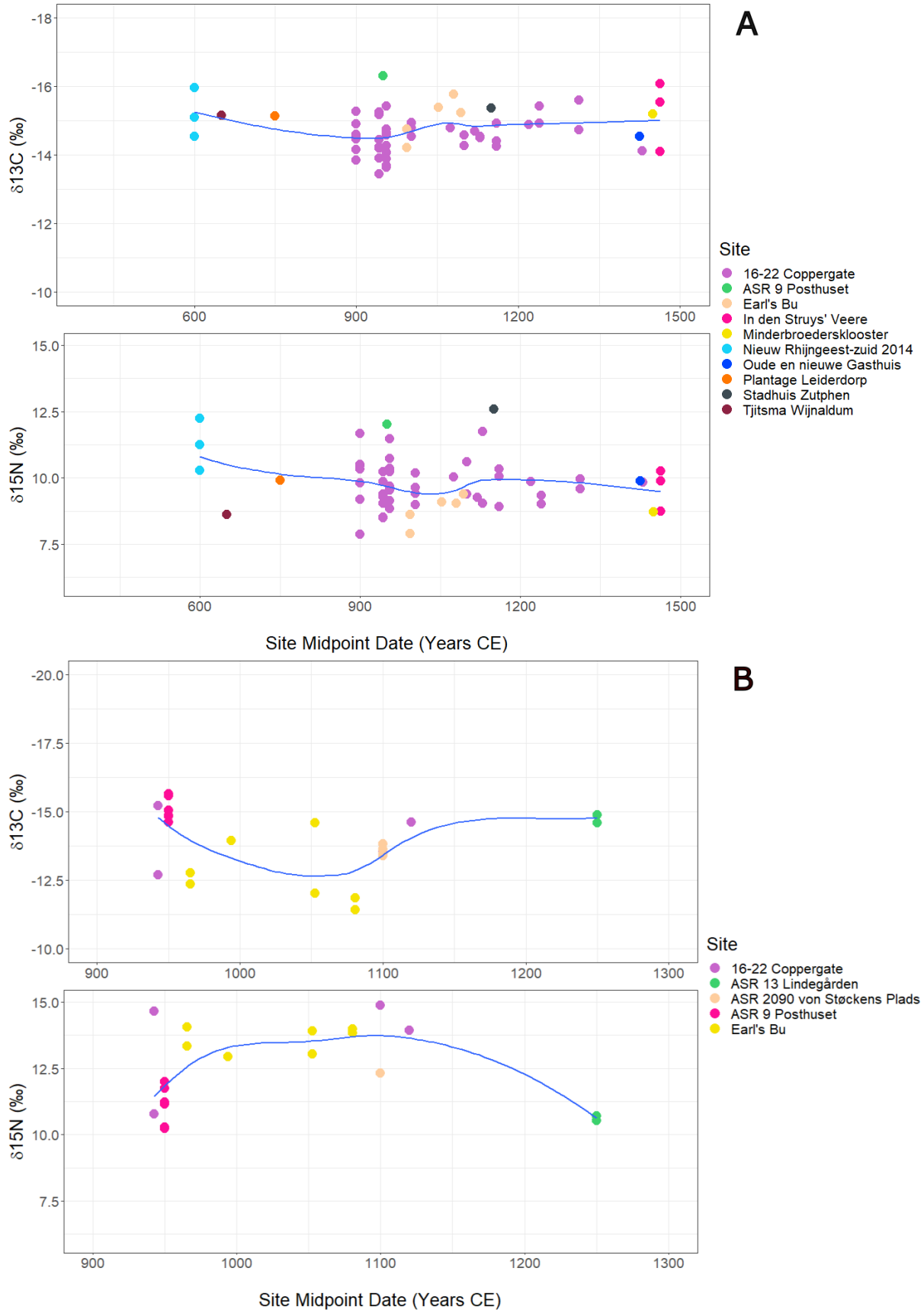


FIGURE 9.13: Time series plots tracking changes in δ^{13}C and δ^{15}N values over time for A.) *Salmo salar* and B.) *Salmo trutta* samples.

The timeseries produced for those samples identified as sea trout does show slightly more variation in both bulk carbon and nitrogen values, however the overall sample size is smaller (n=26), the time period of interest is shorter (900-1300 CE), and there are only three regions represented (York, Orkney, Ribe). The δ^{13}C values are again quite homogeneous across the observed time period, with a range of between -11.41‰ and -17.19‰. While it initially appears that δ^{13}C values increase over time from the year 1100CE onward, the average values from the individual sites listed after that time period– ASR 2090 von Støckens Plads, 16-22 Coppergate and ASR 13 Lindegården– are actually consistent with values observed from earlier time periods at 16-22 Coppergate, and those from earlier time periods in the region of Ribe. Similarly, the δ^{15}N values included in the timeseries show what might, at first glance, be considered an observable increase and then decrease in δ^{15}N values over time. However, the two post-1100CE samples from 16-22 Coppergate are consistent with one of the samples from pre-1000CE, and the samples from both ASR 2090 von Støckens Plads and ASR 13 Lindegården are consistent with values seen at the earlier ASR 9 Posthuset site. While it is clear that variations in δ^{15}N and δ^{13}C values seen in these fish species are not temporally determined, the spatial variations both within this archaeological North Sea basin sample and across a wide geographic region are much more clearly evident.

Isotope Niche Space Analysis

Isotope niche space analysis was applied to bulk stable isotope data from four taxa– haddock (n=26), Northern pike (n=11), and the two *Salmo* sp. ecotypes of interest, migratory Atlantic salmon (n=62) and sea trout (n=26). (NB: the exceptional outlier *Salmo salar* sample LMQ_NL_salmo_102 was removed for this set of analyses, as it's δ^{15}N is 6.2‰ higher than the next-closest sample in the group and may unnecessarily skew the results). The two comparative taxa were chose as they both met the minimum sample threshold for analysis using the rKIN package, and are examples of relatively large piscivorous fish in their respective environments which can be compared to adults of both *Salmo* sp. ecotypes in terms of both size and broad diet. Figure 14 is a combined bi-plot image demonstrating the visual aspects of isotope niche width calculations for the four species, using the kernel utilization density (KUD), standard ellipse area (SEA), and minimum convex polygon (MCP) methods.

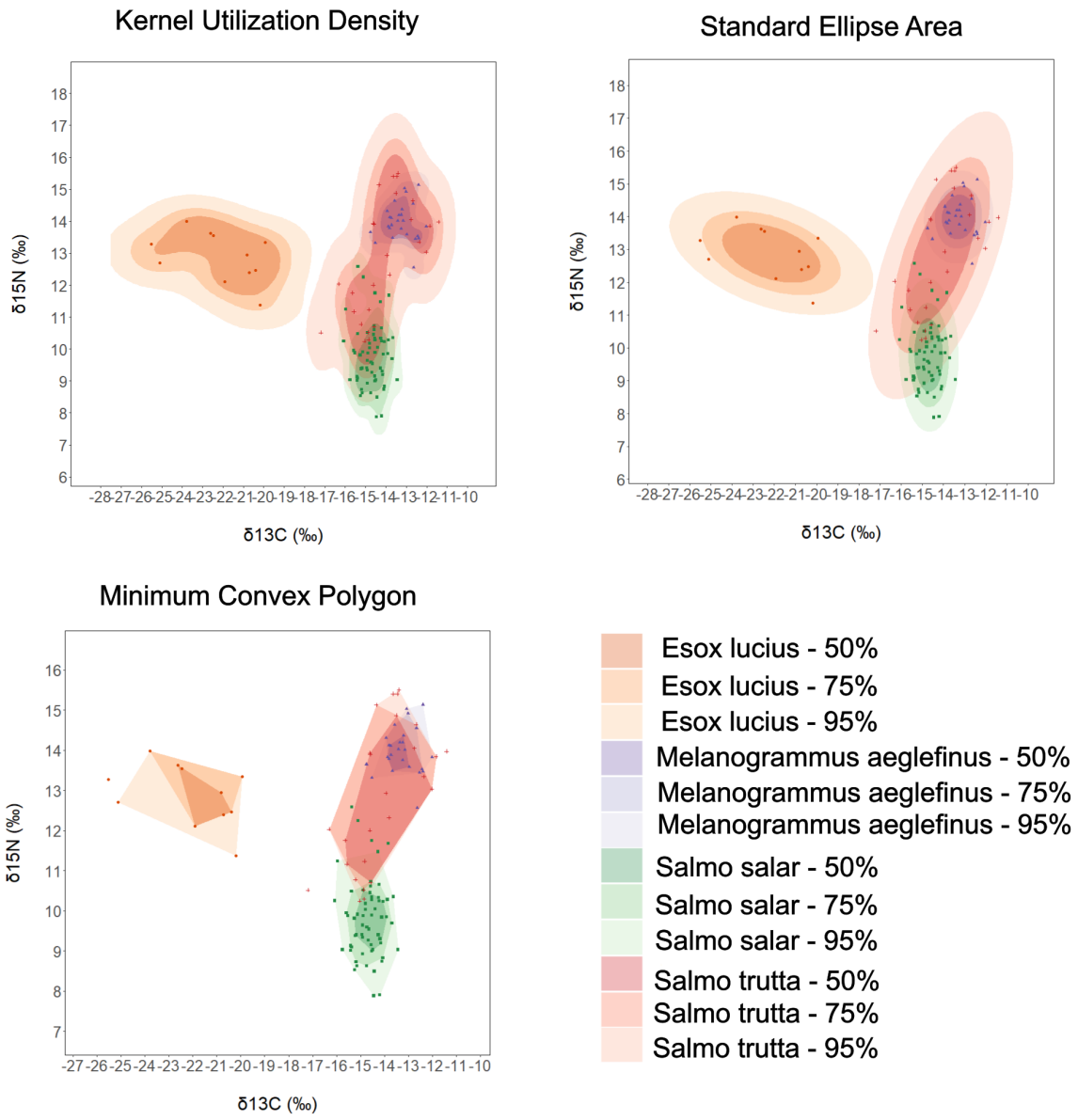


FIGURE 9.14: Combined bi-plot figures displaying Kernel Utilization Density, Standard Ellipse Area, and Minimum Convex Polygons at 50%, 75%, and 95% confidence intervals. Freshwater Northern pike (*Esox lucius*) and marine haddock (*Melanogrammus aeglefinus*) values are compared to those samples identified as *Salmo salar* and *Salmo trutta*.

The largest observed isotope niche width is found in the sea trout group, demonstrating it's wide ranges of both δ^{15}N and δ^{13}C values(10.24‰ to 15.50‰, and -17.19‰ to -11.41‰, respectively). Northern pike display the second largest isotope niche width, which is more highly influenced by variation in their δ^{13}C values, ranging from -25.5‰ to -19.93‰, and likely due to geographic differences in the local river systems they originated from before entering the archaeological record. Compared to sea trout and pike, the haddock and salmon groups have significantly narrower calculated isotopic niche sizes, and are isotopically homogenous in nature. This is especially interesting, as both groups samples (haddock n=26, salmon n=63) come from sites across the entire

study area, covering the entirety of the North Sea. As expected, the freshwater pike samples occupy isotope niche spaces entirely separate, by all method calculations, from the haddock, salmon and sea trout samples (Table 7). Similarly, the groupings of Atlantic salmon and haddock samples display no overlap in niche space despite comparable marine δ^{13}C values. This is consistent with their positions as a marine demersal (bottom feeding) fish (haddock) and migratory pelagic (open water column) fish (salmon) with no expected overlap in foraging choice or trophic positioning. There is, however, significant overlap apparent between the calculated isotope niche spaces for haddock and sea trout for all three methods. Sea trout samples with δ^{15}N values higher than 12.93‰ (n=14) overlap entirely with the haddock set, and the majority of the samples from both taxa (n= 38, out of a total 52 samples) are from sites located in the northern North Sea and Wadden Sea regions. The higher δ^{15}N values in sea trout are most likely a product of their reported post-migration foraging strategy of staying within 100km of coastline and feeding primarily in shallow, highly productive waters of the estuarine or neritic (coastal) zones (B. Jonsson and N. Jonsson 2007; Kristensen et al. 2019). This means that though the haddock and sea trout samples from this study show significant overlap and occupy similar isotopic niche spaces, the sea trout are likely not competing directly for prey with demersal haddock– which tend to occupy deeper, fully marine environments (Cohen 1990; Svetovidov 1984).

Method	**Northern Pike**			**Haddock**			**Atlantic salmon**			**Sea trout**		
	50%	75%	95%	50%	75%	95%	50%	75%	95%	50%	75%	95%
KUD	8.8	16.3	29.7	1.8	3.8	7.7	2.6	5.4	11.6	11.3	20.6	38.5
SEA	5.9	11.8	25.7	1.7	3.4	7.2	2.4	4.8	10.3	8.5	17.0	36.8
MCP	1.6	3.6	7.9	0.5	1.6	2.8	1.4	3.0	6.7	7.9	11.4	12.5

TABLE 9.7: Comparison of estimates of isotope niche size from kernel utilization density, standard ellipse area, and minimum convex polygon methods for Atlantic salmon, trout, Atlantic cod, and Northern pike.

Method	**Haddock-Salmon**			**Haddock-Trout**			**Pike-Salmon**		
	50%	75%	95%	50%	75%	95%	50%	75%	95%
KUD	0.00	0.00	0.00	0.97	1.00	1.00	0.00	0.00	0.00
SEA	0.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00	0.00
MCP	0.00	0.00	0.00	1.00	1.00	1.00	0.00	0.00	0.00
Method	**Pike-Trout**			**Salmon-Trout**			**Trout-Salmon**		
	50%	75%	95%	50%	75%	95%	50%	75%	95%
KUD	0.00	0.00	0.00	0.38	0.51	0.77	0.09	0.14	0.23
SEA	0.00	0.00	0.00	0.01	0.36	0.68	0.01	0.01	0.20
MCP	0.00	0.00	0.00	0.00	0.01	0.18	0.00	0.00	0.10

TABLE 9.8: Comparison of pairwise overlap estimates for pairings of haddock, pike, salmon and trout, reported for each method.

The wide isotopic niche space occupied by sea trout results in a fairly high degree of overlap between the salmon and trout groups, with higher overlaps calculated using the KUD and SEA methods than the MCP method (Table 8). In order to investigate regional variation in isotope niche space and niche overlaps for sea trout and

salmon, regional groupings were created based on the source location of the archaeological samples. Salmon from the Earl's Bu site in Orkney (n=6) were categorized as "Northern North Sea" in origin, and those from the Coppergate, Oude en nieuwe Gasthuis, In den Struys, Plantage Leiderdorp, Nieuw Rhijngeest-zuid, Minderbroedersklooster, Tjitsma Wijnaldum, and Stadhuis Zutphen sites (n=56) were all classified as "Southern North Sea" in origin. Sea trout samples from Earl's Bu were classified as "Northern North Sea" in origin (n=8), and those from the three Ribe sites and Tjitsma Wijnaldum, were classified as being of "Wadden Sea" origin (n=14). The reason for the distinction between "Northern North Sea" and "Wadden Sea" for sea trout, but not for salmon, is due to the previously mentioned tendency for sea trout to stay within 100km of the coastline, meaning that those sea trout from the northern Dutch and Danish sites are presumed to have fed primarily in the Wadden Sea environment rather than venturing into the open pelagic waters of the northern North Sea as Atlantic salmon do. Two of the groups investigated in this set of rKIN analyses had less than the recommended minimum of 10 samples, however the decision was made to override this using the available "smallSamp()" argument in order to maximise understanding of regional variations between these archaeological assemblages.

Figure 15 presents the results of the three isotopic niche space calculations for salmon and sea trout in isotope bi-plot format, with samples divided by region and ecotype. The widest calculated isotopic niche space (Table 9) is seen in the population of Wadden Sea trout, with the two distinct clusters of δ^{15}N values (those ≤ 12.32‰ and those ≥ 15.15‰) best demonstrated by the plot produced using KUD analysis. There is no evident correlation between these differing δ^{15}N values and site location, time period, or total length estimations, so it is likely this is just evidence of differing individual foraging strategies within the regional population of Wadden Sea sea trout. The calculated isotopic niche space of Northern North Sea trout is also large compared to the two salmon groups, however this is heavily influenced by the outlier sea trout sample with a δ^{13}C value of - 17.19‰. Sea trout in general demonstrate more behavioral plasticity with foraging, often being described as opportunistic feeders, (B. Jonsson and N. Jonsson 2007; Knutsen et al. 2001), and this is reflected in the comparatively larger size of their calculated isotopic niche spaces. The northern North Sea trout and Wadden sea trout populations have relatively low levels of overlap, and their distinction is especially visible in using the MCP polygon estimates which removes the carbon-depleted outlier sample (Figure 15).

While the isotopic characteristics of the overall salmon sample included in this study is very homogeneous compared to the sea trout samples, there is some observable variation in isotopic niche size between the two groupings of salmon. Southern North Sea salmon appear to exhibit both a wider isotopic niche size and display lower average δ^{15}N values (9.88 ± 0.93‰) than their northern North Sea counterparts (8.86 ± 0.48‰). Though there is still a decent amount of overlap both ways between the two groups (Table 10), the lower average δ^{15}N may be indicative of differences in primary foraging environment latitude– δ^{15}N values have been observed to be inversely proportional to latitude, with samples from higher marine latitudes displaying lower δ^{15}N values (Cherel and Hobson 2007; Newsome et al. 2007). This potential influence lends further support to the hypothesized regional populations used in this set of rKIN analysis, which would imply that the salmon and sea trout samples from southern North Sea, northern North Sea, and Wadden sea archaeological sites are, in fact, from different fish populations.

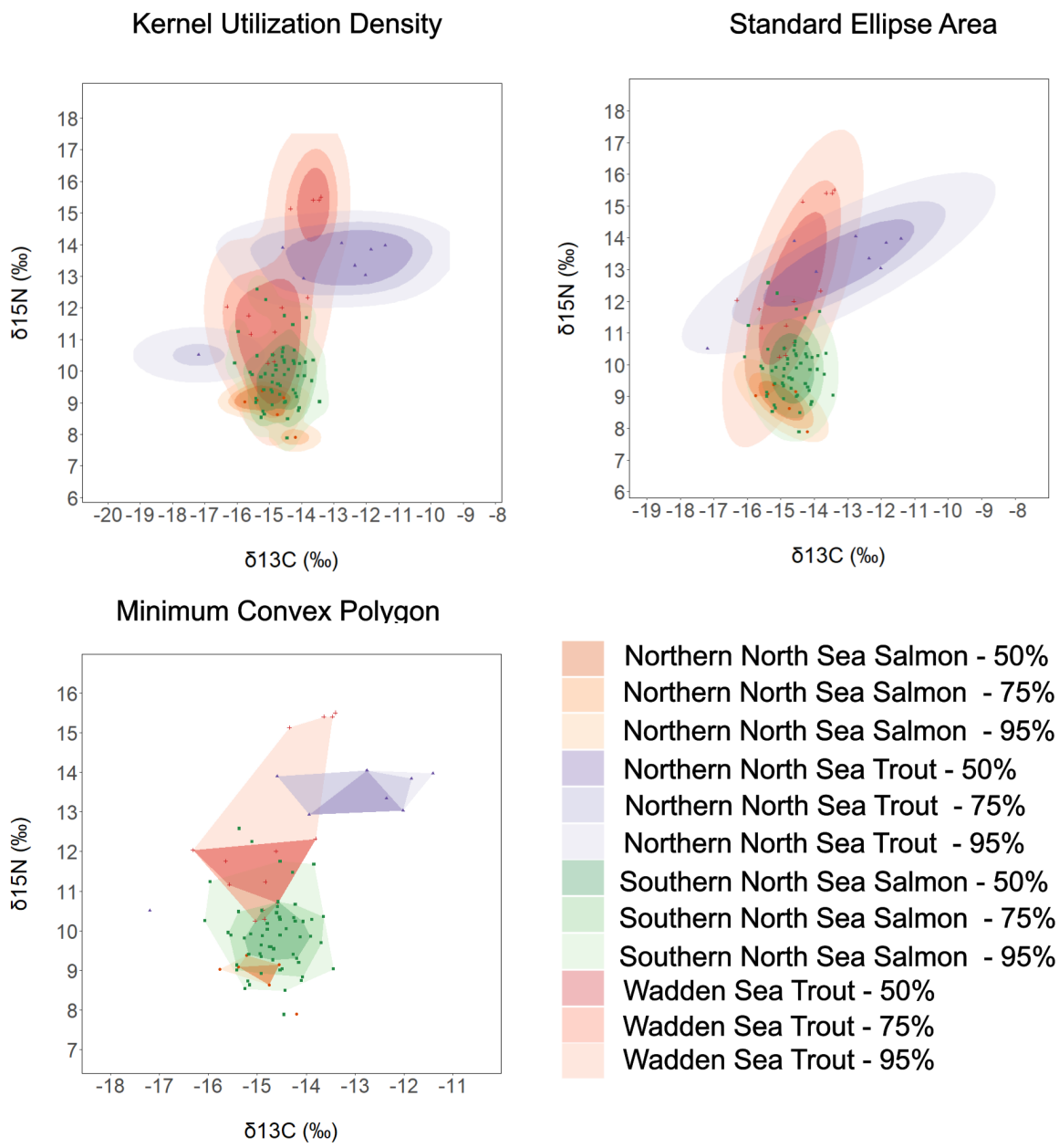


FIGURE 9.15: Combined bi-plot figures displaying Kernel Utilization Density, Standard Ellipse Area, and Minimum Convex Polygons at 50%, 75%, and 95% confidence intervals. Four distinct populations of fish are compared– Northern North Sea Salmon, Northern North Sea Trout, Southern North Sea Salmon, and Wadden Sea Trout.

Method	Northern NS Salmon			Northern NS Trout			Southern NS Salmon			Wadden Sea Trout		
	50%	75%	95%	50%	75%	95%	50%	75%	95%	50%	75%	95%
KUD	1.1	2.3	4.5	5.4	11.3	24.0	2.5	5.2	11.3	7.9	15.3	28.4
SEA	1.0	2.0	4.3	5.9	11.8	25.5	2.3	4.7	10.1	5.7	11.3	24.5
MCP	0.2	0.3	0.5	1.0	2.3	2.6	1.3	2.9	6.5	2.2	2.6	7.6

TABLE 9.9: Comparison of estimates of isotope niche size from kernel utilization density (KUD), standard ellipse area (SEA), and minimum convex polygon (MCP) methods for *Salmo trutta* from the Wadden Sea and Northern North Sea, and *Salmo salar* from both the Northern and Southern North Sea regions.

Method	NNSS-WST			NNSS-NNST			NNSS-SNSS		
	50%	75%	95%	50%	75%	95%	50%	75%	95%
KUD	0.32	0.51	0.74	0.00	0.00	0.15	0.56	0.69	0.78
SEA	0.00	0.26	0.63	0.00	0.00	0.00	0.24	0.60	0.87
MCP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.59	0.93
Method	**NNST-WST**			**NNST-NNSS**			**NNST-SNSS**		
	50%	75%	95%	50%	75%	95%	50%	75%	95%
KUD	0.01	0.27	0.47	0.00	0.00	0.04	0.00	0.00	0.09
SEA	0.36	0.41	0.44	0.00	0.00	0.00	0.00	0.00	0.10
MCP	0.00	0.00	0.23	0.00	0.00	0.00	0.00	0.00	0.00
Method	**SNSS-WST**			**SNSS-NNSS**			**SNSS-NNST**		
	50%	75%	95%	50%	75%	95%	50%	75%	95%
KUD	0.66	0.69	0.88	0.26	0.30	0.31	0.00	0.00	0.18
SEA	0.18	0.48	0.70	0.10	0.25	0.37	0.00	0.00	0.24
MCP	0.00	0.05	0.20	0.00	0.09	0.07	0.00	0.00	0.00
Method	**WST-NNSS**			**WST-NNST**			**WST-SNSS**		
	50%	75%	95%	50%	75%	95%	50%	75%	95%
KUD	0.05	0.08	0.12	0.01	0.20	0.39	0.21	0.23	0.35
SEA	0.00	0.05	0.11	0.37	0.43	0.46	0.08	0.20	0.29
MCP	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.06	0.18

TABLE 9.10: Comparison of pairwise overlap estimates for pairings of regional groupings designated as Wadden Sea Trout (WST), Northern North Sea Salmon (NNSS), Northern North Sea Trout (NNST) and Southern North Sea Salmon (SNSS), reported for each method.

The regional differences demonstrated here by isotope niche space analysis and the pairwise overlap calculations indicate that procurement of salmon and sea trout by occupants of the archaeological sites in these area may have been primarily local. The distinct groupings of sea trout likely reflect local fishing in Wadden Sea environments for sea trout by occupants of the Danish and Dutch sites, involving the Ribe Å and IJssel river systems, the medieval Zuiderzee, and Vlie estuary. The groupings of northern North Sea salmon and southern North Sea salmon do have significant overlap, and a larger sample size of northern North Sea salmon would clarify

whether the difference between the two groupings here is indicative of fish sourced from different populations. If the northern North Sea salmon samples included here are representative of typical isotopic niche spaces occupied by salmon from that region, this could have implications for study of salmon trade. This would indicate that southern North Sea sites, like Coppergate, were not necessarily importing salmon that were harvested from northern North Sea populations. This cannot be definitively tested until a more robust assemblage of northern North Sea archaeological salmon bulk isotope data is available, but it does showcase the potential utility of the rKIN package for investigating long distance trade in the North Sea.

Transatlantic Variation in *Salmo* sp. Isotope Palaeoecology

In order to adequately contextualize the geographic differences observed in both bulk carbon and nitrogen values in archaeological salmon samples from this thesis, δ^{15}N and δ^{13}C data was sourced from published *Salmo salar* and *Salmo trutta* isotope datasets. Figure 16 illustrates mean δ^{15}N and δ^{13}C data values from five distinct groups of data– North Sea basin archaeological sites from this study, modern Canadian samples, modern European samples, Canadian archaeological sites, and European archaeological sites. As this thesis represents the largest dataset of published archaeological salmon values, and the only dataset of medieval salmon values, the European archaeological comparisons are limited to only two sites– the medieval Knowth site, in County Louth, Ireland and a palaeolithic site at Trou de Frontal in Namur, Belgium (Bocherens, Baryshnikov, and Van Neer 2014; Guiry, Needs-Howarth, et al. 2016). Similarly, archaeological Canadian sites only represent pre-contact Late Woodland period (circa 1300-1550 CE) sites from Quebec and Ontario (Guiry, Needs-Howarth, et al. 2016). Modern data was sourced from studies of bulk isotope values in regional populations of modern salmon from both Europe and Canada, with mean values available from European samples taken in Scotland, England, Ireland, Wales, and Spain, as well as from Canadian samples taken in the Samiajij Miawpukek First Nation, Nova Scotia, New Brunswick, Nunavik, Quebec, and Labrador (Almodóvar et al. 2020; Dempson et al. 2010; Dixon et al. 2012; Guiry, Needs-Howarth, et al. 2016; R. Jones et al. 1998; McCarthy and Waldron 2000; O'Toole et al. 2020; Sinnatamby, Dempson, and Power 2008; Trueman 2022). Suess corrections were applied to all modern European and Canadian samples where the fish were expected to have fed primarily in the Subpolar North Atlantic region, either in the original publications or prior to being incorporated into this dataset (Clark et al. 2021).

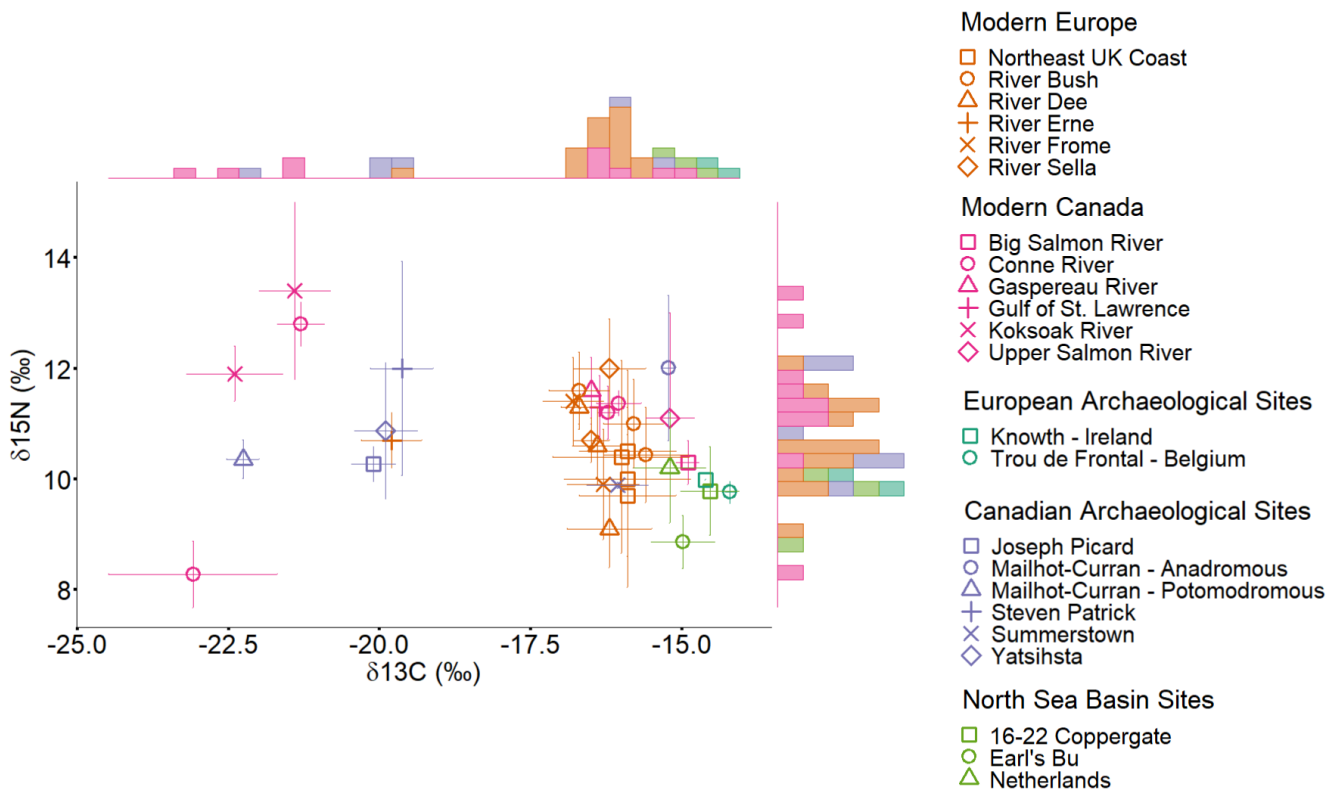


FIGURE 9.16: Isotope bi-plot reporting mean δ^{13}C and δ^{15}N values for five groups of *Salmo salar* samples; North Sea Basin archaeological sites, Modern Canada, Modern Europe, Canadian Archaeological sites, and European archaeological sites. Marginal histograms on each axis illustrate the proportions of a given isotopic value for each group.

Figure 16 shows a division of distinct Atlantic salmon ecotypes, with several populations of potamodromous (freshwater migratory) visible from some of the modern Canadaian Koksoak River population, some of the Conne River (Samiajij Miawpukek) population, the River Erne population in Ireland, and archaeological materials from the Canadian Joseph Picard, Mailhot-Curran, Steven Patrick, and Yatsihtsa sites located on Lake Ontario and along the St. Lawrence River (Dempson et al. 2010; Guiry, Needs-Howarth, et al. 2016; R. Jones et al. 1998; McCarthy and Waldron 2000). This assignment of these samples to the potamodromous salmon ecotype is consistent with conclusions made by the original analysts, and is especially expected in semi-isolated lacustrine environments like Lake Ontario and Loch Ness (Guiry, Needs-Howarth, et al. 2016; R. Jones et al. 1998). The remaining mean values displayed in Figure 16 are considered to represent anadromous Atlantic salmon which migrate from their source rivers to feeding locations across the subpolar-North Atlantic region. The North Sea basin means represented here include those for 16-22 Coppergate, Earl's Bu, and seven Dutch sites. What previously appear to have been quite significantly different regional archaeological salmon groups from the North Sea basin area, are, in this wider geographic context, much more homogeneous. The samples from Coppergate, Earl's Bu, and the Netherlands are, on average, more carbon enriched than those from modern European anadromous salmon populations (-14.90 ± 0.54‰ vs.-16.36 ± 0.36‰), and this is consistent with the other European archae-

ological sites (Knowth = -14.61 ± 0.00‰; Trou de Frontal= -14.2 ± 0.08‰). Samples from the Northeast coast of the UK provide some of the most direct modern comparisons to the archaeological samples from the 16-22 Coppergate site. There are four sets of Northeast coast data, with an averaged δ^{13}C value of -15.93 ± 0.95‰ and δ^{15}N value of 10.15 ± 1.4‰– compare to the Coppergate mean δ^{13}C values of -14.53 ± 0.49‰ and mean δ^{15}N values of 9.78 ± 0.80‰. Taken altogether, it appears that the bulk carbon and nitrogen values for archaeological anadromous salmon from this North Sea Basin dataset are within the overall acceptable range of observed values from modern and archaeological European and Canadian populations of Atlantic salmon (δ^{13}C range -18.7‰ to -13.8‰; δ^{15}N range 6.97‰ to 14.80‰).

Figure 17 illustrates mean δ^{15}N and δ^{13}C values from the North Sea basin archaeological sea trout data obtained from 16-22 Coppergate, Earl's Bu, and the three Ribe sites, compared to modern European trout data. The three modern sets of isotope data are comprised of freshwater brown trout from Loch Awe in Scotland (McCarthy and Waldron 2000), sea trout from the Irish Sea off the coast of Northern Ireland (McCarthy and Waldron 2000), and sea trout from the Dutch Wadden Sea (Poiesz et al. 2021). As expected for the nitrogen-enriched coastal/estuarine Wadden Sea environment, the sea trout data from that region displays much higher mean δ^{15}N values (16.0 ± 0.19‰) and lower mean δ^{13}C values (-19.54 ± 0.29‰). Similarly, the Loch Awe freshwater trout show typically low δ^{15}N values and δ^{13}C values (9.2 ± 1.5‰ and -22.5 ± 1.3‰, respectively). As with the archaeological salmon samples in Figure 16, the archaeological sea trout samples all display comparatively higher carbon values than those from the modern trout populations. In fact, the carbon values from the North Sea sites show an increase ranging between 1.84-3.23‰ over those from modern Irish Sea sea trout (mean -16.50 ± 1.2‰), and is likely due to geographic differences in baseline isotopic carbon values between the two bodies of water. An unexpected difference between modern and archaeological material is seen in the case of the Dutch Wadden Sea sea trout and Ribe sea trout, which we would have expected to show more similar δ^{13}C and δ^{15}N, given the likely primary foraging environment of the Ribe sea trout would be the Danish portion of the Wadden Sea. The significant differences in both carbon and nitrogen values may be explained by the sampling strategy used for the Wadden Sea study– sea trout were captured in the spring as they exited an estuarine area at the furthest southern point of the Dutch Wadden sea (Poiesz et al. 2021). These samples were likely younger fish, with very little chance to feed extensively in the pelagic zone beyond the Wadden Sea, which would explain their enriched nitrogen and carbon values (McCarthy and Waldron 2000; Poiesz et al. 2021) compared to the Ribe samples which were, presumably, adult fish which were harvested for food upon returning close to shore after marine feeding.

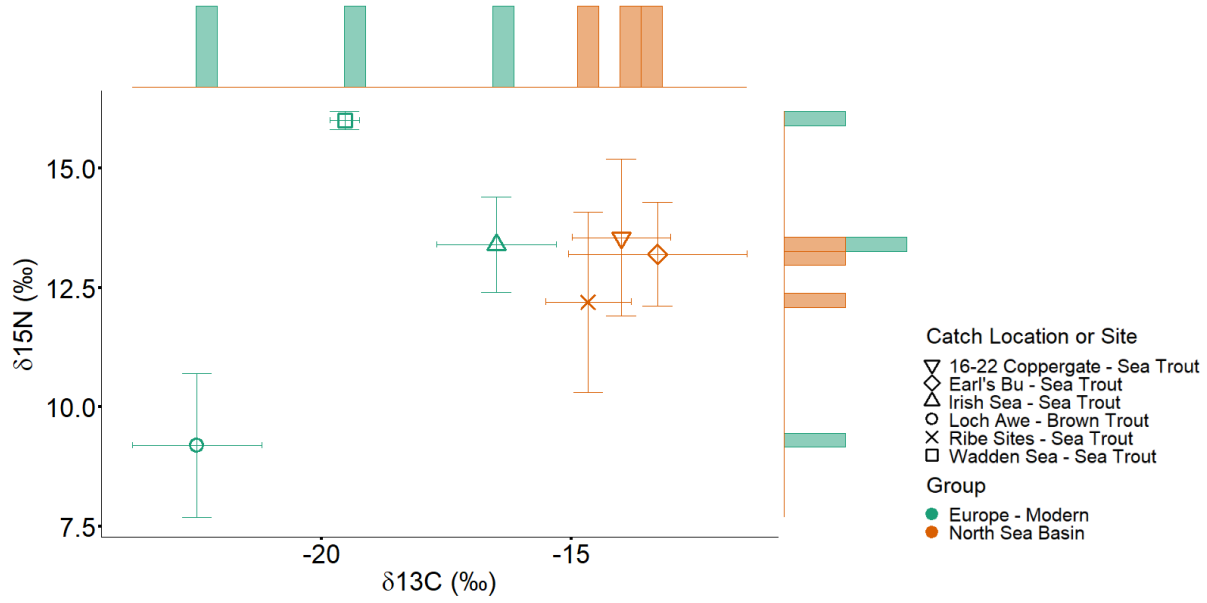


FIGURE 9.17: Isotope bi-plot reporting mean δ^{13}C and δ^{15}N values for several groups of *Salmo trutta* samples; Brown trout from Loch Awe - Scotland, sea trout from the Irish Sea and Dutch Wadden Sea, and sea trout samples from the 16-22 Coppergate, Earl's Bu, and Ribe archaeological sites. Marginal histograms on each axis illustrate the proportions of a given isotopic value for each group.

9.6.4 Cultural Differences in Medieval *Salmo* sp. Exploitation

In addition to the observed variations in isotopic characteristics seen in the sample sets of comparative species, Atlantic salmon, sea trout, and *Salmo* sp., there are some conclusions that can be drawn about geographic, and therefore cultural, differences in the exploitation of *Salmo* sp. fishes during the broadly Medieval Period. Based on the overall proportions of ZooMS-identified indviduals, with 63 *Salmo salar* and 27 *Salmo trutta*, it would be easy to conclude that Atlantic salmon were preferred over sea trout in the medieval North Sea basin area. However, it is clear that this is not the case when the data are broken down and viewed by individual site. In the Netherlands it does appear to hold true that salmon (n=11) are more prevalent than trout (n=1), however, despite investigating materials from 8 dutch sites the overall Dutch sample of *Salmo* sp. remains was exceptionally small compared to those found in Coppergate, ASR9 Posthuset and Earl's Bu. These small sample sizes are consistent with observed trends in small *Salmo* sp. assemblages found at Dutch archaeological sites from the Medieval Period (see Chapter 7). The issue of low survival rates of *Salmo* sp. remains in the Netherlands does impact the ability to draw concrete conclusions about preferences for salmon or trout, but historical evidence from the Netherlands does suggest an economic and cultural importance placed on anadromous salmon. Various sources refer to the concept of salmon, along with allis shad and sturgeon, being used as *vroonvis* – taxes payable in fish to local nobility or the crown (Bob Beerenhout 2011; Dijkstra, Verhoeven, and Straten 2016; Frits Laarman and Lauwerier 1996). The duration of this practice in the Netherlands is fairly well established, with references as early as 1306 to the right of the Count of Holland to take a portion of income from local salmon fisheries (Lenders and Verberk 2018). The concept of Atlantic salmon as highly prized fish whose value must in some way be shared with nobility or royalty is also mentioned in conjunction with archaeological fish remains from earlier time periods, for

example at the Stadhuis Zutphen (1125-1175 CE) and Plantage Leiderdorp (650-850 CE) sites – though Dijkstra et al. are careful to mention that it is uncertain how prevalent or well-enforced the *vroonvis* right was in the Early Medieval Period (Bob Beerenhout 2011; Dijkstra, Verhoeven, and Straten 2016). In addition to the *vroonvis* concept influencing preference for salmon, it is also asserted by at least one Dutch zooarchaeologist that access to sea trout in the Netherlands was restricted to locations closer to the coast and which were seasonally active during the summer (E. Esser 2000). Interestingly, the same zooarchaeologist did positively identify the sole Dutch *Salmo trutta* specimen, at the Oude en nieuwe Gasthuis site– a site with comparatively closer sea and river access, however the individual is not a sea trout as originally recorded but a freshwater brown trout (E. Esser 1992).

Contrary to the scarce assemblages of *Salmo* sp. remains seen across the Netherlands, the 16-22 Coppergate site clearly demonstrates both a large assemblage of *Salmo* sp. specimens (n=260, 53 sampled) as well as a higher prevalence of *Salmo salar* identifications (n=44) within the site assemblage. Even the 4 unspecified *Salmo* sp. individuals from the Coppergate site are likely anadromous salmon, according to their relatively depleted δ^{15}N values. This results in an assemblage that is likely comprised of 47 (92.2%) *Salmo salar* samples and only 4 (7.8%) *Salmo trutta* samples, all of which can be identified as anadromous sea trout based on their enriched δ^{15}N values and typically marine δ^{13}C values. The *Salmo* sp. remains sampled for this study from Coppergate came from contexts dating between 850-1500 CE, and is fairly representative of the full *Salmo* sp. assemblage (n=260) recorded for the site. It is important to note that the Coppergate site is anomalous among the wider landscape of English sites with reported *Salmo* sp. remains, most of which report less than 10 identified *Salmo* sp. bones (see Chapter 7). This means that the prevalence of anadromous salmon seen within the sub-assemblage reported here can likely be interpreted as being characteristic of the site itself, rather than England in general, meaning that throughout multiple periods of cultural and political fluctuations the city's desire for salmon remained consistent. The modern day Ouse does not support any significant sea trout populations, and evidence suggests that it never has– unlike the Rivers Tyne, Wear, and Esk to the north (GOV.UK 2022). The question then becomes, how do sea trout fit into the foodways of York– were these individuals incidental catches within the local York environment of the River Ouse, or targeted catches from further afield? Interestingly, the four sea trout individuals from Coppergate were recovered from contexts dating from approximately 930-1160 CE, a period of fairly significant political changes that saw York in the hands of Scandinavian, Anglo-Saxon, and Norman rulers (R. A. Hall 2014, 2011).

Earl's Bu was also under Scandinavian control, though, unlike York's relatively short Scandinavian period, the Orcadian Norse period spanned from approximately the late-9th to late-13th centuries, with the site occupied by Norse or Orcadian Norse individuals for the majority of that time (Anderson 1873; J. H. Barrett, Beukens, et al. 2000; Batey 2021; J. Harland 2006, 2019). The site itself is mentioned in the Orkneyinga Saga, as an estate originally built by Earl Paul Haakonsson in the early-mid 12th-century CE but which likely was occupied by Norse settlers from the late 9th-century Viking period (J. H. Barrett, Beukens, et al. 2000; Batey 2021; J. Harland 2006, 2019). Unlike Coppergate, the data from Earl's Bu reflects a much different fishing strategy for *Salmo* sp. fishes, with 9 of the total 16 samples identified as either *Salmo trutta* or *c.f. Salmo trutta*, and the remaining 7 as *Salmo salar* or *c.f. Salmo salar*. When additional samples from Earl's Bu are added, which have ZooMS identifications but no associated bulk stable isotope data, the proportions increase to 15 *Salmo trutta* and 10 *Salmo salar* (See Chapter 7). While there are endogenous populations of brown and sea trout in the Orkney islands, there are no current or past populations of Atlantic salmon found in the archipelago's small streams and lochs (Thomson 2015). The fact that 40% of the samples from Earl's Bu can be identified as Atlantic salmon suggests that the inhabitants of the site were importing salmon from a different environment. Norse salmon fishing was accomplished using a variety of techniques, including hook and line, spear, and net technology (DaSent 1866;

Fulk 2012). A particular type of salmon and sea trout fishing, using what are called *haaf* nets, is still practised in the Solway Firth of Scotland, and involves wading in estuarine waters using a long repositionable net apparatus to capture salmon as they migrate. Haaf netting is likely based on techniques used by Norse fishers (Scott 2015), and is possibly one of the ways the salmon and sea trout found at Earl's Bu were harvested– but only in the case of sea trout that was locally caught or salmon which was processed for preservation prior to transport to Orkney. While salmon can occasionally be caught in marine environments using a hook and line setup, it's much more common for them to be landed in estuarine or river environments while they migrate. With no migrating salmon entering the waters immediately surrounding Earl's Bu, the salmon caught with net techniques would likely have either been caught just across the Pentland Firth in Caithness if consumed fresh, and if imported from further afield they would have been dried or salted to preserve them. While both Atlantic salmon and migratory sea trout are found at Earl's Bu, it appears that the consumption patterns involving these two fish differed. Norse textual references record distinct terms for sea trout (*birtingr*), freshwater brown trout (*aurriði*), and Atlantic salmon (*lax*)– though there are conflicting translations of *aurriði(a)* as both "trout" and "salmon-trout" (Fulk 2012; Gade and Marold 2017; Ross 2017). In fact, one of the surviving explicit descriptions of fishing in the Norse period can be found in a stanza of poetry by the *skald* Sigvatr Þórðarson– which tells of fishing for sea trout with a fishing line in seaweed-filled estuarine waters (Fulk 2012). The modern day Bay of Firth was referred to as the Aurriðafjörd, or Trout Fjord, in the Orkneyinga Saga, which describes how this body of water is visible from the hill by Orfjara (Anderson 1873). While it appears that the inhabitants of Earl's Bu exploited the locally available sea trout more than salmon, the existence of salmon at the site allows us to ponder whether these specially imported, prestigious fish were included in politically-important feasts held at the Earl's drinking hall over the years of his rule– events also recorded in the Orkneyinga Saga (Anderson 1873).

The three Danish sites at Ribe– ASR 9 "Posthuset", ASR 13 "Lindegården", and ASR 2090 "von Støckens Plads"– tell a story of much clearer preference for sea trout over salmon from the initial marketplace settlement circa 700 CE through to the 13th/14th centuries. The biomolecular sample presented in this study is comprised of 15 specimens with associated bulk stable isotope and ZooMS data; one *Salmo salar*, two *c.f. Salmo trutta* and 12 *Salmo trutta*. In addition to these samples, a further 31 samples were analysed using ZooMS in order to determine species, with 7 identified as *Salmo salar* and 24 as *Salmo trutta* (See Chapter 8). This total sub-assemblage is then divided into 37 (82.2%) individuals identified via ZooMS and/or bulk stable isotope analysis as anadromous sea trout, and 8 (17.8%) individuals identified as anadromous salmon. Unlike Orkney, the region surrounding Ribe has historically been home to robust populations of both anadromous Atlantic salmon and sea trout– in fact, the Ribe Å river has one of the few surviving naturally breeding salmon and sea trout stocks in Denmark today (Feveile 2006; Sivebæk 2023). There is at least some evidence of medium-sized wattle-lined boats being used to transport live cattle and other goods along watercourses in Denmark by the 13th-century CE– it stands to reason that the transport of live fish may also have been occurring prior to this point (Ayers 2016). There is evidence from the ASR 9 Posthuset site for production of boats, nets, and perhaps even *fiskegærde* (fish fences) or *ruser* (weirs) (Feveile 2006). The overwhelming ratio of sea trout to salmon seen at Ribe throughout several distinct occupation periods seems to suggest either a massive difference in past availability of salmon in the Ribe Å, or a clear preference for sea trout over salmon by the medieval inhabitants of Ribe. It may also have been the case that equal numbers of salmon and sea trout were fished from the Wadden Sea estuary or river mouth in Ribe, but the majority of salmon were destined for trade and processed elsewhere after being caught while the sea trout were processed and eaten locally within the settlement.

9.7 Conclusion

The results of this study clearly indicate that there exists great variation in bulk carbon and nitrogen values both across the *Salmo* sp. ecotype categories identified here, and within the ecotype categories themselves. There are variety of observations and conclusions that can be made about the icthyoarchaeological dataset presented here, the first being that the two most significant groups in this study are anadromous Atlantic salmon and anadromous sea trout, both of which were economically and culturally important taxa within various medieval North Sea fisheries. While mistaken identifications of pike and cod bones as *Salmo* sp. did occur within 6.6% of the ZooMS sample presented here, ZooMS analysis did aid in the identification of several samples that were previously unidentified or misidentified in their original fish bone assemblages. Variations in *Salmo* sp. prevalence exists on a regional scale, with the 16-22 Coppergate site consisting of primarily (92.2%) *Salmo salar* individuals, Earl's Bu consisting of 60% *Salmo trutta* and 40% *Salmo salar* individuals, and the three Ribe sites consisting of primarily (82.2%) *Salmo trutta* individuals. Isotopic characteristics of comparative taxa like Atlantic cod, haddock, eel, pike, and cyprinids were all as expected for individuals from a varied set of archaeological sites around the North Sea basin area. Reasonable hypotheses of both species and ecotype can be made for samples without associated ZooMS data, based on what is known about the bulk carbon and nitrogen characteristics of regionally distinct populations of anadromous salmon and anadromous sea trout. Finally, variations in bulk carbon and nitrogen values for salmon and sea trout from the medieval North Sea basin area are regionally dependent, rather than a result of change over time. There are, of course, some improvements that can be made upon the analysis presented here, which include; further work on establishing Suess correction data for the North Sea, adding further archaeological salmon data to explore the use of isotope niche space analysis to track archaeological Atlantic salmon primary foraging locations in the North Sea, and improving regression formulas for both Atlantic salmon and sea trout in order to confirm or reject TL-δ^{15}N correlations. Nevertheless, this study constitutes the largest published dataset of bulk carbon and nitrogen values from North Sea archaeological salmon, and sea trout of any geographic or temporal origin. It contributes key pre-modern baseline bulk carbon and nitrogen data for two of the most economically and culturally important salmonid species of the North Sea basin area, shedding light on pre-industrial environmental conditions for these threatened fish. Additionally, it provides useful contextual information for the discussion of medieval fisheries, trade networks, and environmental change.

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Chapter 10

Discussion and Conclusions

10.1 Introduction

The chapters up to this point have been focused on describing material sources, reviewing the state-of-the-art, and reporting results in more-or-less standalone article format. This means that, while there is an appropriate amount of discussion for the datasets reported in each article, there have been discussion topics that did not make the final edit. These topics tend to include more of the interpretive discourse focused on medieval cultural conceptions and human-environment interactions, and which are further grounded in anthropological theory. The first topic of discussion is the final dataset of archaeological remains of *Salmo* sp. fishes explored within this thesis. Following will be a cumulative discussion of human-salmon interactions in the Medieval Period, including examinations of commercialization of salmon fishing and trade, characteristics of medieval fish populations, and efforts to protect salmon and sea trout populations in the past, present and future. Finally, the chapter, and thesis, will end with a conclusion section which summarizes the main contributions of this work, connections to other disciplines, and future research.

10.2 The *Salmo* sp. Dataset

10.2.1 Sampling Limitations

This thesis presents one of the largest single datasets of archaeological *Salmo* sp. biomolecular data, with 194 total samples (Figure 1, section 2.2), from 16 archaeological sites located in modern day England, Scotland, Denmark and the Netherlands. Despite its size, the compilation of this final biomolecular dataset is perhaps not as comprehensive as first intended, with significant barriers to further sampling including factors like material availability, destructive sampling permissions, quality control criteria, and accessibility issues created by the ongoing COVID-19 pandemic. Not only were there difficulties with accessing certain recorded materials–including inadequate storage solutions and declined requests for sampling permission– but there were also inconsistencies in record keeping that made it difficult to match published records to physical remains upon review. This is, unfortunately, a very common problem in archaeology in general, especially when working primarily with so-called "legacy" collections rather than those which have been newly excavated. Most assemblages were recorded and stored according to the standard practices of their time, and the differences in opinion about zooarchaeological material assessment, recording, organisation, and storage that make our discipline so vibrant and diverse can, unfortunately, also be a barrier to research. As it is, the current biomolecular sample could be expanded in a variety of ways, not least by ensuring that all samples with available bulk stable isotope results also have corresponding ZooMS identification; 10 samples with only isotopes data were the result of failed MALDI runs/time constraints, and can be re-attempted in the future. In terms of individual sites, the Netherlands has the greatest diversity of samples in this thesis, due in part to ease of access to archaeological materials. The Netherlands has a centralized repository for zooarchaeological information (BoneInfo), and the invaluable cooperation of the Cultural Heritage Agency of the Netherlands (RCE) allowed for ease of contact with site excavators, collections managers, and storage facilities. Sourcing more samples from Scotland, England, and other areas of Denmark would strengthen the current dataset, as would the addition of samples from France, northwestern Germany, and Belgium. Adding sites from these areas would provide a more comprehensive overview of the geographical and cultural variation in *Salmo* sp. exploitation in the study region. Additionally, more samples from agricultural settlements, early monastic sites, and industrial fishing sites would be beneficial for drawing more concrete conclusions about changes over time in *Salmo* sp. exploitation.

Nevertheless, the material and data presented in this thesis is the result of concerted efforts to present a

selection of *Salmo* sp. bones from archaeological sites which vary in geographic location, occupation period, cultural group, and site type. The materials from this thesis come from Early Medieval marketplaces, urban and rural settlements, high status residences, and ecclesiastical settings. (Table 1)

Site Name	***Salmo* sp. samples**	**Date Range (Years CE)**	**Site Type**
16-22 Coppergate	61	400-1720	Early Trading; Urban
ASR 13 Lindegården	2	1200-1300	Urban
ASR 2090 von Støckens Plads	4	1000-1200	Urban
ASR 9 Posthuset	46	700-1200	Early Trading
Earl's Bu	25	750-1220	High Status
Heveskesklooster	1	900-1610	Ecclesiastical
Huis Malburg	1	900-1499	Rural
In den Struys' Veere	3	1425-1500	Urban
Johan van Oldenbarneveltlaan	2	450-700	Early Trading
Kasteel Voorst	2	1280-1362	High Status
Minderbroedersklooster	20	1175-1500	Ecclesiastical
Nieuw Rhijngeest-zuid	15	475-725	Early Trading
Oude en nieuwe Gasthuis Delft	3	1400-1450	Ecclesiastical
Plantage Leiderdorp	1	650-850	Rural
Stadhuis Zutphen	1	1125-1175	High Status
Tjitsma Foarryp Wijnaldum	7	550-950	Rural

TABLE 10.1: Archaeological Sites and the Characteristics

10.2.2 Strengths of the Dataset

While the dataset does have it's limitations, it still represents 7.7% of the recorded archaeological *Salmo* sp. bones (n=2515) reviewed in Chapter 7. A sample of this size with associated biomolecular data provides an excellent opportunity to make general conclusions about the state of medieval *Salmo* sp. exploitation in the North Sea region, the assemblage characteristics of each site, and the reliability of traditional archaeological methods for correctly identifying *Salmo* sp. samples and drawing conclusions about their presence and absence. The final *Salmo* sp. dataset presented in this thesis is made up of 194 samples, with varying types of biomolecular data associated with each sample (Figure 1) including those with zooarchaeology by mass spectrometry (ZooMS) identifications (total n=120) and bulk stable isotope (SI) data (total n=184).

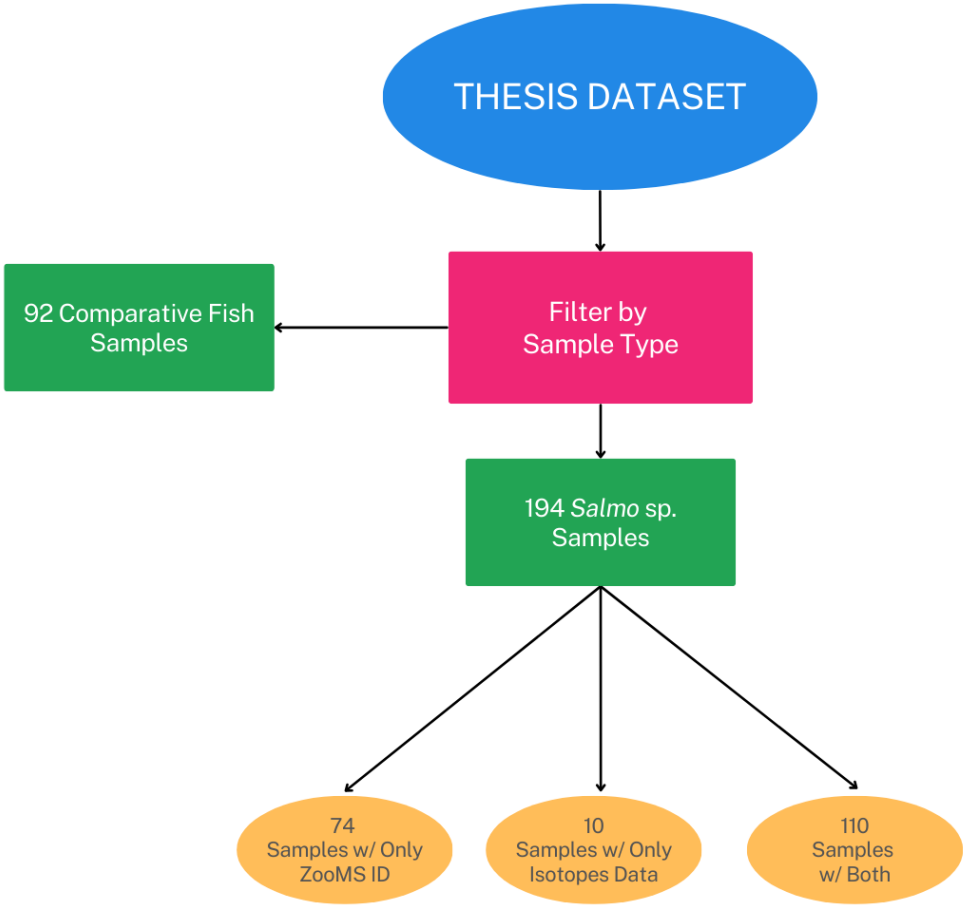


FIGURE 10.1: Flowchart demonstrating how the *Salmo* sp. dataset is broken down in this thesis.

The primary strength of this dataset lies in it's reliable species identifications made using collagen peptide fingerprinting techniques. ZooMS identifications of *Salmo salar* and *Salmo trutta* are more reliable than simple morphological identifications, which tend to be overly generalised due to lack of distinctive morphology between the two species' most commonly recovered remains (see Chapter 3). These reliable identifications are what set the general results of this thesis dataset apart from the published ichthyoarchaeological material reviewed as part of Chapter 7, in which generalized conclusions about changes in *Salmo* sp. presence and absence over time were made using the published data. While the majority of ZooMS identifications were of *Salmo salar* (n=122, 66.30%), the fact that one third of the studied remains were identified as *Salmo trutta* has called into question assumptions made about the "default" status of Atlantic salmon. Generally, morphological identification methods tend to either remain conservative and only classify remains that could belong to either species as "*Salmo* sp." or "salmonid", or, if species determinations are being made they rely on the assumption that larger bones (generally vertebrae) will be from Atlantic salmon, and smaller ones from Brown/sea trout.

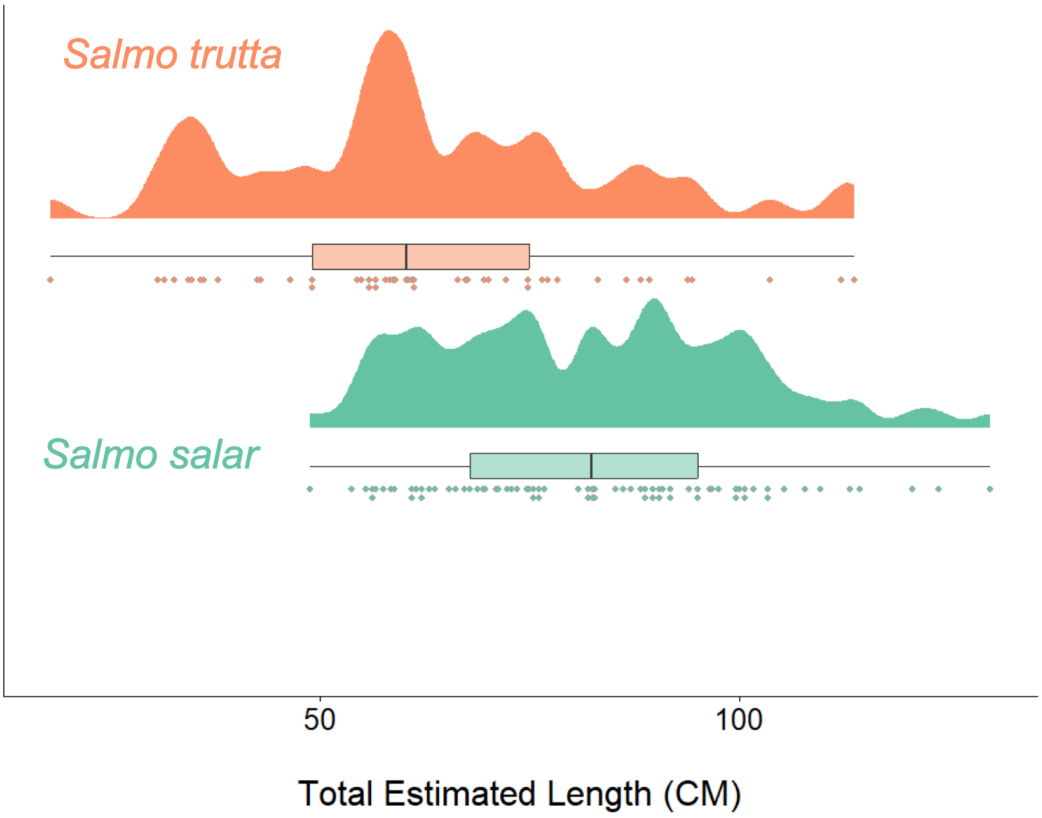


FIGURE 10.2: Graphical representation of the set of ZooMS-identified *Salmo salar* and *Salmo trutta* samples with associated total length estimations. NB: The TL estimations for *Salmo trutta* are based on an application of the Atlantic salmon TL regression formula from (Watt, Pierce, and Boyle 1997), as there is no regression formula available for trout.

In fact, while the average estimated total length (TL) of *Salmo salar* samples from this study is 82.45cm, compared to an average 62.40cm for *Salmo trutta*, there is considerable overlap between the range of estimated total lengths seen in the two species (Figure 2). The *Salmo salar* samples with estimated total lengths (n=77) range between 48.93 to 130cm, and 75.5% (n=37) of the *Salmo trutta* samples with estimated TL data (n=49) lie completely within that range. When the *Salmo trutta* group is filtered by ecotype, the overlap becomes even more significant, with 24/26 samples falling within a range of 55.86 to 113.75cm. Of the 13 vertebrae which are believed to belong to migratory Atlantic salmon and sea trout estimated at <100cm in length, three of them are from sea trout, and two of those sea trout samples are larger than 50% of the <100cm salmon samples. These data confirm that there needs to be more flexibility in assumptions made about *Salmo* sp. remains based on size– large vertebrae cannot be taken as solid indication of an Atlantic salmon, and ZooMS analysis is, at present, the most reliable and cost effective method of identifying these fish to species in the archaeological record.

Another strength of this thesis dataset involves the second chemical analytical method used– bulk stable isotope analysis of carbon and nitrogen isotopes. The total isotope dataset of 212 samples is one of the largest multi-species datasets of medieval archaeological fish remains, and the subset of 120 *Salmo* sp. samples is the largest dataset of archaeological salmonid isotope data currently available from any period in Europe. By conducting a targeted study of a single genus, *Salmo*, this thesis provides invaluable historic baseline isotopic infor-

mation about two species which have been economically important in the area since at least the Roman period, and through to today. One of the major conclusions of this isotopic study is that variations in bulk carbon and nitrogen values for *Salmo salar* and *Salmo trutta* specimens do not appear to vary on a temporal scale, but instead show variation by region and regional population (See Chapter 9). This insight into past differences in fish foraging ecology, combined with accurate ZooMS identifications of the archaeological remains, has resulted in a unique opportunity to not only examine species prevalence, but also that of ecotypes – behaviorally distinct populations of a given species. Chapter 8 outlines the combined biomolecular approach to identifying *Salmo* sp. ecoptypes in the archaeological record, namely migratory Atlantic salmon, migratory sea trout, and freshwater brown trout. One of the major outcomes of the case studies in Chapter 8 was the discovery that initial assumptions about the relative importance of freshwater brown trout in this medieval assemblage were incorrect, and that the migratory ecotype of *Salmo trutta*, the sea trout, is not only more prevalent than brown trout, but is, in some locations, more prevalent than salmon.

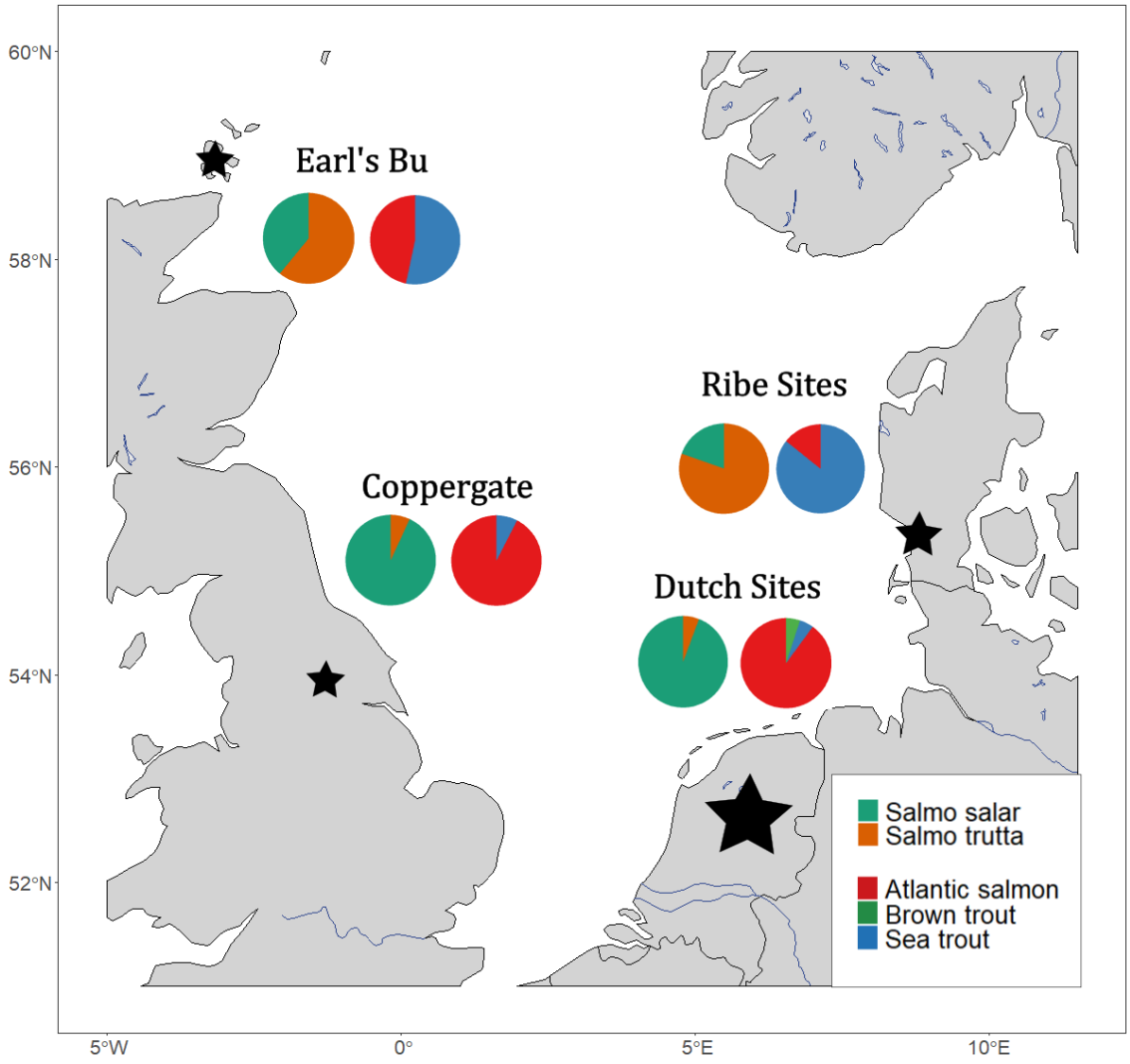


FIGURE 10.3: Map of the North Sea study area displaying proportions of sea trout and Atlantic salmon ecotypes (total n=109), as well as proportions of ZooMS IDs (total n=184), from the four sites/regions of 16-22 Coppergate, Earl's Bu, the three Ribe sites, and all Dutch sites.

Figure 3 illustrates the differences in proportions seen amongst both the set of *Salmo* sp. samples with available ZooMS identifications (n=184) and those with both ZooMS identifications and bulk stable isotope data, leading to the assignment of ecotype categories (n=109). The samples designated as "Atlantic salmon" are those which display typically "marine" high δ^{13}C values and ZooMS IDs of *Salmo salar*, sea trout are those which display typically "marine" high δ^{13}C values and ZooMS IDs of *Salmo trutta*, and brown trout are those which display typically "freshwater" low δ^{13}C values and ZooMS IDs of *Salmo trutta*.

10.3 Salmon and Sea Trout in the Medieval North Sea Basin

10.3.1 Compatibility with North Sea *Salmo* sp. Review

In addition to these regional differences in species/ecotype presence, there are also some general observable differences in presence and absence through time of samples identified via ZooMS. Figure 4 below aims to assess how temporal differences seen in the set of ZooMS-identified archaeological samples (n=120) compare to those included in the Chapter 7 review of archaeological *Salmo* sp. materials (n=1917). The top plot (Figure 4A) is a reproduction of a multivariate comparison of total fish NIPS and *Salmo* sp. NISP over time from archaeological sites and contexts dated to between 450-1650CE, and the bottom plot (Figure 4B) shows changes in identified sample numbers for both species through time, with an added variable of site type. It's clear that the materials sampled for this thesis follow a similar pattern established in the NSAS review, with the majority of fish, unidentified *Salmo* sp. remains, and identified *Salmo salar* and *Salmo trutta* specimens concentrated in the periods from c. 900-1350CE. There are likely several reasons for this, including preservation, and therefore sampling, bias for sites from those periods. This may merely be reflecting the fact that there has historically been a larger interest in so-called "High Medieval" archaeological material across the northwestern European region, which has resulted in more sites excavated, more materials recovered, and therefore more fish samples available to study. Sites from this period may not necessarily have been selected to the exclusion of later or earlier periods, but often they do contain more large, undisturbed urban deposits which makes them disproportionately represented in the archaeological record. Indeed, the existence of large, complex trading and/or urban sites like 16-22 Coppergate or Ribe ASR 9 Posthuset further complicates the dataset by unduly influencing the total numbers despite only representing two individual sites.

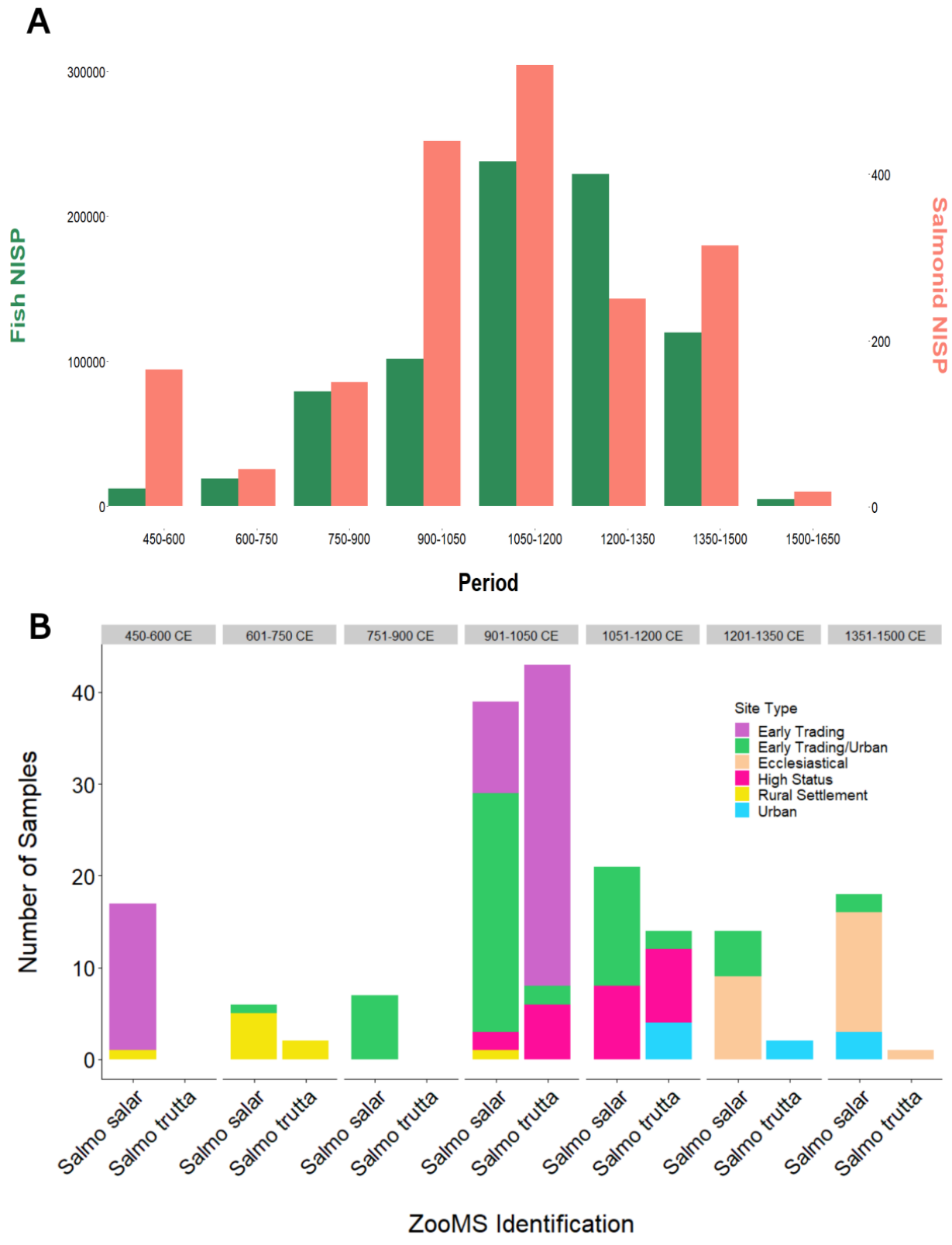


FIGURE 10.4: Comparison of graphs representing sample numbers (NISP) through time. Plot A is a reproduction of a plot from Chapter 7: the North Sea *Salmo* sp. Review, indicating both the pattern of all fish NISP through time (green, left axis) and salmonid fishes (peach, right axis). Plot B demonstrates differences through time between the number of samples in this thesis dataset identified as *Salmo salar* and *Salmo trutta*, with bar fill colors indicating the type of site the samples were recovered from.

This being said, this examination of ZooMS-identified samples through time does confirm some of the observations made within Chapter 7, and provides a more comprehensive understanding of species differences within the wider *Salmo* sp. data reviewed there. Attempts to infer historic trends in *Salmo trutta* presence using the data from this thesis is constrained by the fact that the majority of samples (49 out of a total 62) are from two sites– Earl's Bu and ASR 9 Posthuset. Additionally, 44.2% of salmon samples are from a single site, 16-22 Coppergate, which influences potential interpretations of *Salmo salar* trends through time. However, even with these limiting factors, there do seem to be some repetition of patterns seen in the NSAS datasets, with a higher recorded presence of both species starting from c. 900 CE. Even looking at Coppergate on it's own (represented in green in Plot 4B) there is a demonstrable increase in *Salmo salar* presence from the 751-900CE period to the 901-1050CE period, followed by a steady decline in presence in the following three periods. The Coppergate site is an example of a North Sea trading settlement which expands and urbanizes over time, with excellent preservation of *Salmo* sp. remains, several successive well-dated periods of occupation and demonstrable cultural change (Hall 2014; Hall and Hunter-Mann 2002; Harland, A. K. Jones, and D. C. Orton 2016). I propose that Coppergate may be used as a proxy for similar trading/urban sites across the region which have less comprehensive ichthyoarchaeological assemblages, and it is likely that, were ZooMS analysis of large *Salmo* sp. assemblages performed, similar temporal patterns would emerge. This is based on the patterns seen in both the NSAS *Salmo* sp. assemblages as well as the overall ZooMS assemblage from this study– all of which align with observations made about the so-called medieval "Fish Event Horizon", which proposes an intensification of wholesale fishing effort in the decades surrounding c. 1000 CE (Barrett, Locker, and Roberts 2004a,b).

Interestingly, the patterning seen in this ZooMS dataset also appears to mirror observations made in Chapter 7 about proportional increases in *Salmo* sp. presence at high status and ecclesiastical sites during later periods from c. 1051-1500 CE. In the period from 1200-1500 CE the three ecclesiastical sites (Minderbroedersklooster, Heveskesklooster, and Oude en nieuwe Gasthuis) both have the largest proportion of identified *Salmo salar* remains, independent of whether Coppergate is included. This pattern of the highest proportions of identified salmon bones being found at ecclesiastical sites not only mirrors the overall trends seen in Chapter 7, but also affirms documentary and historical evidence for ecclesiastical involvement in and, in some cases, control of fishing rights and local fisheries in the High-Late Medieval Period (R. C. Hoffmann 2015; R. Miller 2003). Additionally, as discussed in Chapter 6, there is ample evidence within documentary records for local church institutions across the North Sea basin having a vested economic interest in not only fisheries in general, but salmon fisheries specifically (R. Hoffmann 2012; R. C. Hoffmann 2015; R. C. Hoffmann and Ross 2019; M. J. Miller, Capriles, and Hastorf 2010). More thorough analysis of the available ecclesiastical documentary records, in comparison to archaeological records from the same time periods, would provide a more comprehensive understanding of religious consumption of *Salmo* sp. fishes. Similarly, beginning during the c. 901-1050 CE period we see a proportional increase in the presence of both species at high status sites (primarily Earl's Bu, but also the Dutch site of Stadhuis Zutphen), even as overall presence begins to decline post-1051 CE. It is important to remain cognizant of the fact that this sample data is limited by a low number of sites, and heavily imbalanced inter-assemblage variation within categories due to the inclusion of sites like ASR 9 Posthuset, 16-22 Coppergate, and Earl's Bu which have proportionally larger numbers of recovered *Salmo* sp. compared to other sites in their respective site type categories. That being said, the visualization of these overall increases and declines, and shifts in site type representation through time, is still a useful metric for understanding access to salmon and sea trout during the Medieval Period.

Reported declines in Atlantic salmon availability during the High-Late Medieval Period, beginning c. 1200 CE, have been documented both within the results of this thesis (see Chapters 6 and 9), but also within work

by other environmental historians, archaeologists, and historical ecologists (R. C. Hoffmann 2015; Lenders et al. 2016; Sear et al. 2022). Although there is comparatively little research on declines in sea trout populations in the same region and time periods, some assessments of modern sea trout, and other anadromous North Atlantic species, population declines do indicate that they would be susceptible to similar environmental and anthropogenic pressures as salmon (Limburg and Waldman 2009; I. E. Moore 2020; Walday and Kroglund 2002). It is undeniable that both anthropogenic and natural changes to the global and regional environment occurred during the period from 500-1500 CE, including soil degradation and erosion, fluctuations in sea temperature and surface pressure, forest clearing and land development, and volcanic activity (e.g. Berglund 2003; Björklund et al. 2023; Bradley, Hughes, and Diaz 2003; Coombes, Chiverrell, and Barber 2009; R. Hoffmann 2014; Mann et al. 2009; McCormick et al. 2012; Mensing et al. 2016; J. W. Moore 2002; O'Sullivan 2008; Schofield et al. 2022; Trouet et al. 2009). The oft-debated "Medieval Warm Period", more accurately termed the "Medieval Climate Anomaly" (MCA) (Björklund et al. 2023; Mann et al. 2009; Trouet et al. 2009), was a period of reportedly warm and dry summers combined with milder winters beginning c. 950CE and continuing until c. 1200 CE when the climactic changes that preceded the so-called "Little Ice Age" (LIA) of c. 1450-1850 first began (Bradley, Hughes, and Diaz 2003; H. H. Lamb 1972, 1965). It is now hypothesized that the major mechanisms behind the MCA were a persistent positive North Atlantic Oscillation (NAO) mode, higher solar irradiance, and an increase in volcanic-derived atmospheric aerosols (Mann et al. 2009; Trouet et al. 2009). The reversal or removal of these factors, along with regional and global shifts in oceanic and atmospheric conditions, resulted in "La-Niña-like" conditions precipitating the LIA, which was characterized by a moister and colder overall environment in Northern Europe (R. Hoffmann 2014; H. H. Lamb 1972, 1965; Mann et al. 2009; Trouet et al. 2009). In the context of these well-documented climactic, atmospheric, and oceanic phenomena it would be easy to ascribe the noted increases and decreases in *Salmo* sp. presence at medieval archaeological sites solely to natural environmental changes, but anthropogenic changes to the environment, especially within estuarine and riverine habitats cannot be discounted.

It's these anthropogenic environmental changes in European rivers that are the focus of the previously discussed reviews of the impact of damming, fishing activity, and agricultural development on migratory fish species (Hansen et al. 2014; R. Hoffmann 2012; R. C. Hoffmann 2015, 2023; R. C. Hoffmann and Ross 2019; Lenders et al. 2016; Prummel and Heinrich 2005). The hypotheses presented within these various sources are that human fishing, agricultural, and waterpower activity all contributed to the noted declines in migratory fish populations, especially that of salmon and, by extension, sea trout. Waterway manipulation during the Medieval Period included the redirection of water for mills, the construction of massive weirs and fish traps in river and estuarine environments, and damming of rivers to create artificial ponds (Lenders et al. 2016; Prummel and Heinrich 2005). These human activities were likely not the most significant source of declines in salmon and sea trout stocks, as suggested by Lenders et al 2016, but more likely an equal contributor along with cyclical climactic fluctuations like the Atlantic Multidecadal/North Atlantic Oscillation, MCA, and LIA (Sear et al. 2022). A combination of intensified human fishing activity during the 10th-11th century transition, which was likely influenced by favorable oceanic conditions established during the MCA, led to over-exploitation of fish resources which, when combined with human modification of riverine and estuarine environments led to population collapses. These collapses may be visible in the archaeological record via reported presence/absence of *Salmo* sp. remains, and are further supported by the noted shifts in prevalence of *Salmo* sp. remains at high status and ecclesiastical sites.

10.3.2 Ecotypes, Economic Value, and "Prestige"

The higher incidence rate of anadromous sea trout than hypothesized (Figure 3, Section 2.2) is indicative of a broader pattern of exploitation during the Medieval Period in which the anadromous migration strategy is "king", rather than a single species or ecotype of fish. While this thesis deals with three ecotypes of the *Salmo* genus, several other culturally and economically important fish taxa display anadromous migration strategies, including sturgeon, lampreys, and some whitefish. The socioeconomic importance of anadromous fish is not necessarily predicated solely on their migration strategy, but the anthropogenic "success" of these fish as indicators of prestige, measures of wealth, and sources of high value food is certainly dependent on the evolutionary success of anadromy. Anadromous migration strategies bring with them larger overall body size, more robust fat and protein structures, higher fecundity, and a predictable seasonal availability (McDowall 2001). Subjective factors like flavor, aesthetic desirability, and perhaps even symbolic meaning certainly influence which species or ecotype is considered to be "prestigious" in a given area, but it also seems that local availability of large, powerfully built anadromous species like salmon and sea trout, has a not-insignificant impact on their presence at archaeological North Sea basin sites during the Medieval Period. It's clear that the presence/absence of sea trout, salmon and freshwater trout is highly site-dependent, with some sites with comparatively large *Salmo* sp. presence, like Coppergate, showing a clear majority of salmon over sea trout, while the higher prevalence of sea trout at Earl's Bu is likely due to local availability of sea trout and lack of a local salmon population. The higher incidence rate of sea trout identifications made at a site like ASR 9 Posthuset in Ribe, which has a river with significant modern and historic salmon and sea trout populations, is perhaps more indicative of cultural preference for one fish over the other.

Whatever the reasons for preference of salmon or sea trout, the anadromous ecotypes of these fish dominate medieval assemblages of *Salmo* sp. specimens, and this raises questions of where these fish ecotypes fit within the "fish event horizon" first identified by Barrett et al. 2004, and subsequently expanded upon by various ichthyoarchaeological researchers (Barrett, D. Orton, et al. 2011; Fuller et al. 2012; Lotze 2007; Milner et al. 2008; D. C. Orton et al. 2014; Perdikaris and Mcgovern 2009, etc.). These expanded arguments hinge upon the fact that there are differing degrees of geographic and temporal variability in marine fishing intensification seen in the Medieval Period across northern Europe (Barrett, D. Orton, et al. 2011; Fuller et al. 2012; Lotze 2007). However, all discussions of fishing intensification during the c. 10th-11th century period focus on either marine or freshwater species, leaving a fairly uncertain view of the importance of diadromous species exploitation during the same period. This is further complicated by the fact that most of these migratory fish, both anadromous and catadromous, are high value and/or prestige species like eel, sturgeon, lamprey, and, of course, salmon. What is certain is that there was an overall intensification in fishing effort during this period, which is mirrored in the uptick in salmon NISPs reported at archaeological sites of all kinds during this period (see Chapter 7). However, unlike cod, there have always been reported cyclical fluctuations in Atlantic salmon availability. These fluctuations are both on a yearly level, with both seaward and riverine migrations, but also potentially on a multidecadal scale influenced by climactic changes (Friedland et al. 2003; Sear et al. 2022).

The question remains, then, whether sea trout and salmon can be treated as a monolithic "migratory *Salmo* sp." grouping when discussing not only the position of these fish within a broader trend in fishing intensification, but also local concepts of "prestige". I would argue that, for the most part, salmon and sea trout would both have been considered a higher value "marine" fish when thinking in terms of rapidly expanding fisheries during the 10th-11th century period. While the intensification of salmon and sea trout fishing was likely not as heavily dependent on fishing technology changes as that of herring and cod, their exploitation was naturally influenced by increased demand for fish during the medieval urbanization period (R. Hoffmann 2000; R. C. Hoffmann 2023;

R. I. Moore 2000). Documentary and literary evidence do seem to imply that salmon were of a higher value, both in terms of "prestige" and monetary worth (see Chapter 6), but it may be that these concepts of value and even prestige were also dependent on the availability of each fish in a given location. This being said, migratory Atlantic salmon still inhabit a significantly large portion of the medieval archaeological, documentary, literary, and artistic record and, by extension the general cultural value of the period.

As more studies have been conducted on medieval fisheries and archaeological fish bone evidence, it has become clear that the specialization and commercialization of human fishing activity played a key role in the development of proto-capitalist and, later, capitalist economic systems (e.g. Barrett 2019; Barrett, Locker, and Roberts 2004a,b; Barrett and D. C. Orton 2016; R. C. Hoffmann 2005; Kowaleski 2003; J. W. Moore 2002; Pitcher and Lam 2015; Serjeantson and Woolgar 2006). While debates abound as to the exact characterisation of medieval social and economic structures and whether they can be accurately described as "feudal" or "capitalist" (Brown 1974; Katz 1993; J. W. Moore 2002; Roach 2015), it is clear that a high value group of fish, like salmon and sea trout, would have played an important role in not only the success of a societal-level economy, but also the local economic success of individual fishers. Marx and Engels both characterized the class of immediate producers as one of the driving forces behind medieval economic development in their discourses on the development of historical materialism and the many local and regional transitions from a mode of feudalistic to capitalistic production (Engels 1970; Katz 1993; Marx and Engels 1968). This production class in the Early-High Medieval Period included artisan fishers as well as those who processed and sold fish, rendering them the basis of an exploding economic force that would change the very fabric of western European society once the second round of, primarily cod, fishing intensification began in the Early Modern period (Holm et al. 2019). Commercial fisheries were certainly not unique to the Medieval Period surrounding the 10th-11th century transition, after all evidence for massive commercial fishing and processing endeavors abounds from the Roman period across Europe, North Africa and West Asia (Barrett 2019; Marzano 2018). What was unique about this period was the scale of intensification in comparison to previous declines in the post-Roman period, as well as the overwhelming evidence within the archaeological record for increases and, later, subsequent declines in the presence of *Salmo* sp. fishes at differing types of sites across the archaeological North Sea basin area. These shifts indicate a potential change in ability to procure salmon and sea trout, resulting in the wealthier strata of society not only having easier access to these fish through increased capital, but having increased control over fishing activity and proto-conservation efforts intended to preserve valuable salmon stocks.

10.4 *Salmo* sp. Biogeography and Conservation

10.4.1 Medieval Biogeography of Salmon and Sea Trout

Biogeography, at it's broadest, is the study of how biological diversity of varying kinds is distributed across both space and time (Gubbay 2014; Jenkins and Ricklefs 2011). While ecological studies are often focused on narrower population-level changes within groups, biogeographical approaches have historically investigated biological diversity on a deep-time, higher-order, and even global scale (Jenkins and Ricklefs 2011). There are instances of overlap between the two fields, especially when concerning regional variations over time scales on the order of hundreds or thousands of years (Jenkins and Ricklefs 2011)– precisely the area of study occupied by archaeological isotope and species data like that produced for this study. This provides a unique opportunity at the intersections of archaeology, ecology, and biogeography, to incorporate archaeological data into our understanding of biogeographic patterns for particular species– an archaeobiogeography. This concept has only been explored in

one previous publication, looking at archaeological remains of extinct Caribbean rice rats (Durocher et al. 2021), and is not well-defined. A proposed definition of archaeobiogeography would be the exploration of past variations in biological diversity using palaeoecological data, like species identifications and isotopic characteristics, derived from animal remains recovered from archaeological sites. This archaeobiogeographic data is inextricably linked to the human populations that hunted, fished, bought, sold, cooked, and consumed the animals in question, and therefore they cannot be taken as a direct representation of past fish population characteristics.

That being said, archaeobiogeographic data from the Atlantic salmon and sea trout studied in this thesis does provide some insight into the ways prehistoric populations of these fish differed from historic and modern ones. For example, this study confirms the presence of Atlantic salmon and sea trout at archaeological sites in regions where both species have become almost completely extinct, if not severely threatened, such as the southern Netherlands and York. We see higher concentrations of sea trout remains in more northerly sites, and observed differences in isotope characteristics indicate population-level differences in both δ^{15}N and δ^{13}C values from sea trout originating from the northern North Sea and Wadden Sea (see Chapter 9). Confident ZooMS-based identifications and bulk stable isotope data from archaeological material from these discrete populations provide a snapshot of Atlantic salmon and sea trout population characteristics in the North Sea region through an archaeological lens. The hope is that these data may help inform regional baseline estimations beyond the historic period, and in doing so contribute to modern conservation ecology goals.

10.4.2 Salmon and Sea Trout Conservation

As discussed previously in Chapter 5, there is considerable historic evidence for what may be termed "conservation" practices in northwestern Europe, with the earliest legislation concerned with protecting the health of salmon populations introduced in Scotland in the 14th century (Barrett 2019; Barrett, Nicholson, and Cerón-Carrasco 1999; Bennema and Rijnsdorp 2015; R. Hoffmann 2012; R. C. Hoffmann 2010, 2015, 2023; Lenders et al. 2016; Prummel and Heinrich 2005; Sear et al. 2022). Most conservation practices of the Late Medieval-Early Modern period involved the restriction of damming activity, the development of moveable weirs, and introduction of limited seasons and catches for salmon (Bennema and Rijnsdorp 2015; R. C. Hoffmann 2010, 2015, 2023). However, unlike most modern conservation movements, these early practices were primarily motivated by the truest definition of "conservation"– namely protecting and managing valuable natural resources for future exploitation (Meyer 1997; Minteer and Corley 2007). This stands in opposition to the concept of "preservation" first introduced to the public consciousness via the work of John Muir, which aimed not only to protect ecosystems from human damage but also, ultimately, from human exploitation (Meyer 1997; Minteer and Corley 2007). This early concept of preservation underscores much of what may be deemed as the modern global conservation movement, with many conservationists aiming to develop and champion both the scientific and moral arguments for protecting and encouraging biodiversity (Ghasemi and Kyle 2021; Minteer and Corley 2007). These arguments are certainly the motivation behind modern groups like the North Atlantic Salmon Conservation Organization and the Atlantic Salmon Trust, but it is unlikely they were influential on the moves for conservation of salmon stocks made by those in power during the Medieval Period.

This being said, there have been numerous calls within the last decade for the better integration of palaeobiological, archaeological, and historical information into modern conservation ecology approaches (Barak et al. 2016; Barnosky et al. 2017; Davies, Colombo, and Hanley 2014; Grace et al. 2019; Izdebski et al. 2016; J. Jones and Britton 2019; Nieto-Lugilde et al. 2021). These appeals focus on the incorporation of archaeological and palaeontological data relating to environmental conditions, species biodiversity and biogeography, and prehistorical ecology into modern ecological models and planning. Though the recovery and analysis of palaeonviron-

mental data has been a key part of archaeological research for decades (Dincauze 1987), there remain several barriers to effective inclusion of palaeoenvironmental data into conservation ecology research. These include the occasional misalignment of research priorities between archaeology and ecology, insufficient infrastructure for storing and disseminating this data, perceptions within the ecological community that long-term archaeological data is purely descriptive, and a shortage of accessible and/or coordinated data (Davies, Colombo, and Hanley 2014). While issues like data infrastructure and the perceptions of the ecological community at-large are not ones which can be solved by a single doctoral thesis study, steps can certainly be taken towards making this newly produced data on archaeological salmon and sea trout populations more accessible, as well as identifying the value this research may offer.

The combined biomolecular approach outlined in Chapter 8 provides not only a clearer picture of isotopic baselines in past regional populations, but also expands our collective knowledge of the historic biogeography of different *Salmo* ecotypes– in particular anadromous sea trout. Incorporating archaeological bulk isotopic data on environmental conditions, foraging strategy, and fish origins into modern and historic datasets will allow for more robust ecological isotope modelling and provide wider context for long-term changes in species isotope ecology. Similarly, the application of ZooMS and bulk stable isotope analysis to archaeological material as a pre-screening tool for identifying pre-industrial and pre-agricultural populations of salmon and sea trout is cheaper and, potentially, less destructive than ancient DNA analysis. Identifying these groups in different regions would allow for the isolation of salmon and sea trout populations that were unaffected by the associated anthropogenic changes from later time periods, in turn providing opportunities for further biomolecular or genetic analysis of long-term changes. Finally, there is the potential for palaeoecological data to provide a metric by which the success, or failure, of modern reintroduction and restoration ecology efforts can be measured (Grace et al. 2019). Some researchers in particular have called for the consultation of historical and palaeoecolgical data in order to identify species recovery targets for taxa included on the IUCN Red List and other conservation status inventories, and at least one user-created database (ConservationArchive) has been developed to aid this appeal (Grace et al. 2019). Atlantic salmon were last assessed by the IUCN as "least concern" nearly 30 years ago in 1996, and currently have no associated population distribution data available (Centre 1996). This fact alone makes the incorporation of archaeologically-derived salmon palaeoenvironmental and biogeographical data critical for the accurate assessment and successful conservation of Atlantic salmon today.

10.5 Future Work and Conclusions

10.5.1 Future Work

The incorporation of the biomolecular data presented in this thesis into modern ecological approaches to preservation/conservation of Atlantic salmon and sea trout is one of several potential future avenues of research focused on archaeological *Salmo* sp. material. In addition to re-analyzing the small assemblage of inconclusively identified *Salmo* sp. remains in the hopes of providing a conclusive species identification, it would also be beneficial to re-run the bulk stable isotope analysis of key samples which did not produce adequate results. Bulk sulphur (δ^{34}S) isotope analysis of some samples from this thesis dataset has been conducted already, but as results were not available prior to writing-up they were not included. Incorporating these, and any further sulphur isotope samples, into the intersite isotope analysis of archaeological *Salmo* sp. remains (Chapter 9) would be particularly beneficial for understanding more about estuarine feeding habitats of migratory salmon and sea trout (Nehlich et al. 2010). Another isotopic line of inquiry that may prove particularly interesting for the anal-

ysis of these migratory ecotypes is incremental stable isotope analysis of single vertebrae, a method which has been conducted on modern masu salmon samples and archaeological tuna (Andrews et al. 2023; Matsubayashi et al. 2017). Expanding the preliminary documentary analysis presented in Chapter 6 will also likely contribute more to our understanding of medieval shifts in salmon availability, and perhaps provide an economic model for interpreting declines and resurgences in historical salmon populations. The most important continuation of this current research involves enlarging the biomolecular sample of medieval archaeological *Salmo* sp. by incorporating a wider array of sites and time periods. This would provide more data to refine the proposed isotope niche space-based sourcing method, as well as adding to the multi-isotope baselines presented within this thesis. Additionally, now that it is clear sea trout played a larger role than anticipated in the medieval *Salmo* sp. fishing landscape, future sampling could target areas known for robust sea trout populations in order to determine the extent of their role in the region's economic and cultural landscape. Finally, the application of high-throughput ZooMS analysis of morphologically identified *Salmo* sp. remains from archaeological sites will further refine our understanding of temporal and spatial changes in exploitation and availability.

10.5.2 Research Questions

While the potential for future work is compelling, the data presented in this thesis provides a valuable contribution to the world of ichthyoarchaeology , which connects directly to the research questions posed in Section 1.2 of the Introduction chapter. These questions have been answered throughout the thesis in various ways, but are repeated and the answers briefly summarized here.

How can archaeological *Salmo* sp. bones be identified better?

Are traditional zooarchaeological methods based on morphology reliable? What are the unique osteological characteristics of Salmo sp. fishes that distinguish them from other commonly exploited species in the North Sea region? In Chapter 3 traditional zooarchaeological methods for identifying *Salmo* sp. bones were discussed at length, with the conclusion that they are reliable at a higher taxonomic level for determining whether a given bone belongs to the *Salmo* genus, predominantly based on the unique "honeycomb" bone texture/patterning seen within the genus. For the most part, however, you cannot differentiate between *Salmo salar* and *Salmo trutta* bones based on morphology alone, due to the poor survival rates of diagnostic bones like the vomer or supraethmoid. Additionally, the majority of archaeologically-recovered *Salmo* sp. bones tend to be vertebrae, which are effectively indistinguishable between the two species of interest. **Is ZooMS analysis more reliable? Can ecotypes of Salmo sp. fish be identified using a combination of ZooMS and bulk stable isotope analysis? What are the isotopic difference between *Salmo* sp. fishes and other taxa, and are they as expected?** Chapters 3-5, 7 and 8 provided evidence about the reliability of zooarchaeology by mass spectrometry for differentiating between *Salmo salar* and *Salmo trutta* specimens. It is clear that this analytical method is highly effective at identifying archaeological fish bones to species, and Chapter 8 outlines a novel biomolecular method for identifying ecotypes within the species groups themselves. Finally, Chapter 8 demonstrates the ability to differentiate isotopically between Atlantic salmon and other groups of economically import archaeological fish species. The observed differences between these fish groups are in line with expectations based on modern isotopic data.

How did human exploitation of these fish change over time in the North Sea basin area?

Are there regional differences in exploitation visible through time? Are there different cultural or economic perceptions of Atlantic salmon, sea trout, and brown trout in the study area? The results of this thesis indicate that, while there are clear temporal differences in exploitation of *Salmo* sp. fishes visible in the archaeological materials through time, these were not regionally dependent but more closely tied to social class (see Chapter 7). These differences in exploitation patterns are closely related to the different cultural and economic perceptions of the fish identified throughout the thesis, with Atlantic salmon having historically been valued more as a signifier of "prestige" than either sea trout or freshwater trout (see Chapter 6). **Did human activity impact wild *Salmo* sp. populations through time, and are reported declines in population visible in the archaeological record? What does the archaeological "landscape" of *Salmo* sp. fishes look like in the medieval North Sea region?** Reviews of archaeological materials and historical documents (Chapters 6 and 7) did indicate that declines in the availability of salmon and trout are visible in the medieval North Sea basin area, but that there are other factors at play. It's likely that overfishing, anthropogenic climate change, and natural population fluctuations clashed to create a "perfect storm" of overall population decline in *Salmo* sp. fishes at various points in the broadly medieval period. There is some evidence for recovery in the past when human groups changed their actions, but the extent to which this is possible in the modern period is still unknown. The "archaeological landscape" of *Salmo* sp. fishes was most clearly reported in Chapter 7, but discussions relating to this question can be found throughout Chapters 6-9.

What differences are observable between ancient populations of Salmo sp. Fish and modern populations?

Are these differences regionally or temporally dependent? Can they be quantified isotopically? When exploring observable differences between ancient and modern populations of *Salmo* sp. fishes, it was clear that regional differences are far more common than temporal ones. There were clear regional differences between isotopic characteristics of salmon and sea trout, which formed the basis of rKIN analysis in Chapter 8. **What benefit is there to understanding past population baselines for Salmo sp. fisheries? Can archaeological fish remains contribute to modern conservation efforts for threatened species?** It is clear that there are benefits to exploring past populations of *Salmo* sp. fishes isotopically, and from a biogeographic perspective. Conclusions from this thesis establish baselines beyond the historic period, shedding light on pre-industrial characteristics of the populations in question. This, when coupled with the wider research into presence/absence patterns, provides a better understanding of how past populations may have recovered from reported declines. Finally, it is clear that the study of archaeological fish remains can contribute to modern conservation science, but that there are difficulties with integrating archaeological data into ecological research.

10.5.3 Conclusions

In summary, three overarching conclusions can be made about this thesis research as a whole, which each, in turn, have numerous inferences and opportunities for discussion.

First, this thesis has demonstrated that increases and decreases over time in *Salmo* sp. presence and absence are visible at medieval archaeological sites across the North Sea basin area. These increases coincide with an overall intensification of medieval exploitation of marine taxa seen around the 10th-11th century CE, which occurred concurrently with a medieval climate anomaly and increased urbanisation across northwestern Europe. Over-exploitation of *Salmo* sp. fish during this period on a regional level was complicated by the end of favourable climactic conditions, leading to a larger-than-normal decline in fish survival and return rates. When

coupled with anthropogenic environmental change, this led to regional population collapses. Decreases associated with these regional population collapses and fluctuations are visible in the archaeological record, however there is also evidence for disproportionate access to the remaining *Salmo* sp. stocks by ecclesiastical and high status groups across the study area.

Second, in addition to providing the largest to-date published dataset of archaeological Atlantic salmon and anadromous sea trout biomolecular data, this thesis provides further resolution about the palaeoecological characteristics of these taxa during the Medieval Period. Observed variations in bulk stable carbon and nitrogen isotope characteristics in Atlantic salmon are on a regional, but not temporal scale, with no evidence found for diachronic changes at sites with sufficiently large sample sizes and time-depth. Additionally, isotope niche space analysis of sea trout from distinct regions of the North Sea indicates observable differences between regional populations, and may reflect local fishing at the associated archaeological sites rather than long-distance trade. It is presumed that combined biomolecular analysis of more Atlantic salmon samples from the northern North Sea region may provide similar evidence for population-level differences (or similarities) in this ecotype group.

Finally, species identification based on morphology alone does not allow us to develop a clear understanding of both past human exploitation patterns and past species/ecotype biogeography. These thesis has demonstrated that ecotypes of *Salmo* sp. fish can be identified using a combination of bulk stable isotope and ZooMS analysis, which provides a cheaper alternative to methods which require DNA analysis. Through this method, it has become clear that anadromous sea trout were present at a higher-than-expected rate across medieval North Sea basin sites. When the affiliated grant funding for this thesis was sought, the main focus was on differentiating *Salmo salar* and *Salmo trutta*, with an explicit focus on the migratory and freshwater ecotypes of these species. It was assumed that most significant contribution would be to clarify and refine identification protocols for salmon and trout, and that this would clarify the roles of salmon and prestige fish and trout as a species of more utilitarian exploitation during the period. It was also generally assumed that the larger specimens identified morphologically as *Salmo* sp. would be identified primarily as Atlantic salmon and the smaller specimens and freshwater brown trout. However, the identification rates of migratory sea trout have been far higher than anticipated, and they actually make up the majority of finds at four out of the sixteen studied archaeological sites. The presence of sea trout at these sites further complicates our view of medieval salmon and trout fisheries, which do not appear to be as binary as previously thought. The unexpectedly common incidence of these fish on some medieval archaeological sites is not only evidence of their importance during the Medieval Period, but also another interesting direction of study in terms of past and present biogeography and conservation efforts.

The assemblages of sea trout documented here show that regional differences in availability of large migratory *Salmo* sp. fish may dictate which are predominant at a given site, and there may be potential regional or cultural preferences for one species over another. These three categories of conclusions span a methodologically, temporally, and geographically diverse set of data which provides useful insight into past consumption patterns and availability of economically and culturally important *Salmo* sp. taxa. The datasets and research presented here demonstrate that the archaeological record can pick up where the historical record leaves off, and confirm or contradict long-held assumptions about these so-called "King of Fish".

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Appendices

A North Sea Archaeological Salmo sp. Review Data

Imq_NSASR_number	Site Name	Date Start (CE)	Date End (CE)	Fish NISP	Salmo sp. NISP	Data Source	Salmo sp. Site?
Imq_NSASR_0001	Mindets tomt	1025	1125-1150	1035	0	NSS	no
Imq_NSASR_0002	Mindets tomt	1225	1350	3382	0	NSS	no
Imq_NSASR_0003	Mindets tomt	1350	1624	98	0	NSS	no
Imq_NSASR_0004	Søndre Felt	1350	1500	281	0	NSS	no
Imq_NSASR_0005	Dreggen	1170	1300	100	0	NSS	no
Imq_NSASR_0006	Dreggen	1300	1332	196	0	NSS	no
Imq_NSASR_0007	Dreggen	1332	1527	140	0	NSS	no
Imq_NSASR_0008	Kaupang	800	810	23	0	NSS	no
Imq_NSASR_0009	Kaupang	840	980	250	0	NSS	no
Imq_NSASR_0010	Kaupang	800	980	46	0	NSS	no
Imq_NSASR_0011	Kaupang	800	980	30	0	NSS	no
Imq_NSASR_0012	Kaupang	800	980	2	0	NSS	no
Imq_NSASR_0013	Marktplatz	601	1000	4	0	NSS	no
Imq_NSASR_0014	Marktplatz	1290	1310	5	0	NSS	no
Imq_NSASR_0015	Marktplatz	1301	1400	2	0	NSS	no
Imq_NSASR_0016	Langenstraße 5, Wertpapierbörse	1401	1500	4	0	NSS	no
Imq_NSASR_0017	Böttcherstraße	1201	1300	9	0	NSS	no
Imq_NSASR_0018	Langenstraße 31-35	1001	1200	1	0	NSS	no
Imq_NSASR_0019	Schlachte 36-38, Hotel Überfluss	1183	1200	104	0	NSS	no
Imq_NSASR_0020	Geeren, Radio Bremen	801	1300	9	0	NSS	no
Imq_NSASR_0021	Geeren, Radio Bremen	1201	1500	8	0	NSS	no
Imq_NSASR_0022	Carl-Ronning-Straße, Stern-Kino	1401	1500	233	0	NSS	no
Imq_NSASR_0023	Dionysius-Kirche	901	1000	1	0	NSS	no
Imq_NSASR_0024	Dionysius-Kirche	1301	1500	12	0	NSS	no
Imq_NSASR_0025	Dominikanerkloster Norden	1400	1450	31	0	NSS	no
Imq_NSASR_0026	Dominikanerkloster Norden	1401	1531	4	0	NSS	no
Imq_NSASR_0027	Dominikanerkloster Norden	1201	1600	8	0	NSS	no
Imq_NSASR_0028	Wrack Darss 40	1300	1310	7	0	NSS	no
Imq_NSASR_0029	Heilige Geestkapel	1350	1368	8	0	NSS	no
Imq_NSASR_0030	Heilige Geestkapel	1350	1368	356	0	NSS	no
Imq_NSASR_0031	Heilige Geestkapel	1368	1368	3	0	NSS	no
Imq_NSASR_0032	Heilige Geestkapel	1350	1470	22	0	NSS	no
Imq_NSASR_0033	Hopmarkt	1475	1500	4	0	NSS	no
Imq_NSASR_0034	Hopmarkt	1475	1500	525	0	NSS	no
Imq_NSASR_0035	Hopmarkt	1475	1500	64	0	NSS	no
Imq_NSASR_0036	Hopmarkt	1475	1500	1347	0	NSS	no
Imq_NSASR_0037	Hopmarkt	1475	1500	41	0	NSS	no
Imq_NSASR_0038	Hopmarkt	1475	1500	527	0	NSS	no
Imq_NSASR_0039	Hopmarkt	1475	1500	345	0	NSS	no
Imq_NSASR_0040	Hopmarkt	1475	1500	60	0	NSS	no
Imq_NSASR_0041	Hopmarkt	1475	1500	285	0	NSS	no
Imq_NSASR_0042	Hopmarkt	1475	1500	463	0	NSS	no
Imq_NSASR_0043	Hopmarkt	1475	1500	222	0	NSS	no
Imq_NSASR_0044	Hopmarkt	1475	1500	639	0	NSS	no
Imq_NSASR_0045	Hopmarkt	1300	1400	4	0	NSS	no
Imq_NSASR_0046	Hopmarkt	1300	1400	3	0	NSS	no
Imq_NSASR_0047	Hopmarkt	1300	1400	8	0	NSS	no
Imq_NSASR_0048	Hopmarkt	1475	1525	99	0	NSS	no
Imq_NSASR_0049	Hopmarkt	1475	1525	87	0	NSS	no
Imq_NSASR_0050	Hopmarkt	1475	1525	263	0	NSS	no
Imq_NSASR_0051	Hopmarkt	1475	1525	2	0	NSS	no
Imq_NSASR_0052	Hopmarkt	1475	1525	20	0	NSS	no
Imq_NSASR_0053	Hopmarkt	1475	1525	57	0	NSS	no
Imq_NSASR_0054	Hopmarkt	1475	1525	138	0	NSS	no
Imq_NSASR_0055	Oude Vismarkt	1300	1400	57	0	NSS	no
Imq_NSASR_0056	Pontstraat parking	1300	1500	7	0	NSS	no
Imq_NSASR_0057	Priester Daensplein	1200	1400	6	0	NSS	no
Imq_NSASR_0058	Priester Daensplein	1200	1400	11	0	NSS	no
Imq_NSASR_0059	Priester Daensplein	1300	1500	2	0	NSS	no
Imq_NSASR_0060	Priester Daensplein	1300	1500	2	0	NSS	no
Imq_NSASR_0061	Priester Daensplein	1300	1500	6	0	NSS	no
Imq_NSASR_0062	Priester Daensplein	1300	1500	1	0	NSS	no
Imq_NSASR_0063	Stadhuis	1175	1225	12	0	NSS	no
Imq_NSASR_0064	Stadhuis	1175	1225	7	0	NSS	no
Imq_NSASR_0065	Stadhuis	1100	1150	83	0	NSS	no
Imq_NSASR_0066	Stadhuis	1175	1250	1	0	NSS	no
Imq_NSASR_0067	Stadhuis	1200	1300	27	0	NSS	no
Imq_NSASR_0068	Stadhuis	1203	1300	1677	0	NSS	no
Imq_NSASR_0069	Stadhuis	1325	1375	2	0	NSS	no
Imq_NSASR_0070	Stadhuis	1325	1375	18	0	NSS	no
Imq_NSASR_0071	Stadhuis	1325	1375	404	0	NSS	no

lmq_NSASR_0072	Sint-Martensplein	1125	1175	1	0	NSS	no
lmq_NSASR_0073	Woestijne	1475	1525	7	0	NSS	no
lmq_NSASR_0074	Woestijne	1475	1525	200	0	NSS	no
lmq_NSASR_0075	Woestijne	1475	1525	87	0	NSS	no
lmq_NSASR_0076	Woestijne	1475	1525	112	0	NSS	no
lmq_NSASR_0077	Woestijne	1475	1525	33	0	NSS	no
lmq_NSASR_0078	Woestijne	1475	1525	3	0	NSS	no
lmq_NSASR_0079	Woestijne	1475	1525	92	0	NSS	no
lmq_NSASR_0080	Woestijne	1475	1525	12	0	NSS	no
lmq_NSASR_0081	Woestijne	1475	1525	53	0	NSS	no
lmq_NSASR_0082	Woestijne	1475	1525	18	0	NSS	no
lmq_NSASR_0083	Woestijne	1475	1525	1	0	NSS	no
lmq_NSASR_0084	Woestijne	1475	1525	6	0	NSS	no
lmq_NSASR_0085	Woestijne	1475	1525	51	0	NSS	no
lmq_NSASR_0086	Woestijne	1475	1525	34	0	NSS	no
lmq_NSASR_0087	Burchtgracht	1300	1400	10	0	NSS	no
lmq_NSASR_0088	Burchtgracht	1300	1400	217	0	NSS	no
lmq_NSASR_0089	Stadsparking	1000	1200	4	0	NSS	no
lmq_NSASR_0090	No site name	1100	1200	1	0	NSS	no
lmq_NSASR_0091	No site name	1100	1200	12	0	NSS	no
lmq_NSASR_0092	Assenede 831	1100	1200	35	0	NSS	no
lmq_NSASR_0093	Parc communal	1300	1400	863	0	NSS	no
lmq_NSASR_0094	Prinsenhof	1250	1350	1	0	NSS	no
lmq_NSASR_0095	Prinsenhof	1250	1350	2	0	NSS	no
lmq_NSASR_0096	Prinsenhof	1250	1350	3	0	NSS	no
lmq_NSASR_0097	Prinsenhof	1200	1400	32	0	NSS	no
lmq_NSASR_0098	Prinsenhof	1300	1400	39	0	NSS	no
lmq_NSASR_0099	Prinsenhof	1300	1400	1259	0	NSS	no
lmq_NSASR_0100	Prinsenhof	1300	1400	931	0	NSS	no
lmq_NSASR_0101	Prinsenhof	1300	1400	3	0	NSS	no
lmq_NSASR_0102	Prinsenhof	1300	1500	2	0	NSS	no
lmq_NSASR_0103	Prinsenhof	1300	1500	505	0	NSS	no
lmq_NSASR_0104	Prinsenhof	1300	1500	11	0	NSS	no
lmq_NSASR_0105	Arme Klaren	1350	1400	34	0	NSS	no
lmq_NSASR_0106	Arme Klaren	1350	1400	202	0	NSS	no
lmq_NSASR_0107	Arme Klaren	1350	1400	12	0	NSS	no
lmq_NSASR_0108	Arme Klaren	1350	1400	5	0	NSS	no
lmq_NSASR_0109	Arme Klaren	1350	1400	48	0	NSS	no
lmq_NSASR_0110	Arme Klaren	1350	1400	140	0	NSS	no
lmq_NSASR_0111	Arme Klaren	1350	1400	19	0	NSS	no
lmq_NSASR_0112	Arme Klaren	1350	1400	35	0	NSS	no
lmq_NSASR_0113	Arme Klaren	1350	1400	49	0	NSS	no
lmq_NSASR_0114	Arme Klaren	1350	1400	119	0	NSS	no
lmq_NSASR_0115	Arme Klaren	1350	1400	16	0	NSS	no
lmq_NSASR_0116	Arme Klaren	1350	1400	8	0	NSS	no
lmq_NSASR_0117	Arme Klaren	1350	1400	158	0	NSS	no
lmq_NSASR_0118	Arme Klaren	1350	1400	308	0	NSS	no
lmq_NSASR_0119	Arme Klaren	1350	1400	4	0	NSS	no
lmq_NSASR_0120	Arme Klaren	1350	1400	62	0	NSS	no
lmq_NSASR_0121	Arme Klaren	1350	1400	188	0	NSS	no
lmq_NSASR_0122	Arme Klaren	1350	1400	9	0	NSS	no
lmq_NSASR_0123	Arme Klaren	1350	1400	13	0	NSS	no
lmq_NSASR_0124	Arme Klaren	1350	1400	35	0	NSS	no
lmq_NSASR_0125	Arme Klaren	1350	1400	138	0	NSS	no
lmq_NSASR_0126	Arme Klaren	1350	1400	7	0	NSS	no
lmq_NSASR_0127	Arme Klaren	1350	1400	37	0	NSS	no
lmq_NSASR_0128	Arme Klaren	1350	1400	154	0	NSS	no
lmq_NSASR_0129	Arme Klaren	1350	1400	19	0	NSS	no
lmq_NSASR_0130	Arme Klaren	1350	1400	5	0	NSS	no
lmq_NSASR_0131	Arme Klaren	1350	1400	161	0	NSS	no
lmq_NSASR_0132	Arme Klaren	1350	1400	314	0	NSS	no
lmq_NSASR_0133	Arme Klaren	1350	1400	12	0	NSS	no
lmq_NSASR_0134	Arme Klaren	1375	1425	33	0	NSS	no
lmq_NSASR_0135	Arme Klaren	1375	1425	228	0	NSS	no
lmq_NSASR_0136	Arme Klaren	1375	1425	24	0	NSS	no
lmq_NSASR_0137	Eenmansstraat	1275	1425	67	0	NSS	no
lmq_NSASR_0138	Hotel Traviata	1200	1500	260	0	NSS	no
lmq_NSASR_0139	Hotel Traviata	1200	1600	59	0	NSS	no
lmq_NSASR_0140	Hotel Traviata	1200	1600	195	0	NSS	no
lmq_NSASR_0141	Rijke Klarenwijk	1250	1350	14	0	NSS	no
lmq_NSASR_0142	Sint-Katelijnewijk	1325	1375	19	0	NSS	no
lmq_NSASR_0143	Sint-Katelijnewijk	1350	1425	9	0	NSS	no

lmq_NSASR_0144	Sint-Katelijnewijk	1400	1500	6	0	NSS	no
lmq_NSASR_0145	Villers en Dinantstraat	1200	1250	3	0	NSS	no
lmq_NSASR_0146	Villers en Dinantstraat	1275	1325	3	0	NSS	no
lmq_NSASR_0147	Villers en Dinantstraat	1325	1375	2	0	NSS	no
lmq_NSASR_0148	Villers en Dinantstraat	1350	1425	5	0	NSS	no
lmq_NSASR_0149	Villers en Dinantstraat	1200	1250	2	0	NSS	no
lmq_NSASR_0150	Villers en Dinantstraat	1200	1300	20	0	NSS	no
lmq_NSASR_0151	Villers en Dinantstraat	1250	1325	2	0	NSS	no
lmq_NSASR_0152	Villers en Dinantstraat	1225	1275	681	0	NSS	no
lmq_NSASR_0153	Villers en Dinantstraat	1275	1350	7	0	NSS	no
lmq_NSASR_0154	Villers en Dinantstraat	1300	1350	7	0	NSS	no
lmq_NSASR_0155	Zuidstraat	1300	1600	77	0	NSS	no
lmq_NSASR_0156	Zuidstraat	1200	1500	6	0	NSS	no
lmq_NSASR_0157	Zuidstraat	1300	1600	2	0	NSS	no
lmq_NSASR_0158	Zuidstraat	1300	1600	1	0	NSS	no
lmq_NSASR_0159	Saint Salvatorsabbey	1100	1300	2	0	NSS	no
lmq_NSASR_0160	Saint Salvatorsabbey	1100	1300	21	0	NSS	no
lmq_NSASR_0161	Saint Salvatorsabbey	1400	1500	11	0	NSS	no
lmq_NSASR_0162	Saint Salvatorsabbey	1350	1450	109	0	NSS	no
lmq_NSASR_0163	Saint Salvatorsabbey	1350	1450	102	0	NSS	no
lmq_NSASR_0164	Castrum	975	1025	44	0	NSS	no
lmq_NSASR_0165	Castrum	975	1025	22	0	NSS	no
lmq_NSASR_0166	Portus	975	1025	10	0	NSS	no
lmq_NSASR_0167	Belfortstraat	1100	1200	170	0	NSS	no
lmq_NSASR_0168	Belfortstraat	1100	1200	220	0	NSS	no
lmq_NSASR_0169	Kammerstraat	1100	1200	12	0	NSS	no
lmq_NSASR_0170	Nieuwe Beestenmarkt	700	800	15	0	NSS	no
lmq_NSASR_0171	Sint-Baafsplein 8	1100	1200	48	0	NSS	no
lmq_NSASR_0172	Sint-Baafsplein 8	1100	1200	540	0	NSS	no
lmq_NSASR_0173	Sint-Baafsplein 8	1100	1200	325	0	NSS	no
lmq_NSASR_0174	St-Michiels	1200	1300	29	0	NSS	no
lmq_NSASR_0175	St-Michiels	1200	1300	1	0	NSS	no
lmq_NSASR_0176	St-Michiels	1000	1200	192	0	NSS	no
lmq_NSASR_0177	St-Michiels	1000	1200	2	0	NSS	no
lmq_NSASR_0178	St-Michiels	1200	1500	232	0	NSS	no
lmq_NSASR_0179	St-Michiels	1200	1500	20	0	NSS	no
lmq_NSASR_0180	St-Michiels	1400	1600	122	0	NSS	no
lmq_NSASR_0181	St-Michiels	1400	1600	16	0	NSS	no
lmq_NSASR_0182	Tweekerkenstraat	900	1100	88	0	NSS	no
lmq_NSASR_0183	Tweekerkenstraat	900	1100	111	0	NSS	no
lmq_NSASR_0184	Wijzemansstraat	1250	1325	3	0	NSS	no
lmq_NSASR_0185	Wijzemansstraat	1250	1325	26	0	NSS	no
lmq_NSASR_0186	Wijzemansstraat	1250	1325	12	0	NSS	no
lmq_NSASR_0187	Wijzemansstraat	1250	1325	1	0	NSS	no
lmq_NSASR_0188	Wijzemansstraat	1250	1325	9	0	NSS	no
lmq_NSASR_0189	Wijzemansstraat	1250	1325	3	0	NSS	no
lmq_NSASR_0190	Wijzemansstraat	1100	1225	30	0	NSS	no
lmq_NSASR_0191	Wijzemansstraat	1100	1225	86	0	NSS	no
lmq_NSASR_0192	Wijzemansstraat	1100	1225	49	0	NSS	no
lmq_NSASR_0193	Wijzemansstraat	1100	1225	30	0	NSS	no
lmq_NSASR_0194	Wijzemansstraat	1100	1225	11	0	NSS	no
lmq_NSASR_0195	Wijzemansstraat	1100	1225	3	0	NSS	no
lmq_NSASR_0196	Wijzemansstraat	1200	1300	1	0	NSS	no
lmq_NSASR_0197	Wijzemansstraat	1200	1300	5	0	NSS	no
lmq_NSASR_0198	Wijzemansstraat	1200	1300	2	0	NSS	no
lmq_NSASR_0199	Wijzemansstraat	1100	1225	2	0	NSS	no
lmq_NSASR_0200	Wijzemansstraat	1100	1225	19	0	NSS	no
lmq_NSASR_0201	Wijzemansstraat	1100	1225	12	0	NSS	no
lmq_NSASR_0202	Veldstraat	1100	1200	1	0	NSS	no
lmq_NSASR_0203	Veldstraat	1300	1400	1	0	NSS	no
lmq_NSASR_0204	Veldstraat	1400	1500	134	0	NSS	no
lmq_NSASR_0205	Zwarte laag	1175	1200	57	0	NSS	no
lmq_NSASR_0206	Zwarte laag	1175	1200	33	0	NSS	no
lmq_NSASR_0207	Zwarte laag	1175	1200	243	0	NSS	no
lmq_NSASR_0208	Zwarte laag	1175	1200	15	0	NSS	no
lmq_NSASR_0209	Zwarte laag	1150	1175	36	0	NSS	no
lmq_NSASR_0210	Zwarte laag	1150	1175	81	0	NSS	no
lmq_NSASR_0211	Zwarte laag	1150	1175	274	0	NSS	no
lmq_NSASR_0212	Zwarte laag	1150	1175	41	0	NSS	no
lmq_NSASR_0213	Zwarte laag	1125	1150	21	0	NSS	no
lmq_NSASR_0214	Zwarte laag	1125	1150	37	0	NSS	no
lmq_NSASR_0215	Zwarte laag	1125	1150	185	0	NSS	no

lmq_NSASR_0216	Zwarte laag	1125	1150	23	0	NSS	no
lmq_NSASR_0217	Zwarte laag	1100	1125	25	0	NSS	no
lmq_NSASR_0218	Zwarte laag	1100	1125	42	0	NSS	no
lmq_NSASR_0219	Zwarte laag	1100	1125	187	0	NSS	no
lmq_NSASR_0220	Zwarte laag	1100	1125	25	0	NSS	no
lmq_NSASR_0221	Zwarte laag	1025	1050	26	0	NSS	no
lmq_NSASR_0222	Zwarte laag	1025	1050	129	0	NSS	no
lmq_NSASR_0223	Zwarte laag	1025	1050	10	0	NSS	no
lmq_NSASR_0224	Zwarte laag	1012	1037	3	0	NSS	no
lmq_NSASR_0225	Zwarte laag	1012	1037	24	0	NSS	no
lmq_NSASR_0226	Zwarte laag	1012	1037	15	0	NSS	no
lmq_NSASR_0227	Zwarte laag	1000	1025	10	0	NSS	no
lmq_NSASR_0228	Zwarte laag	1000	1025	30	0	NSS	no
lmq_NSASR_0229	Zwarte laag	1000	1025	132	0	NSS	no
lmq_NSASR_0230	Zwarte laag	1000	1025	32	0	NSS	no
lmq_NSASR_0231	Zwarte laag	987	1012	2	0	NSS	no
lmq_NSASR_0232	Zwarte laag	987	1012	17	0	NSS	no
lmq_NSASR_0233	Zwarte laag	987	1012	108	0	NSS	no
lmq_NSASR_0234	Zwarte laag	987	1012	15	0	NSS	no
lmq_NSASR_0235	Zwarte laag	975	1000	3	0	NSS	no
lmq_NSASR_0236	Zwarte laag	975	1000	9	0	NSS	no
lmq_NSASR_0237	Zwarte laag	975	1000	101	0	NSS	no
lmq_NSASR_0238	Zwarte laag	975	1000	20	0	NSS	no
lmq_NSASR_0239	Zwarte laag	950	975	1	0	NSS	no
lmq_NSASR_0240	Zwarte laag	950	975	15	0	NSS	no
lmq_NSASR_0241	Zwarte laag	950	975	126	0	NSS	no
lmq_NSASR_0242	Zwarte laag	950	975	21	0	NSS	no
lmq_NSASR_0243	Zwarte laag	937	962	10	0	NSS	no
lmq_NSASR_0244	Zwarte laag	937	962	36	0	NSS	no
lmq_NSASR_0245	Zwarte laag	937	962	8	0	NSS	no
lmq_NSASR_0246	Oude Markt	1275	1325	4	0	NSS	no
lmq_NSASR_0247	HII/P3b	1400	1500	693	0	NSS	no
lmq_NSASR_0248	H87/P10	1400	1500	370	0	NSS	no
lmq_NSASR_0249	Lakenhalle	1200	1300	25	0	NSS	no
lmq_NSASR_0250	No site name	1400	1425	37	0	NSS	no
lmq_NSASR_0251	No site name	1400	1425	3697	0	NSS	no
lmq_NSASR_0252	Hof ter Hille	1050	1150	95	0	NSS	no
lmq_NSASR_0253	Hof ter Hille	1000	1100	34	0	NSS	no
lmq_NSASR_0254	Hof ter Hille	1000	1150	393	0	NSS	no
lmq_NSASR_0255	Hof ter Hille	1000	1150	612	0	NSS	no
lmq_NSASR_0256	Hof ter Hille	1000	1150	2218	0	NSS	no
lmq_NSASR_0257	Hof ter Hille	900	1100	5	0	NSS	no
lmq_NSASR_0258	Hof ter Hille	900	1100	1	0	NSS	no
lmq_NSASR_0259	Hof ter Hille	1025	1150	8	0	NSS	no
lmq_NSASR_0260	Hof ter Hille	1150	1200	107	0	NSS	no
lmq_NSASR_0261	Hof ter Hille	900	1100	1	0	NSS	no
lmq_NSASR_0262	Hof ter Hille	900	1150	1	0	NSS	no
lmq_NSASR_0263	Hof ter Hille	900	1100	73	0	NSS	no
lmq_NSASR_0264	Hof ter Hille	900	1100	56	0	NSS	no
lmq_NSASR_0265	Hof ter Hille	900	1000	15	0	NSS	no
lmq_NSASR_0266	Hof ter Hille	875	1025	1	0	NSS	no
lmq_NSASR_0267	Hof ter Hille	900	950	1698	0	NSS	no
lmq_NSASR_0268	Hof ter Hille	900	1100	4	0	NSS	no
lmq_NSASR_0269	Hof ter Hille	1000	1100	102	0	NSS	no
lmq_NSASR_0270	Franse dwangburcht	1415	1550	2	0	NSS	no
lmq_NSASR_0271	OLV hospitaal	1350	1450	21	0	NSS	no
lmq_NSASR_0272	Schouwburgplein	1150	1225	5	0	NSS	no
lmq_NSASR_0273	Schouwburgplein	1150	1225	3	0	NSS	no
lmq_NSASR_0274	Schouwburgplein	1150	1225	4	0	NSS	no
lmq_NSASR_0275	Abdij van Herkenrode	1200	1300	39	0	NSS	no
lmq_NSASR_0276	Abdij van Herkenrode	1200	1300	108	0	NSS	no
lmq_NSASR_0277	Abdij van Herkenrode	1450	1525	31	0	NSS	no
lmq_NSASR_0278	Abdij van Herkenrode	1450	1525	224	0	NSS	no
lmq_NSASR_0279	Abdij van Herkenrode	1450	1525	18	0	NSS	no
lmq_NSASR_0280	Chateau - LC9	1000	1100	2	0	NSS	no
lmq_NSASR_0281	Oude Werf	650	1025	11	0	NSS	no
lmq_NSASR_0282	Oude Werf	650	1025	65	0	NSS	no
lmq_NSASR_0283	Oude Werf	650	1025	115	0	NSS	no
lmq_NSASR_0284	Vesaliusstraat	1300	1400	2	0	NSS	no
lmq_NSASR_0285	Vesaliusstraat	1300	1400	21	0	NSS	no
lmq_NSASR_0286	Vesaliusstraat	1300	1400	52	0	NSS	no
lmq_NSASR_0287	Grote Markt	1200	1400	17	0	NSS	no

Imq_NSASR_0288	Burcht	1275	1350	175	0	NSS	no
Imq_NSASR_0289	Burcht	1275	1350	18	0	NSS	no
Imq_NSASR_0290	Ganzendries	1275	1325	129	0	NSS	no
Imq_NSASR_0291	Ganzendries	1275	1325	300	0	NSS	no
Imq_NSASR_0292	Ganzendries	1275	1325	13	0	NSS	no
Imq_NSASR_0293	Ganzendries	1275	1325	641	0	NSS	no
Imq_NSASR_0294	Ganzendries	1275	1325	25	0	NSS	no
Imq_NSASR_0295	Ganzendries	1275	1325	99	0	NSS	no
Imq_NSASR_0296	Ganzendries	1275	1325	148	0	NSS	no
Imq_NSASR_0297	K 42	1400	1425	4	0	NSS	no
Imq_NSASR_0298	Kazerne Dossin	1325	1350	252	0	NSS	no
Imq_NSASR_0299	Kazerne Dossin	1325	1350	1289	0	NSS	no
Imq_NSASR_0300	Kazerne Dossin	1325	1350	65	0	NSS	no
Imq_NSASR_0301	Kazerne Dossin	1325	1350	325	0	NSS	no
Imq_NSASR_0302	Kazerne Dossin	1275	1325	133	0	NSS	no
Imq_NSASR_0303	Kazerne Dossin	1275	1325	128	0	NSS	no
Imq_NSASR_0304	Kazerne Dossin	1325	1375	59	0	NSS	no
Imq_NSASR_0305	Kazerne Dossin	1325	1375	1930	0	NSS	no
Imq_NSASR_0306	Kazerne Dossin	1325	1375	1945	0	NSS	no
Imq_NSASR_0307	Kazerne Dossin	1325	1375	26	0	NSS	no
Imq_NSASR_0308	Kazerne Dossin	1325	1375	171	0	NSS	no
Imq_NSASR_0309	Kazerne Dossin	1325	1375	242	0	NSS	no
Imq_NSASR_0310	Kazerne Dossin	1325	1375	35	0	NSS	no
Imq_NSASR_0311	Lamot	800	1200	26	0	NSS	no
Imq_NSASR_0312	Lamot	800	1200	52	0	NSS	no
Imq_NSASR_0313	Lamot	800	1200	37	0	NSS	no
Imq_NSASR_0314	Lamot	800	1200	7	0	NSS	no
Imq_NSASR_0315	Lamot	800	1200	334	0	NSS	no
Imq_NSASR_0316	Lamot	800	1200	560	0	NSS	no
Imq_NSASR_0317	Lamot	800	1200	329	0	NSS	no
Imq_NSASR_0318	Lamot	800	1200	229	0	NSS	no
Imq_NSASR_0319	Lamot	800	1200	150	0	NSS	no
Imq_NSASR_0320	Lamot	800	1200	163	0	NSS	no
Imq_NSASR_0321	Lamot	1050	1150	2	0	NSS	no
Imq_NSASR_0322	Lamot	1050	1150	14	0	NSS	no
Imq_NSASR_0323	Lamot	1050	1150	9	0	NSS	no
Imq_NSASR_0324	Lamot	1050	1150	16	0	NSS	no
Imq_NSASR_0325	Lamot	1050	1150	22	0	NSS	no
Imq_NSASR_0326	Lamot	1050	1150	27	0	NSS	no
Imq_NSASR_0327	Lamot	1050	1150	24	0	NSS	no
Imq_NSASR_0328	Lamot	1050	1150	9	0	NSS	no
Imq_NSASR_0329	Steen	1275	1325	362	0	NSS	no
Imq_NSASR_0330	Steen	1275	1325	144	0	NSS	no
Imq_NSASR_0331	Steen	1275	1325	1474	0	NSS	no
Imq_NSASR_0332	Steen	1275	1325	178	0	NSS	no
Imq_NSASR_0333	Steen	1275	1325	34	0	NSS	no
Imq_NSASR_0334	Steen	1275	1325	1173	0	NSS	no
Imq_NSASR_0335	Steen	1275	1325	41	0	NSS	no
Imq_NSASR_0336	No site name	1200	1500	254	0	NSS	no
Imq_NSASR_0337	Chateau des comtes Mechelen	1000	1100	9	0	NSS	no
Imq_NSASR_0338	Chateau des comtes Mechelen	1000	1100	255	0	NSS	no
Imq_NSASR_0339	Chateau des comtes Monnikerede	1275	1325	315	0	NSS	no
Imq_NSASR_0340	Chateau des comtes Namur	1300	1500	92	0	NSS	no
Imq_NSASR_0341	Chateau des comtes Namur	1000	1200	10	0	NSS	no
Imq_NSASR_0342	Grognon	1150	1300	19	0	NSS	no
Imq_NSASR_0343	Grognon	1150	1300	8	0	NSS	no
Imq_NSASR_0344	Grognon	1150	1300	174	0	NSS	no
Imq_NSASR_0345	Grognon	1200	1400	5	0	NSS	no
Imq_NSASR_0346	Grognon	1300	1500	93	0	NSS	no
Imq_NSASR_0347	Grognon	1300	1500	268	0	NSS	no
Imq_NSASR_0348	Grognon	1475	1525	31	0	NSS	no
Imq_NSASR_0349	Grognon	1475	1525	52	0	NSS	no
Imq_NSASR_0350	Grognon	1475	1525	412	0	NSS	no
Imq_NSASR_0351	Grognon	1100	1200	19	0	NSS	no
Imq_NSASR_0352	Grognon	1100	1200	8	0	NSS	no
Imq_NSASR_0353	Grognon	1100	1200	174	0	NSS	no
Imq_NSASR_0354	Grognon	1475	1525	32	0	NSS	no
Imq_NSASR_0355	Grognon	1475	1525	52	0	NSS	no
Imq_NSASR_0356	Grognon	1475	1525	413	0	NSS	no
Imq_NSASR_0357	Mussenpad	600	800	1	0	NSS	no
Imq_NSASR_0358	Mussenpad	600	800	35	0	NSS	no
Imq_NSASR_0359	Abdij van Sint-Cornelius en Sint-Cyprianus	1100	1200	43	0	NSS	no

Imq_NSASR_0360	Abdij van Sint-Cornelius en Sint-Cyprianus	1100	1200	64	0	NSS	no
Imq_NSASR_0361	Abdij van Sint-Cornelius en Sint-Cyprianus	1100	1200	74	0	NSS	no
Imq_NSASR_0362	Abdij van Sint-Cornelius en Sint-Cyprianus	1100	1200	38	0	NSS	no
Imq_NSASR_0363	Mijnplein	1400	1600	578	0	NSS	no
Imq_NSASR_0364	Mijnplein	1400	1600	97	0	NSS	no
Imq_NSASR_0365	Mijnplein	1400	1600	2328	0	NSS	no
Imq_NSASR_0366	Mijnplein	1400	1600	560	0	NSS	no
Imq_NSASR_0367	Mijnplein	1400	1600	49	0	NSS	no
Imq_NSASR_0368	Mijnplein	1400	1600	280	0	NSS	no
Imq_NSASR_0369	Mijnplein	1400	1600	21	0	NSS	no
Imq_NSASR_0370	Mijnplein	1400	1600	45	0	NSS	no
Imq_NSASR_0371	Mijnplein	1400	1600	104	0	NSS	no
Imq_NSASR_0372	Mijnplein	1400	1600	59	0	NSS	no
Imq_NSASR_0373	Mijnplein	1400	1600	16	0	NSS	no
Imq_NSASR_0374	Mijnplein	1400	1600	1981	0	NSS	no
Imq_NSASR_0375	Lalaign	1250	1500	21	0	NSS	no
Imq_NSASR_0376	Rijke Klaren	1475	1525	4	0	NSS	no
Imq_NSASR_0377	Rijke Klaren	1475	1525	195	0	NSS	no
Imq_NSASR_0378	Rijke Klaren	1475	1525	89	0	NSS	no
Imq_NSASR_0379	No site name	700	900	3	0	NSS	no
Imq_NSASR_0380	Boudelo-abdij	1300	1600	13	0	NSS	no
Imq_NSASR_0381	Boudelo-abdij	1300	1600	37	0	NSS	no
Imq_NSASR_0382	Boudelo-abdij	1300	1600	41	0	NSS	no
Imq_NSASR_0383	Boudelo-abdij	1300	1600	23	0	NSS	no
Imq_NSASR_0384	No site name	1300	1600	37	0	NSS	no
Imq_NSASR_0385	No site name	1300	1600	20	0	NSS	no
Imq_NSASR_0386	No site name	1300	1600	11	0	NSS	no
Imq_NSASR_0387	No site name	1300	1600	193	0	NSS	no
Imq_NSASR_0388	No site name	1300	1600	303	0	NSS	no
Imq_NSASR_0389	No site name	1300	1600	68	0	NSS	no
Imq_NSASR_0390	No site name	1300	1600	15	0	NSS	no
Imq_NSASR_0391	No site name	1300	1600	14	0	NSS	no
Imq_NSASR_0392	No site name	1300	1600	2076	0	NSS	no
Imq_NSASR_0393	No site name	1300	1600	1775	0	NSS	no
Imq_NSASR_0394	Cloître	500	1100	28	0	NSS	no
Imq_NSASR_0395	Cloître	500	700	84	0	NSS	no
Imq_NSASR_0396	Cloître	500	700	168	0	NSS	no
Imq_NSASR_0397	t Klooster	1450	1550	12	0	NSS	no
Imq_NSASR_0398	t Klooster	1450	1550	116	0	NSS	no
Imq_NSASR_0399	Molenstraat/Oude Vest	1400	1500	2	0	NSS	no
Imq_NSASR_0400	Molenstraat/Oude Vest	1400	1500	1377	0	NSS	no
Imq_NSASR_0401	Burseplein	1200	1400	58	0	NSS	no
Imq_NSASR_0402	Van de Perrehuis	1325	1400	408	0	NSS	no
Imq_NSASR_0403	Van de Perrehuis	1325	1575	12	0	NSS	no
Imq_NSASR_0404	Van de Perrehuis	1400	1450	25	0	NSS	no
Imq_NSASR_0405	Jansstraat 46/Gerechtsgebouw	1100	1800	372	0	NSS	no
Imq_NSASR_0406	Tiellandtweg	450	1050	51	0	NSS	no
Imq_NSASR_0407	Kasteel van Eindhoven	1420	1486	13	0	NSS	no
Imq_NSASR_0408	De Dorpen	1100	1300	64	0	NSS	no
Imq_NSASR_0409	Huis Malburg	1050	1249	214	0	NSS	no
Imq_NSASR_0410	Huis Malburg	1250	1499	22	0	NSS	no
Imq_NSASR_0411	Huis ter Kleef	1400	1573	16	0	NSS	no
Imq_NSASR_0412	Huis ter Kleef	1400	1573	17	0	NSS	no
Imq_NSASR_0413	Huis ter Kleef	1400	1573	85	0	NSS	no
Imq_NSASR_0414	Huis ter Kleef	1400	1573	105	0	NSS	no
Imq_NSASR_0415	Huis ter Kleef	1400	1573	10	0	NSS	no
Imq_NSASR_0416	Huis ter Kleef	1400	1573	21	0	NSS	no
Imq_NSASR_0417	Huis ter Kleef	1200	1300	87	0	NSS	no
Imq_NSASR_0418	Huis ter Kleef	1200	1300	57	0	NSS	no
Imq_NSASR_0419	Huis ter Kleef	1200	1300	30	0	NSS	no
Imq_NSASR_0420	Huis ter Kleef	1400	1500	7	0	NSS	no
Imq_NSASR_0421	Huis ter Kleef	1400	1500	77	0	NSS	no
Imq_NSASR_0422	Huis ter Kleef	1400	1500	43	0	NSS	no
Imq_NSASR_0423	Huis ter Kleef	1250	1573	178	0	NSS	no
Imq_NSASR_0424	Huis ter Kleef	1250	1573	316	0	NSS	no
Imq_NSASR_0425	Huis ter Kleef	1250	1573	37	0	NSS	no
Imq_NSASR_0426	Huis ter Kleef	1250	1573	188	0	NSS	no
Imq_NSASR_0427	St. Nicolaasgasthuis	1300	1400	2348	0	NSS	no
Imq_NSASR_0428	St. Nicolaasgasthuis	1400	1550	373	0	NSS	no
Imq_NSASR_0429	Berghuijskazerne	1000	1250	2	0	NSS	no
Imq_NSASR_0430	Berghuijskazerne	1200	1350	31	0	NSS	no
Imq_NSASR_0431	Berghuijskazerne	1350	1400	15	0	NSS	no

Imq_NSASR_0432	Berghuijskazerne	1400	1560	107	0	NSS	no
Imq_NSASR_0433	Berghuijskazerne	1400	1560	501	0	NSS	no
Imq_NSASR_0434	De Beyerd	1450	1550	85	0	NSS	no
Imq_NSASR_0435	Maasboulevard	1150	1360	2	0	NSS	no
Imq_NSASR_0436	Maasboulevard	1400	1600	160	0	NSS	no
Imq_NSASR_0437	Winston bioscoop	1275	1300	16	0	NSS	no
Imq_NSASR_0438	Winston bioscoop	1300	1400	28	0	NSS	no
Imq_NSASR_0439	Winston bioscoop	1400	1500	21	0	NSS	no
Imq_NSASR_0440	Winston bioscoop	1200	1280	2	0	NSS	no
Imq_NSASR_0441	Winston bioscoop	1280	1310	23	0	NSS	no
Imq_NSASR_0442	Winston bioscoop	1280	1310	880	0	NSS	no
Imq_NSASR_0443	Winston bioscoop	1310	1350	1	0	NSS	no
Imq_NSASR_0444	Winston bioscoop	1310	1350	99	0	NSS	no
Imq_NSASR_0445	Winston bioscoop	1350	1400	6	0	NSS	no
Imq_NSASR_0446	Winston bioscoop	1400	1575	2	0	NSS	no
Imq_NSASR_0447	Winston bioscoop	1400	1575	57	0	NSS	no
Imq_NSASR_0448	Gat in de Markt 01.101	891	1000	6	0	NSS	no
Imq_NSASR_0449	Gat in de Markt 01.101	1000	1050	1	0	NSS	no
Imq_NSASR_0450	Gat in de Markt 01.101	1000	1050	19	0	NSS	no
Imq_NSASR_0451	Gat in de Markt 01.101	1050	1170	1	0	NSS	no
Imq_NSASR_0452	Gat in de Markt 01.101	1050	1170	13	0	NSS	no
Imq_NSASR_0453	Gat in de Markt 01.101	1170	1350	458	0	NSS	no
Imq_NSASR_0454	Gat in de Markt 01.101	1170	1350	256	0	NSS	no
Imq_NSASR_0455	Stenen Kamer/Linge	1050	1250	115	0	NSS	no
Imq_NSASR_0456	Stenen Kamer/Linge	1250	1550	29	0	NSS	no
Imq_NSASR_0457	A2-sportpark Strijland	575	675	33	0	NSS	no
Imq_NSASR_0458	A2-sportpark Strijland	650	725	381	0	NSS	no
Imq_NSASR_0459	A2-sportpark Strijland	715	775	511	0	NSS	no
Imq_NSASR_0460	Bethlehemstraat - Voogdijstraat	1400	1500	22	0	NSS	no
Imq_NSASR_0461	Bethlehemstraat - Voogdijstraat	1200	1400	2	0	NSS	no
Imq_NSASR_0462	Elfhuizen	1300	1400	177	0	NSS	no
Imq_NSASR_0463	Huys te Werve	1400	1600	73	0	NSS	no
Imq_NSASR_0464	Huys te Werve	1400	1600	112	0	NSS	no
Imq_NSASR_0465	Huys te Werve	1400	1600	88	0	NSS	no
Imq_NSASR_0466	Bolwerk	1300	1350	3	0	NSS	no
Imq_NSASR_0467	Bolwerk	1350	1450	373	0	NSS	no
Imq_NSASR_0468	Bolwerk	1375	1438	1214	0	NSS	no
Imq_NSASR_0469	Bolwerk	1438	1500	35	0	NSS	no
Imq_NSASR_0470	Bruggestraat 8-10	1300	1350	76	0	NSS	no
Imq_NSASR_0471	Bruggestraat 8-10	1200	1300	479	0	NSS	no
Imq_NSASR_0472	Bruggestraat 8-10	1300	1400	1032	0	NSS	no
Imq_NSASR_0473	Bruggestraat 8-10	1400	1500	263	0	NSS	no
Imq_NSASR_0474	Kerkstraat	1175	1232	390	0	NSS	no
Imq_NSASR_0475	Kerkstraat	1232	1575	3	0	NSS	no
Imq_NSASR_0476	Achterom	1350	1450	1000	0	NSS	no
Imq_NSASR_0477	Achterom	1450	1500	38	0	NSS	no
Imq_NSASR_0478	Het Regthuys	1350	1450	2036	0	NSS	no
Imq_NSASR_0479	Groot Olmen	475	675	2	0	NSS	no
Imq_NSASR_0480	Groot Olmen	700	750	2	0	NSS	no
Imq_NSASR_0481	Groot Olmen	750	850	1	0	NSS	no
Imq_NSASR_0482	Groot Olmen	700	800	33	0	NSS	no
Imq_NSASR_0483	Voorstraat 244, Mijnsherenherberg	1300	1585	388	0	NSS	no
Imq_NSASR_0484	Voorstraat 244, Mijnsherenherberg	1300	1585	283	0	NSS	no
Imq_NSASR_0485	Middelhof	1400	1600	28	0	NSS	no
Imq_NSASR_0486	Middelhof	1400	1600	132	0	NSS	no
Imq_NSASR_0487	Middelhof	1400	1600	2	0	NSS	no
Imq_NSASR_0488	Middelhof	1400	1600	4	0	NSS	no
Imq_NSASR_0489	Middelhof	1400	1600	418	0	NSS	no
Imq_NSASR_0490	Middelhof	1400	1600	785	0	NSS	no
Imq_NSASR_0491	Dorestad	725	899	2	0	NSS	no
Imq_NSASR_0492	Westnieuwlandgebied	1300	1450	37	0	NSS	no
Imq_NSASR_0493	Westnieuwlandgebied	1400	1500	223	0	NSS	no
Imq_NSASR_0494	Westnieuwlandgebied	1400	1525	74	0	NSS	no
Imq_NSASR_0495	Hoogeland Zuidweg	700	1000	40	0	NSS	no
Imq_NSASR_0496	Korte Begijnestraat	1400	1450	12	0	NSS	no
Imq_NSASR_0497	Korte Begijnestraat	1400	1450	68	0	NSS	no
Imq_NSASR_0498	Korte Begijnestraat	1400	1450	47	0	NSS	no
Imq_NSASR_0499	Korte Begijnestraat	1400	1450	50	0	NSS	no
Imq_NSASR_0500	Krijtstraat	1300	1425	3	0	NSS	no
Imq_NSASR_0501	Krijtstraat	1300	1425	58	0	NSS	no
Imq_NSASR_0502	Langestraat 115/117	1400	1500	27	0	NSS	no
Imq_NSASR_0503	City Building (Binnenrotte)	1000	1100	2	0	NSS	no

lmq_NSASR_0504	City Building (Binnenrotte)	1000	1100	49	0	NSS	no
lmq_NSASR_0505	Langestraat 3-5	1350	1450	107	0	NSS	no
lmq_NSASR_0506	Langestraat 3-5	1350	1450	151	0	NSS	no
lmq_NSASR_0507	Speelmansstraat	1000	1400	131	0	NSS	no
lmq_NSASR_0508	St. Jacobsstraat	1000	1400	96	0	NSS	no
lmq_NSASR_0509	Marnixlaan	1392	1580	5	0	NSS	no
lmq_NSASR_0510	Marnixlaan	1392	1580	81	0	NSS	no
lmq_NSASR_0511	Marnixlaan	1392	1580	616	0	NSS	no
lmq_NSASR_0512	Marnixlaan	1392	1580	19	0	NSS	no
lmq_NSASR_0513	Marnixlaan	1392	1580	234	0	NSS	no
lmq_NSASR_0514	Marnixlaan	1392	1580	61	0	NSS	no
lmq_NSASR_0515	Sint Janskerkhof	1175	1250	6	0	NSS	no
lmq_NSASR_0516	Sint Janskerkhof	1250	1275	6	0	NSS	no
lmq_NSASR_0517	Sint Janskerkhof	1275	1325	17	0	NSS	no
lmq_NSASR_0518	Sint Janskerkhof	1300	1425	109	0	NSS	no
lmq_NSASR_0519	Rijksweg 9	1250	1400	72	0	NSS	no
lmq_NSASR_0520	St. Agnesklooster	1400	1500	216	0	NSS	no
lmq_NSASR_0521	Regulierenklooster	1430	1550	141	0	NSS	no
lmq_NSASR_0522	d'Engelsche Boomgaert	1275	1351	140	0	NSS	no
lmq_NSASR_0523	Helenius de Cockschool	1300	1500	31	0	NSS	no
lmq_NSASR_0524	Ganzenmarkt	1425	1500	34	0	NSS	no
lmq_NSASR_0525	Breestraat/Peperstraat	1200	1500	3	0	NSS	no
lmq_NSASR_0526	Breestraat/Peperstraat	1250	1560	40	0	NSS	no
lmq_NSASR_0527	Breestraat/Peperstraat	1250	1450	3	0	NSS	no
lmq_NSASR_0528	Breestraat/Peperstraat	1250	1450	58	0	NSS	no
lmq_NSASR_0529	Breestraat/Peperstraat	1250	1500	16	0	NSS	no
lmq_NSASR_0530	Klokkenveld	1392	1580	34	0	NSS	no
lmq_NSASR_0531	Klokkenveld	1392	1580	3	0	NSS	no
lmq_NSASR_0532	Klokkenveld	1392	1580	37	0	NSS	no
lmq_NSASR_0533	Klokkenveld	1392	1580	18	0	NSS	no
lmq_NSASR_0534	Klokkenveld	1392	1580	6	0	NSS	no
lmq_NSASR_0535	Klokkenveld	1392	1580	24	0	NSS	no
lmq_NSASR_0536	Klokkenveld	1392	1580	3	0	NSS	no
lmq_NSASR_0537	Klokkenveld	1392	1580	5	0	NSS	no
lmq_NSASR_0538	Keizershof	1475	1500	148	0	NSS	no
lmq_NSASR_0539	Plantage	750	850	106	0	NSS	no
lmq_NSASR_0540	Kastanjelaan	700	900	49	0	NSS	no
lmq_NSASR_0541	Kastanjelaan	700	900	47	0	NSS	no
lmq_NSASR_0542	Kastanjelaan	525	1250	4	0	NSS	no
lmq_NSASR_0543	Nieuw Rhijngeest-zuid	475	725	3	0	NSS	no
lmq_NSASR_0544	Minderbroedersklooster	1375	1400	117	0	NSS	no
lmq_NSASR_0545	Minderbroedersklooster	1400	1425	74	0	NSS	no
lmq_NSASR_0546	Brooklands	500	700	188	0	NSS	no
lmq_NSASR_0547	East Kent Access Road EXEKA09	500	1500	1242	0	NSS	no
lmq_NSASR_0548	St. John's	1100	1500	620	0	NSS	no
lmq_NSASR_0549	Sandwick North	600	1600	32	0	NSS	no
lmq_NSASR_0550	Sandwick North	1000	1200	355	0	NSS	no
lmq_NSASR_0551	Sandwick North	1000	1200	2176	0	NSS	no
lmq_NSASR_0552	Sandwick North	1100	1300	163	0	NSS	no
lmq_NSASR_0553	Sandwick North	1100	1300	713	0	NSS	no
lmq_NSASR_0554	Sandwick North	1200	1400	869	0	NSS	no
lmq_NSASR_0555	Sandwick	1150	1200	142	0	NSS	no
lmq_NSASR_0556	Sandwick	1150	1200	43	0	NSS	no
lmq_NSASR_0557	Sandwick	1200	1300	1096	0	NSS	no
lmq_NSASR_0558	Sandwick	1200	1300	171	0	NSS	no
lmq_NSASR_0559	Sandwick	1200	1300	39	0	NSS	no
lmq_NSASR_0560	Sandwick	1250	1400	1029	0	NSS	no
lmq_NSASR_0561	Sandwick	1250	1400	399	0	NSS	no
lmq_NSASR_0562	Scalloway	1300	1500	43	0	NSS	no
lmq_NSASR_0563	Scalloway	300	900	2	0	NSS	no
lmq_NSASR_0564	Scalloway	300	900	494	0	NSS	no
lmq_NSASR_0565	Scalloway	300	1000	765	0	NSS	no
lmq_NSASR_0566	Scalloway	1300	1500	4	0	NSS	no
lmq_NSASR_0567	St. Boniface	250	750	1329	0	NSS	no
lmq_NSASR_0568	St. Boniface	1100	1250	9279	0	NSS	no
lmq_NSASR_0569	St. Boniface	600	1600	1372	0	NSS	no
lmq_NSASR_0570	Quoygrew	900	1000	2786	0	NSS	no
lmq_NSASR_0571	Quoygrew	900	1000	1348	0	NSS	no
lmq_NSASR_0572	Quoygrew	1000	1300	3473	0	NSS	no
lmq_NSASR_0573	Quoygrew	1000	1300	3597	0	NSS	no
lmq_NSASR_0574	Quoygrew	1000	1200	3080	0	NSS	no
lmq_NSASR_0575	Quoygrew	1000	1200	1838	0	NSS	no

lmq_NSASR_0576	Quoygrew	1400	1600	5720	0	NSS	no
lmq_NSASR_0577	Quoygrew	1000	1200	297	0	NSS	no
lmq_NSASR_0578	Quoygrew	1000	1200	476	0	NSS	no
lmq_NSASR_0579	Quoygrew	1375	1425	159	0	NSS	no
lmq_NSASR_0580	Tuquoy	800	1200	4	0	NSS	no
lmq_NSASR_0581	Tuquoy	1050	1200	757	0	NSS	no
lmq_NSASR_0582	Tuquoy	1200	1600	1805	0	NSS	no
lmq_NSASR_0583	Tuquoy	1050	1250	20	0	NSS	no
lmq_NSASR_0584	Tuquoy	1050	1200	253	0	NSS	no
lmq_NSASR_0585	Tuquoy	1200	1400	297	0	NSS	no
lmq_NSASR_0586	Tuquoy	1200	1600	311	0	NSS	no
lmq_NSASR_0587	Tuquoy	800	1200	44	0	NSS	no
lmq_NSASR_0588	Tuquoy	1050	1250	99	0	NSS	no
lmq_NSASR_0589	Tuquoy	1050	1200	983	0	NSS	no
lmq_NSASR_0590	Tuquoy	1200	1400	4221	0	NSS	no
lmq_NSASR_0591	Brough of Birsay	300	1050	5	0	NSS	no
lmq_NSASR_0592	Brough of Birsay	640	880	3	0	NSS	no
lmq_NSASR_0593	Brough of Birsay	890	1190	32	0	NSS	no
lmq_NSASR_0594	Brough of Birsay	750	1600	46	0	NSS	no
lmq_NSASR_0595	Brough of Birsay	750	1600	448	0	NSS	no
lmq_NSASR_0596	Brough of Birsay	890	1190	22	0	NSS	no
lmq_NSASR_0597	Brough Road	300	1600	4	0	NSS	no
lmq_NSASR_0598	Brough Road	600	1100	360	0	NSS	no
lmq_NSASR_0599	Brough Road	600	1200	11	0	NSS	no
lmq_NSASR_0600	Brough Road	600	1100	255	0	NSS	no
lmq_NSASR_0601	Brough Road	600	1100	32	0	NSS	no
lmq_NSASR_0602	Brough Road	600	900	236	0	NSS	no
lmq_NSASR_0603	Brough Road	300	1600	19	0	NSS	no
lmq_NSASR_0604	Brough Road	300	1600	70	0	NSS	no
lmq_NSASR_0605	Brough Road	600	1100	13	0	NSS	no
lmq_NSASR_0606	Brough Road	300	1600	199	0	NSS	no
lmq_NSASR_0607	Brough Road	300	1600	18	0	NSS	no
lmq_NSASR_0608	Brough Road	600	1200	30	0	NSS	no
lmq_NSASR_0609	Brough Road	300	1600	9	0	NSS	no
lmq_NSASR_0610	Brough Road	600	1000	51	0	NSS	no
lmq_NSASR_0611	Beachview Burnside	1020	1320	25	0	NSS	no
lmq_NSASR_0612	Beachview Burnside	1020	1280	3	0	NSS	no
lmq_NSASR_0613	Beachview Burnside	1020	1280	5	0	NSS	no
lmq_NSASR_0614	Beachview Burnside	1020	1280	52	0	NSS	no
lmq_NSASR_0615	Beachview Burnside	1020	1280	70	0	NSS	no
lmq_NSASR_0616	Beachview Burnside	1020	1280	73	0	NSS	no
lmq_NSASR_0617	Beachview Burnside	1020	1280	29	0	NSS	no
lmq_NSASR_0618	Beachview Burnside	1020	1280	700	0	NSS	no
lmq_NSASR_0619	Beachview Burnside	1020	1280	7	0	NSS	no
lmq_NSASR_0620	Beachview Burnside	1020	1280	3	0	NSS	no
lmq_NSASR_0621	Beachview Burnside	1020	1280	70	0	NSS	no
lmq_NSASR_0622	Beachview Burnside	1020	1280	567	0	NSS	no
lmq_NSASR_0623	Beachview Burnside	1020	1280	20	0	NSS	no
lmq_NSASR_0624	Beachview Burnside	1000	1900	2	0	NSS	no
lmq_NSASR_0625	Beachview Studio	980	1206	16	0	NSS	no
lmq_NSASR_0626	Beachview Studio	1000	1300	1	0	NSS	no
lmq_NSASR_0627	Beachview Studio	1001	1410	105	0	NSS	no
lmq_NSASR_0628	Beachview Studio	1000	1300	3	0	NSS	no
lmq_NSASR_0629	Beachview Studio	1020	1280	32	0	NSS	no
lmq_NSASR_0630	Beachview Studio	1020	1280	2	0	NSS	no
lmq_NSASR_0631	Beachview Studio	1000	1300	18	0	NSS	no
lmq_NSASR_0632	Beachview Studio	1000	1300	817	0	NSS	no
lmq_NSASR_0633	Beachview Studio	1000	1300	45	0	NSS	no
lmq_NSASR_0634	Beachview Studio	900	1300	3	0	NSS	no
lmq_NSASR_0635	Beachview Studio	900	1300	161	0	NSS	no
lmq_NSASR_0636	Beachview Studio	900	1300	8	0	NSS	no
lmq_NSASR_0637	Beachview Studio	900	1300	6	0	NSS	no
lmq_NSASR_0638	Beachview Studio	900	1300	10	0	NSS	no
lmq_NSASR_0639	Beachview Studio	900	1300	8	0	NSS	no
lmq_NSASR_0640	Beachview Studio	900	1300	2	0	NSS	no
lmq_NSASR_0641	Beachview Studio	900	1300	209	0	NSS	no
lmq_NSASR_0642	Beachview Studio	1134	1280	2	0	NSS	no
lmq_NSASR_0643	Beachview Studio	1134	1280	1121	0	NSS	no
lmq_NSASR_0644	Beachview Studio	993	1220	69	0	NSS	no
lmq_NSASR_0645	Beachview Studio	900	1300	27	0	NSS	no
lmq_NSASR_0646	Beachview Studio	900	1300	140	0	NSS	no
lmq_NSASR_0647	Beachview Studio	1163	1300	139	0	NSS	no

lmq_NSASR_0648	Beachview Studio	900	1300	23	0	NSS	no
lmq_NSASR_0649	Beachview Studio	900	1300	2	0	NSS	no
lmq_NSASR_0650	Beachview Studio	990	1210	1115	0	NSS	no
lmq_NSASR_0651	Buckquoy	300	800	6	0	NSS	no
lmq_NSASR_0652	Buckquoy	300	800	4	0	NSS	no
lmq_NSASR_0653	Buckquoy	750	1050	2	0	NSS	no
lmq_NSASR_0654	Buckquoy	750	1050	40	0	NSS	no
lmq_NSASR_0655	Saevar Howe	750	950	98	0	NSS	no
lmq_NSASR_0656	Saevar Howe	750	950	122	0	NSS	no
lmq_NSASR_0657	Saevar Howe	750	950	153	0	NSS	no
lmq_NSASR_0658	Brough of Deerness	750	1050	2	0	NSS	no
lmq_NSASR_0659	Brough of Deerness	750	1900	7	0	NSS	no
lmq_NSASR_0660	Brough of Deerness	750	1900	32	0	NSS	no
lmq_NSASR_0661	Brough of Deerness	300	900	1	0	NSS	no
lmq_NSASR_0662	Brough of Deerness	750	1900	1	0	NSS	no
lmq_NSASR_0663	Skaill	750	1600	1981	0	NSS	no
lmq_NSASR_0664	Newark Bay	300	900	1	0	NSS	no
lmq_NSASR_0665	Newark Bay	600	1600	39	0	NSS	no
lmq_NSASR_0666	Newark Bay	600	1600	22	0	NSS	no
lmq_NSASR_0667	Newark Bay	600	1600	2	0	NSS	no
lmq_NSASR_0668	Earl's Bu	750	1200	16	0	NSS	no
lmq_NSASR_0669	Earl's Bu	1000	1200	43	0	NSS	no
lmq_NSASR_0670	Earl's Bu	970	1220	9	0	NSS	no
lmq_NSASR_0671	Earl's Bu	880	1160	16	0	NSS	no
lmq_NSASR_0672	Earl's Bu	1000	1200	189	0	NSS	no
lmq_NSASR_0673	Earl's Bu	1000	1200	39	0	NSS	no
lmq_NSASR_0674	Earl's Bu	990	1190	215	0	NSS	no
lmq_NSASR_0675	Earl's Bu	750	1200	71	0	NSS	no
lmq_NSASR_0676	Earl's Bu	1000	1200	120	0	NSS	no
lmq_NSASR_0677	Earl's Bu	1000	1200	28	0	NSS	no
lmq_NSASR_0678	Earl's Bu	970	1220	308	0	NSS	no
lmq_NSASR_0679	Robert’s Haven	1000	1300	16753	0	NSS	no
lmq_NSASR_0680	Robert’s Haven	750	1600	52	0	NSS	no
lmq_NSASR_0681	Robert’s Haven	1300	1600	301	0	NSS	no
lmq_NSASR_0682	Robert’s Haven	750	1600	85	0	NSS	no
lmq_NSASR_0683	Freswick	300	1050	334	0	NSS	no
lmq_NSASR_0684	Freswick	1000	1400	2161	0	NSS	no
lmq_NSASR_0685	Freswick	1100	1350	295	0	NSS	no
lmq_NSASR_0686	Advocates Close	1100	1300	158	0	NSS	no
lmq_NSASR_0687	Advocates Close	1100	1300	15	0	NSS	no
lmq_NSASR_0688	Berst Ness Knowe of Skea	300	900	667	0	NSS	no
lmq_NSASR_0689	Berst Ness Knowe of Skea	300	900	23	0	NSS	no
lmq_NSASR_0690	Berst Ness Knowe of Skea	300	900	92	0	NSS	no
lmq_NSASR_0691	Berst Ness Knowe of Skea	300	900	87	0	NSS	no
lmq_NSASR_0692	Berst Ness Knowe of Skea	300	900	25	0	NSS	no
lmq_NSASR_0693	Berst Ness Knowe of Skea	300	900	60	0	NSS	no
lmq_NSASR_0694	Berst Ness Knowe of Skea	1150	1450	8	0	NSS	no
lmq_NSASR_0695	Bon Accord	1200	1400	2805	0	NSS	no
lmq_NSASR_0696	Bon Accord	1200	1400	518	0	NSS	no
lmq_NSASR_0697	Bon Accord	1300	1500	373	0	NSS	no
lmq_NSASR_0698	Bon Accord	1200	1400	84	0	NSS	no
lmq_NSASR_0699	Bon Accord	1200	1400	90	0	NSS	no
lmq_NSASR_0700	Bon Accord	1300	1500	25	0	NSS	no
lmq_NSASR_0701	Bon Accord	1200	1400	11	0	NSS	no
lmq_NSASR_0702	Bon Accord	1200	1400	68	0	NSS	no
lmq_NSASR_0703	Bon Accord	1200	1500	4	0	NSS	no
lmq_NSASR_0704	Bon Accord	1200	1500	8	0	NSS	no
lmq_NSASR_0705	Bon Accord	1200	1400	34	0	NSS	no
lmq_NSASR_0706	Bon Accord	1200	1400	9	0	NSS	no
lmq_NSASR_0707	Bon Accord	1200	1500	5	0	NSS	no
lmq_NSASR_0708	Bon Accord	1200	1400	1	0	NSS	no
lmq_NSASR_0709	Stackelbrae	900	1300	6	0	NSS	no
lmq_NSASR_0710	Stackelbrae	900	1300	107	0	NSS	no
lmq_NSASR_0711	Perth High Street	800	1200	10	0	NSS	no
lmq_NSASR_0712	Perth High Street	1150	1200	164	0	NSS	no
lmq_NSASR_0713	Perth High Street	1150	1250	52	0	NSS	no
lmq_NSASR_0714	Perth High Street	1150	1300	4	0	NSS	no
lmq_NSASR_0715	Perth High Street	1200	1300	35	0	NSS	no
lmq_NSASR_0716	Perth High Street	1250	1350	80	0	NSS	no
lmq_NSASR_0717	Perth High Street	1300	1350	673	0	NSS	no
lmq_NSASR_0718	Perth High Street	800	1900	13	0	NSS	no
lmq_NSASR_0719	Perth High Street	800	1900	1	0	NSS	no

lmq_NSASR_0720	Perth High Street	1200	1250	2	0	NSS	no
lmq_NSASR_0721	Castle Hill Pumping Station	1031	1187	522	0	NSS	no
lmq_NSASR_0722	Castle Hill Pumping Station	1044	1223	3302	0	NSS	no
lmq_NSASR_0723	Castle Hill Pumping Station	1000	1600	212	0	NSS	no
lmq_NSASR_0724	Castle Hill Pumping Station	1000	1600	148	0	NSS	no
lmq_NSASR_0725	Castle Hill Pumping Station	1000	1600	264	0	NSS	no
lmq_NSASR_0726	Howe	300	1900	1	0	NSS	no
lmq_NSASR_0727	Castle Street	1200	1400	1	0	NSS	no
lmq_NSASR_0728	Castle Street	1350	1500	78	0	NSS	no
lmq_NSASR_0729	Castle Street	1400	1500	3	0	NSS	no
lmq_NSASR_0730	Castle Street	1400	1500	16	0	NSS	no
lmq_NSASR_0731	Castle Street	1400	1500	2	0	NSS	no
lmq_NSASR_0732	16-18 Netherkirkgate	1200	1400	3	0	NSS	no
lmq_NSASR_0733	16-18 Netherkirkgate	1200	1400	101	0	NSS	no
lmq_NSASR_0734	16-18 Netherkirkgate	1200	1400	495	0	NSS	no
lmq_NSASR_0735	16-18 Netherkirkgate	1350	1500	3	0	NSS	no
lmq_NSASR_0736	16-18 Netherkirkgate	1400	1500	70	0	NSS	no
lmq_NSASR_0737	30-46 Upperkirkgate	1100	1300	44	0	NSS	no
lmq_NSASR_0738	30-46 Upperkirkgate	1200	1400	15	0	NSS	no
lmq_NSASR_0739	30-46 Upperkirkgate	1400	1500	46	0	NSS	no
lmq_NSASR_0740	Gallowgate Middle School	1150	1300	256	0	NSS	no
lmq_NSASR_0741	45-75 Gallowgate	1225	1275	2	0	NSS	no
lmq_NSASR_0742	45-75 Gallowgate	1250	1375	534	0	NSS	no
lmq_NSASR_0743	45-75 Gallowgate	1375	1600	85	0	NSS	no
lmq_NSASR_0744	Kirk Ness	-100	1950	1	0	NSS	no
lmq_NSASR_0745	Kirk Ness	1100	1500	11	0	NSS	no
lmq_NSASR_0746	Holyrood	1300	1500	26	0	NSS	no
lmq_NSASR_0747	Holyrood	1300	1500	81	0	NSS	no
lmq_NSASR_0748	Inveresk Gate	1093	1603	1	0	NSS	no
lmq_NSASR_0749	Arbroath Abbey Visitor Centre	1200	1400	3	0	NSS	no
lmq_NSASR_0750	Arbroath Abbey Visitor Centre	1300	1500	130	0	NSS	no
lmq_NSASR_0751	Scatness	900	1900	221	0	NSS	no
lmq_NSASR_0752	Portmahomack	1200	1500	1823	0	NSS	no
lmq_NSASR_0753	St. Giles' Cathedral	1100	1300	1	0	NSS	no
lmq_NSASR_0754	St. Giles' Cathedral	1200	1400	15	0	NSS	no
lmq_NSASR_0755	St. Giles' Cathedral	1350	1550	64	0	NSS	no
lmq_NSASR_0756	Horse Cross	1100	1275	8	0	NSS	no
lmq_NSASR_0757	Horse Cross	1100	1400	11	0	NSS	no
lmq_NSASR_0758	Horse Cross	1150	1400	9	0	NSS	no
lmq_NSASR_0759	Kirk Site	1175	1225	337	0	NSS	no
lmq_NSASR_0760	Kirk Site	1175	1225	129	0	NSS	no
lmq_NSASR_0761	Kirk Site	1200	1300	77	0	NSS	no
lmq_NSASR_0762	Kirk Site	1200	1300	63	0	NSS	no
lmq_NSASR_0763	Kirk Site	1300	1500	945	0	NSS	no
lmq_NSASR_0764	Kirk Site	1300	1500	90	0	NSS	no
lmq_NSASR_0765	Kirk Site	1475	1525	163	0	NSS	no
lmq_NSASR_0766	Kirk Site	1475	1525	248	0	NSS	no
lmq_NSASR_0767	Inchaffray Abbey	1200	1300	1	0	NSS	no
lmq_NSASR_0768	Holyrood Road, Cannongate Backlands	1300	1600	4	0	NSS	no
lmq_NSASR_0769	Drum Castle	1300	1500	2	0	NSS	no
lmq_NSASR_0770	Brotchie's Steading	-390	1900	1	0	NSS	no
lmq_NSASR_0771	St Ethernan's Monastery	1100	1600	1754	0	NSS	no
lmq_NSASR_0772	St Ethernan's Monastery	400	1900	58	0	NSS	no
lmq_NSASR_0773	Cowgate	1000	1400	12	0	NSS	no
lmq_NSASR_0774	Cowgate	1300	1500	108	0	NSS	no
lmq_NSASR_0775	Spynie Palace	1200	1500	0	0	NSS	no
lmq_NSASR_0776	Jeffrey St	1200	1600	39	0	NSS	no
lmq_NSASR_0777	Bishop's Manor	1350	1500	84	0	NSS	no
lmq_NSASR_0778	Rattray	1150	1250	1	0	NSS	no
lmq_NSASR_0779	Rattray	1150	1250	3	0	NSS	no
lmq_NSASR_0780	Rattray	1200	1350	19	0	NSS	no
lmq_NSASR_0781	Rattray	1200	1500	34	0	NSS	no
lmq_NSASR_0782	Rattray	1200	1550	10	0	NSS	no
lmq_NSASR_0783	Rattray	1300	1500	65	0	NSS	no
lmq_NSASR_0784	Rattray	1300	1550	3	0	NSS	no
lmq_NSASR_0785	Rattray	1425	1550	3	0	NSS	no
lmq_NSASR_0786	Mine Howe	40	1900	55	0	NSS	no
lmq_NSASR_0787	Pool	300	900	1	0	NSS	no
lmq_NSASR_0788	Pool	300	900	7	0	NSS	no
lmq_NSASR_0789	Pool	300	900	1	0	NSS	no
lmq_NSASR_0790	Pool	200	800	3	0	NSS	no
lmq_NSASR_0791	Pool	300	900	2	0	NSS	no

lmq_NSASR_0792	Pool	430	870	61	0	NSS	no
lmq_NSASR_0793	Pool	650	1050	211	0	NSS	no
lmq_NSASR_0794	Pool	660	1030	4568	0	NSS	no
lmq_NSASR_0795	Pool	925	1200	818	0	NSS	no
lmq_NSASR_0796	Pool	925	1200	212	0	NSS	no
lmq_NSASR_0797	Pool	925	1200	308	0	NSS	no
lmq_NSASR_0798	Pool	970	1190	1464	0	NSS	no
lmq_NSASR_0799	Pool	1020	1220	2598	0	NSS	no
lmq_NSASR_0800	Old Scatness	525	900	1884	0	NSS	no
lmq_NSASR_0801	Old Scatness	800	1000	57	0	NSS	no
lmq_NSASR_0802	Old Scatness	825	1000	3928	0	NSS	no
lmq_NSASR_0803	Old Scatness	800	1000	5134	0	NSS	no
lmq_NSASR_0804	Old Scatness	825	1000	507	0	NSS	no
lmq_NSASR_0805	Old Scatness	800	1000	1947	0	NSS	no
lmq_NSASR_0806	1-3 High St, Seaford	1200	1350	24	0	Holmes 2017	no
lmq_NSASR_0807	113-119 High St	900	1000	35	0	Holmes 2017	no
lmq_NSASR_0808	113-119 High St	1200	1300	19	0	Holmes 2017	no
lmq_NSASR_0809	14 Farringdon St	1250	1400	1	0	Holmes 2017	no
lmq_NSASR_0810	14 Farringdon St	1400	1480	4	0	Holmes 2017	no
lmq_NSASR_0811	199 Borough High St	1150	1480	328	0	Holmes 2017	no
lmq_NSASR_0812	51-57 High St	1175	1300	13	0	Holmes 2017	no
lmq_NSASR_0813	52-54 Thames St	1250	1375	5	0	Holmes 2017	no
lmq_NSASR_0814	52-54 Thames St	1300	1600	1	0	Holmes 2017	no
lmq_NSASR_0815	67-69 St Thomas' St	1475	1550	1	0	Holmes 2017	no
lmq_NSASR_0816	7-8 Queen St	1075	1150	9	0	Holmes 2017	no
lmq_NSASR_0817	7-8 Queen St	1175	1175	29	0	Holmes 2017	no
lmq_NSASR_0818	79-80 St Aldates	950	1000	1	0	Holmes 2017	no
lmq_NSASR_0819	79-80 St Aldates	1075	1125	1	0	Holmes 2017	no
lmq_NSASR_0820	79-80 St Aldates	1150	1300	8	0	Holmes 2017	no
lmq_NSASR_0821	79-80 St Aldates	1300	1500	13	0	Holmes 2017	no
lmq_NSASR_0822	Abingdon West Central Redevelopment	1100	1500	302	0	Holmes 2017	no
lmq_NSASR_0823	Aldersgate	1000	1125	83	0	Holmes 2017	no
lmq_NSASR_0824	Aldersgate	1000	1200	46	0	Holmes 2017	no
lmq_NSASR_0825	Aldersgate	1200	1375	49	0	Holmes 2017	no
lmq_NSASR_0826	Aldersgate	1400	1500	6	0	Holmes 2017	no
lmq_NSASR_0827	Alton	1400	1500	13	0	Holmes 2017	no
lmq_NSASR_0828	Arundel House	1400	1550	8	0	Holmes 2017	no
lmq_NSASR_0829	Barton Court Farm	450	550	94	0	Holmes 2017	no
lmq_NSASR_0830	Battle Abbey	1100	1400	53	0	Holmes 2017	no
lmq_NSASR_0831	Billingsgate Buildings	900	1000	110	0	Holmes 2017	no
lmq_NSASR_0832	Brighton Hill South	1000	1400	1	0	Holmes 2017	no
lmq_NSASR_0833	Broad St,	1100	1325	13	0	Holmes 2017	no
lmq_NSASR_0834	Broad St,	1300	1400	7	0	Holmes 2017	no
lmq_NSASR_0835	Camber Castle	1543	1637	954	0	Holmes 2017	no
lmq_NSASR_0836	Chantry St	1200	1300	21	0	Holmes 2017	no
lmq_NSASR_0837	Chantry St	1400	1500	4	0	Holmes 2017	no
lmq_NSASR_0838	Chester Rd	1175	1325	13	0	Holmes 2017	no
lmq_NSASR_0839	Oxford Classics Centre	1200	1300	105	0	Holmes 2017	no
lmq_NSASR_0840	Cook St	700	800	253	0	Holmes 2017	no
lmq_NSASR_0841	Dean Court	1175	1200	1	0	Holmes 2017	no
lmq_NSASR_0842	Dean Court	1300	1500	1	0	Holmes 2017	no
lmq_NSASR_0843	Dean Court	1300	1500	192	0	Holmes 2017	no
lmq_NSASR_0844	Dorter Undercroft, Westminster Abbey	1050	1050	2	0	Holmes 2017	no
lmq_NSASR_0845	Easton La	600	1200	12	0	Holmes 2017	no
lmq_NSASR_0846	Eynsham Abbey	650	900	13	0	Holmes 2017	no
lmq_NSASR_0847	Eynsham Abbey	900	1000	6	0	Holmes 2017	no
lmq_NSASR_0848	Eynsham Abbey	1000	1100	6	0	Holmes 2017	no
lmq_NSASR_0849	Faccombe	1070	1204	2	0	Holmes 2017	no
lmq_NSASR_0850	Faccombe	1418	1430	3	0	Holmes 2017	no
lmq_NSASR_0851	Fennings Wharf	1000	1100	2	0	Holmes 2017	no
lmq_NSASR_0852	Fennings Wharf	1175	1500	1	0	Holmes 2017	no
lmq_NSASR_0853	Fletcher's Croft	1100	1300	2	0	Holmes 2017	no
lmq_NSASR_0854	Friar St	1100	1300	5	0	Holmes 2017	no
lmq_NSASR_0855	Gatehouse Nurseries	1375	1450	2	0	Holmes 2017	no
lmq_NSASR_0856	Graveyard Site	700	800	1	0	Holmes 2017	no
lmq_NSASR_0857	Harding's Field	1300	1350	11	0	Holmes 2017	no
lmq_NSASR_0858	Harding's Field	1375	1425	29	0	Holmes 2017	no
lmq_NSASR_0859	Harding's Field	1450	1500	14	0	Holmes 2017	no
lmq_NSASR_0860	Henly's Garage	900	1125	8	0	Holmes 2017	no
lmq_NSASR_0861	High St	1100	1200	1	0	Holmes 2017	no
lmq_NSASR_0862	Oxford Hinxey Hall	1000	1100	9	0	Holmes 2017	no
lmq_NSASR_0863	Holywell Priory	1150	1350	21	0	Holmes 2017	no

lmq_NSASR_0864	Hospital of St. Mary of Ospringe	1230	1470	30	0	Holmes 2017	no
lmq_NSASR_0865	Ivy St and Brown St	1250	1600	621	0	Holmes 2017	no
lmq_NSASR_0866	Oxford Lincoln College	1100	1400	97	0	Holmes 2017	no
lmq_NSASR_0867	Market	400	600	87	0	Holmes 2017	no
lmq_NSASR_0868	Market	900	1125	20	0	Holmes 2017	no
lmq_NSASR_0869	Market	1100	1300	12	0	Holmes 2017	no
lmq_NSASR_0870	Mount House	1175	1225	13	0	Holmes 2017	no
lmq_NSASR_0871	Mount House	1250	1300	59	0	Holmes 2017	no
lmq_NSASR_0872	National Gallery Basement	700	800	16	0	Holmes 2017	no
lmq_NSASR_0873	Nonsuch Palace	1538	1688	320	0	Holmes 2017	no
lmq_NSASR_0874	North St Car Park	600	1200	54	0	Holmes 2017	no
lmq_NSASR_0875	Peabody Site	700	800	67	0	Holmes 2017	no
lmq_NSASR_0876	Pepper Hill Ln	1000	1100	15	0	Holmes 2017	no
lmq_NSASR_0877	Pevensey Castle	1000	1200	27	0	Holmes 2017	no
lmq_NSASR_0878	Pevensey Castle	1200	1400	17	0	Holmes 2017	no
lmq_NSASR_0879	Poole	1200	1500	99	0	Holmes 2017	no
lmq_NSASR_0880	Poole	1200	1500	29	0	Holmes 2017	no
lmq_NSASR_0881	Quilter's Vault	1100	1200	4	0	Holmes 2017	no
lmq_NSASR_0882	Quilter's Vault	1200	1300	2	0	Holmes 2017	no
lmq_NSASR_0883	Rookery Hill	400	500	2	0	Holmes 2017	no
lmq_NSASR_0884	Ropetackle	1250	1375	1690	0	Holmes 2017	no
lmq_NSASR_0885	Shavards Farm	700	800	261	0	Holmes 2017	no
lmq_NSASR_0886	SOU 29	1400	1500	38	0	Holmes 2017	no
lmq_NSASR_0887	Southampton Castle	1200	1375	122	0	Holmes 2017	no
lmq_NSASR_0888	St Gregory's Priory	1150	1250	28	0	Holmes 2017	no
lmq_NSASR_0889	St Gregory's Priory	1250	1375	117	0	Holmes 2017	no
lmq_NSASR_0890	St Gregory's Priory	1375	1525	245	0	Holmes 2017	no
lmq_NSASR_0891	St Mary Spital	1050	1197	42	0	Holmes 2017	no
lmq_NSASR_0892	St Mary Spital	1197	1235	3	0	Holmes 2017	no
lmq_NSASR_0893	St Mary Spital	1235	1280	11	0	Holmes 2017	no
lmq_NSASR_0894	St Mary Spital	1280	1320	495	0	Holmes 2017	no
lmq_NSASR_0895	St Mary Spital	1350	1400	1344	0	Holmes 2017	no
lmq_NSASR_0896	St Mary Spital	1538	1620	207	0	Holmes 2017	no
lmq_NSASR_0897	St Michael's	1100	1300	770	0	Holmes 2017	no
lmq_NSASR_0898	St Michael's	1300	1500	383	0	Holmes 2017	no
lmq_NSASR_0899	St Saviour	1200	1300	13	0	Holmes 2017	no
lmq_NSASR_0900	St. Andrews church vicarage	1000	1300	1	0	Holmes 2017	no
lmq_NSASR_0901	Stert St	1100	1300	44	0	Holmes 2017	no
lmq_NSASR_0902	Sub-vault of Westminster Abbey	1050	1100	7	0	Holmes 2017	no
lmq_NSASR_0903	Sub-vault of Westminster Abbey	1175	1225	347	0	Holmes 2017	no
lmq_NSASR_0904	The Foundry	1400	1425	69	0	Holmes 2017	no
lmq_NSASR_0905	Trill Mill Stream	900	1000	1	0	Holmes 2017	no
lmq_NSASR_0906	Trinity Chequer	1250	1500	134	0	Holmes 2017	no
lmq_NSASR_0907	Victoria Rd	800	900	9	0	Holmes 2017	no
lmq_NSASR_0908	Victoria Rd	900	1125	151	0	Holmes 2017	no
lmq_NSASR_0909	Victoria Rd	1175	1325	144	0	Holmes 2017	no
lmq_NSASR_0910	Victoria Rd	1375	1400	34	0	Holmes 2017	no
lmq_NSASR_0911	Western Suburb	900	950	174	0	Holmes 2017	no
lmq_NSASR_0912	Western Suburb	1075	1150	548	0	Holmes 2017	no
lmq_NSASR_0913	Western Suburb	1175	1350	502	0	Holmes 2017	no
lmq_NSASR_0914	Wickham Glebe	1100	1300	10	0	Holmes 2017	no
lmq_NSASR_0915	Wickham Glebe	1300	1500	2	0	Holmes 2017	no
lmq_NSASR_0916	Winchester Palace	950	1150	217	0	Holmes 2017	no
lmq_NSASR_0917	Winchester Palace	1200	1525	220	0	Holmes 2017	no
lmq_NSASR_0918	Yarnton	700	1100	1	0	Holmes 2017	no
lmq_NSASR_0919	Alms Ln 76	1400	1525	164	0	Albarella & Pirnie	no
lmq_NSASR_0920	Alms Ln 76	1250	1400	151	0	Albarella & Pirnie	no
lmq_NSASR_0921	Alms Ln 76	1150	1250	61	0	Albarella & Pirnie	no
lmq_NSASR_0922	Alms Ln 76	1000	1100	21	0	Albarella & Pirnie	no
lmq_NSASR_0923	Black Lion Hill	1400	1500	2	0	Albarella & Pirnie	no
lmq_NSASR_0924	Black Lion Hill	1100	1300	2	0	Albarella & Pirnie	no
lmq_NSASR_0925	Bury St Edmunds AML 3270	500	1000	120	0	Albarella & Pirnie	no
lmq_NSASR_0926	Castle Mall AML 85/97	800	1100	280	0	Albarella & Pirnie	no
lmq_NSASR_0927	Castle Mall AML 85/97	1400	1500	294	0	Albarella & Pirnie	no
lmq_NSASR_0928	Castle Mall AML 85/97	1000	1100	142	0	Albarella & Pirnie	no
lmq_NSASR_0929	Castle Mall AML 85/97	800	1100	99	0	Albarella & Pirnie	no
lmq_NSASR_0930	Chopdike Drove GOS22	800	1100	1	0	Albarella & Pirnie	no
lmq_NSASR_0931	Coslany St AML 86/97	1100	1300	2	0	Albarella & Pirnie	no
lmq_NSASR_0932	County Museum (Aylesbury)	1250	1400	28	0	Albarella & Pirnie	no
lmq_NSASR_0933	County Museum (Aylesbury)	1150	1250	10	0	Albarella & Pirnie	no
lmq_NSASR_0934	Dragon Hall, King Street 97-98	1000	1100	1478	0	Albarella & Pirnie	no
lmq_NSASR_0935	Dragon Hall, King Street 97-98	1100	1200	557	0	Albarella & Pirnie	no

lmq_NSASR_0936	Dragon Hall, King Street 97-98	1200	1300	731	0	Albarella & Pirnie	no
lmq_NSASR_0937	Dragon Hall, King Street 97-98	1275	1325	527	0	Albarella & Pirnie	no
lmq_NSASR_0938	Dragon Hall, King Street 97-98	1000	1100	41	0	Albarella & Pirnie	no
lmq_NSASR_0939	Dragon Hall, King Street 97-98	1100	1200	12	0	Albarella & Pirnie	no
lmq_NSASR_0940	Dragon Hall, King Street 97-98	1200	1300	66	0	Albarella & Pirnie	no
lmq_NSASR_0941	Dragon Hall, King Street 97-98	1275	1325	37	0	Albarella & Pirnie	no
lmq_NSASR_0942	Dragon Hall, King Street 97-98	1350	1550	8	0	Albarella & Pirnie	no
lmq_NSASR_0943	Fishergate (Norwich) 85	1000	1100	1	0	Albarella & Pirnie	no
lmq_NSASR_0944	Fishergate (Norwich) 85	1100	1200	13	0	Albarella & Pirnie	no
lmq_NSASR_0945	Fishergate (Norwich) 85	1000	1100	344	0	Albarella & Pirnie	no
lmq_NSASR_0946	Gorhambury 72-82	500	1500	8	0	Albarella & Pirnie	no
lmq_NSASR_0947	Hay Green TSC23	650	850	13	0	Albarella & Pirnie	no
lmq_NSASR_0948	Heigham Street 75-76	1200	1300	1	0	Albarella & Pirnie	no
lmq_NSASR_0949	Heigham Street 75-76	1375	1425	1	0	Albarella & Pirnie	no
lmq_NSASR_0950	Heigham Street 75-76	1475	1575	12	0	Albarella & Pirnie	no
lmq_NSASR_0951	Hertford Castle (outer bailey)	1200	1500	6	0	Albarella & Pirnie	no
lmq_NSASR_0952	Ipswich AML 4578	900	1100	2039	0	Albarella & Pirnie	no
lmq_NSASR_0953	Lincoln sites (bones)	1000	1100	29	0	Albarella & Pirnie	no
lmq_NSASR_0954	Northampton AML 4589	400	650	5	0	Albarella & Pirnie	no
lmq_NSASR_0955	Northampton Green AML 4511	1100	1300	16	0	Albarella & Pirnie	no
lmq_NSASR_0956	Owston Abbey	500	1500	27	0	Albarella & Pirnie	no
lmq_NSASR_0957	Shackerley Mound 81	500	1500	4	0	Albarella & Pirnie	no
lmq_NSASR_0958	Tempsford Park	1250	1400	1	0	Albarella & Pirnie	no
lmq_NSASR_0959	The Shires 88 AML 56/92 Little Ln	1400	1500	17	0	Albarella & Pirnie	no
lmq_NSASR_0960	The Shires 88 AML 56/92 Little Ln	1400	1500	139	0	Albarella & Pirnie	no
lmq_NSASR_0961	The Shires 88 AML 56/92 Little Ln	1350	1400	16	0	Albarella & Pirnie	no
lmq_NSASR_0962	The Shires 88 AML 56/92 St Peter's	1400	1500	9	0	Albarella & Pirnie	no
lmq_NSASR_0963	The Shires 88 AML 56/92 St Peter's	1250	1400	4	0	Albarella & Pirnie	no
lmq_NSASR_0964	The Shires 88 AML 56/92 St Peter's	1400	1500	325	0	Albarella & Pirnie	no
lmq_NSASR_0965	The Shires 88 AML 56/92 St Peter's	1250	1400	63	0	Albarella & Pirnie	no
lmq_NSASR_0966	Thetford 64-70	1000	1100	9	0	Albarella & Pirnie	no
lmq_NSASR_0967	Thetford 64-70	900	1000	10	0	Albarella & Pirnie	no
lmq_NSASR_0968	Third Drove GOS16	400	1000	1	0	Albarella & Pirnie	no
lmq_NSASR_0969	West Cotton 85-89 AML 17/94	1250	1400	1	0	Albarella & Pirnie	no
lmq_NSASR_0970	West Cotton 85-89 AML 17/94	1150	1250	2	0	Albarella & Pirnie	no
lmq_NSASR_0971	West Cotton 85-89 AML 17/94	1250	1400	2	0	Albarella & Pirnie	no
lmq_NSASR_0972	West Cotton 85-89 AML 17/94	1150	1250	1	0	Albarella & Pirnie	no
lmq_NSASR_0973	West Cotton 85-89 AML 17/94	800	1100	1	0	Albarella & Pirnie	no
lmq_NSASR_0974	West Stow (animal husbandry)	400	650	3	0	Albarella & Pirnie	no
lmq_NSASR_0975	Whitefriars St 79	1150	1250	93	0	Albarella & Pirnie	no
lmq_NSASR_0976	Whitefriars St 79	800	1100	50	0	Albarella & Pirnie	no
lmq_NSASR_0977	Woolmonger St 94-7 (St Peters Walk)	800	1100	20	0	Albarella & Pirnie	no
lmq_NSASR_0978	Woolmonger St 94-7 (St Peters Walk)	1000	1100	88	0	Albarella & Pirnie	no
lmq_NSASR_0979	Woolmonger St 94-7 (St Peters Walk)	1000	1100	12	0	Albarella & Pirnie	no
lmq_NSASR_0980	Woolmonger St 94-7 (St Peters Walk)	500	1500	3	0	Albarella & Pirnie	no
lmq_NSASR_0981	Bedern	1275	1400	791	0	LMQ	no
lmq_NSASR_0982	St. Magnus	700	1350	35	0	LMQ	no
lmq_NSASR_0983	Lindisfarne	900	1530	70	0	LMQ	no
lmq_NSASR_0984	Southgate	1100	1200	3973	0	LMQ	no
lmq_NSASR_0985	Church Close	600	1525	2018	0	LMQ	no
lmq_NSASR_0986	Wharram Percy	1200	1500	246	0	LMQ	no
lmq_NSASR_0987	Holy Island Village, Phases 1-3	500	1500	50	0	LMQ	no
lmq_NSASR_0988	Crown Court	1250	1600	1333	0	LMQ	no
lmq_NSASR_0989	Crown Court	1300	1600	1505	0	LMQ	no
lmq_NSASR_0990	41-49 Walmgate	1050	1550	710	0	LMQ	no
lmq_NSASR_0991	Rue de la Collegiale	1100	1350	252	0	Clavel 2001	no
lmq_NSASR_0992	Rue de la Collegiale	1200	1300	65	0	Clavel 2001	no
lmq_NSASR_0993	Moreaucourt Priory	1300	1600	1123	0	Clavel 2001	no
lmq_NSASR_0994	Chateau Thierry	1200	1300	925	0	Clavel 2001	no
lmq_NSASR_0995	Compiegne - l'Hopital general	800	1500	117	0	Clavel 2001	no
lmq_NSASR_0996	Beauvais - L'Isle-Adam	1500	1600	1134	0	Clavel 2001	no
lmq_NSASR_0997	Noyon - Ru d'Orroire	1000	1500	5	0	Clavel 2001	no
lmq_NSASR_0998	Lassigny	1400	1500	5	0	Clavel 2001	no
lmq_NSASR_0999	Guiscard	1400	1500	6	0	Clavel 2001	no
lmq_NSASR_1000	Amiens - St. Germain	1000	1600	1460	0	Clavel 2001	no
lmq_NSASR_1001	Amiens - Restaurant Universitaire	1100	1500	364	0	Clavel 2001	no
lmq_NSASR_1002	Amiens - ZAC Cathedrale	1300	1600	1192	0	Clavel 2001	no
lmq_NSASR_1003	Abbeville - Hotel de Ville	1300	1600	1814	0	Clavel 2001	no
lmq_NSASR_1004	Coquelles	1300	1425	12	0	Clavel 2001	no
lmq_NSASR_1005	Trojborg	1300	1580	278	0	Enghoff 2000	no
lmq_NSASR_1006	Elisenhof	700	1200	497	0	Enghoff 2000	no
lmq_NSASR_1007	Plesse Castle	1400	1500	783	0	Enghoff 2000	no

lmq_NSASR_1008	100 North Street	1100	1600	216	0	LMQ	no
lmq_NSASR_1009	Pontefract Castle	1300	1550	41	0	LMQ	no
lmq_NSASR_1010	Holyrood	1100	1700	106	0	LMQ	no
lmq_NSASR_1011	Blackfriargate	1250	1600	1154	0	LMQ	no
lmq_NSASR_1012	Middleham Castle	1000	1400	6	0	LMQ	no
lmq_NSASR_1013	Marktplatz	1200	1300	1255	2	NSS	yes
lmq_NSASR_1014	Katharinenstraße, Astoria	1200	1300	22	1	NSS	yes
lmq_NSASR_1015	Langenstraße, Ecke Fangturm, Melchers	1100	1200	13	1	NSS	yes
lmq_NSASR_1016	Dominikanerkloster Norden	1200	1325	75	1	NSS	yes
lmq_NSASR_1017	Hopmarkt	1475	1500	20	1	NSS	yes
lmq_NSASR_1018	Hopmarkt	1475	1500	391	10	NSS	yes
lmq_NSASR_1019	Saint Salvatorsabbey	1450	1550	508	1	NSS	yes
lmq_NSASR_1020	Saint Salvatorsabbey	1450	1550	881	1	NSS	yes
lmq_NSASR_1021	Chateau La Roche en Ardenne	1000	1100	13	5	NSS	yes
lmq_NSASR_1022	Chateau La Roche en Ardenne	1000	1100	2373	396	NSS	yes
lmq_NSASR_1023	Chateau La Roche en Ardenne	1000	1100	609	94	NSS	yes
lmq_NSASR_1024	Chateau La Roche en Ardenne	1200	1300	15	5	NSS	yes
lmq_NSASR_1025	Chateau La Roche en Ardenne	1200	1300	940	98	NSS	yes
lmq_NSASR_1026	K 42	1400	1425	2291	10	NSS	yes
lmq_NSASR_1027	Kazerne Dossin	1325	1375	275	2	NSS	yes
lmq_NSASR_1028	Lamot	800	1200	66	1	NSS	yes
lmq_NSASR_1029	Kazerne Dossin	1325	1375	2520	3	NSS	yes
lmq_NSASR_1030	Grognon	1300	1500	337	4	NSS	yes
lmq_NSASR_1031	Grote Markt	1200	1400	2566	3	NSS	yes
lmq_NSASR_1032	Ganzendries	1275	1325	582	1	NSS	yes
lmq_NSASR_1033	Ganzendries	1275	1325	359	3	NSS	yes
lmq_NSASR_1034	Kazerne Dossin	1325	1350	1057	1	NSS	yes
lmq_NSASR_1035	Kazerne Dossin	1325	1350	6891	1	NSS	yes
lmq_NSASR_1036	Kazerne Dossin	1275	1325	383	1	NSS	yes
lmq_NSASR_1037	Lamot	800	1200	822	1	NSS	yes
lmq_NSASR_1038	Steen	1275	1325	9691	9	NSS	yes
lmq_NSASR_1039	Steen	1275	1325	3715	5	NSS	yes
lmq_NSASR_1040	Steen	1275	1325	356	2	NSS	yes
lmq_NSASR_1041	Steen	1275	1325	946	1	NSS	yes
lmq_NSASR_1042	Steen	1275	1325	845	1	NSS	yes
lmq_NSASR_1043	Château des comtes	1000	1100	56	1	NSS	yes
lmq_NSASR_1044	Château des comtes	1000	1100	348	4	NSS	yes
lmq_NSASR_1045	Grognon	1200	1400	1468	4	NSS	yes
lmq_NSASR_1046	Grognon	1300	1500	80	1	NSS	yes
lmq_NSASR_1047	Mijnplein	1400	1600	402	1	NSS	yes
lmq_NSASR_1048	Mijnplein	1400	1600	983	1	NSS	yes
lmq_NSASR_1049	Mijnplein	1400	1600	1267	1	NSS	yes
lmq_NSASR_1050	Mijnplein	1400	1600	120	1	NSS	yes
lmq_NSASR_1051	Cloître	500	700	48	2	NSS	yes
lmq_NSASR_1052	Stadhuis	1125	1175	4346	5	NSS	yes
lmq_NSASR_1053	Wijk bij Duurstede	675	775	345	3	NSS	yes
lmq_NSASR_1054	Wijk bij Duurstede	675	900	128	4	NSS	yes
lmq_NSASR_1055	Wijk bij Duurstede	775	900	2643	58	NSS	yes
lmq_NSASR_1056	Burseplein	800	1200	5524	1	NSS	yes
lmq_NSASR_1057	In den Struys'	1425	1500	2797	6	NSS	yes
lmq_NSASR_1058	Huis ter Kleef	1250	1573	789	1	NSS	yes
lmq_NSASR_1059	Huis ter Kleef	1250	1573	86	1	NSS	yes
lmq_NSASR_1060	Johan van Oldenbarneveltlaan 91-95	450	700	547	8	NSS	yes
lmq_NSASR_1061	Hoogeland Zuidweg	500	750	19	2	NSS	yes
lmq_NSASR_1062	Hoogeland Zuidweg	900	1300	12	1	NSS	yes
lmq_NSASR_1063	Marktenroute/Vismarkt	1300	1350	440	3	NSS	yes
lmq_NSASR_1064	Plantage	650	675	379	1	NSS	yes
lmq_NSASR_1065	Plantage	675	850	74	2	NSS	yes
lmq_NSASR_1066	Plantage	800	850	1466	5	NSS	yes
lmq_NSASR_1067	Kastanjelaan	700	1000	939	2	NSS	yes
lmq_NSASR_1068	Nieuw Rhijngeest-zuid	475	725	1229	17	NSS	yes
lmq_NSASR_1069	Nieuw Rhijngeest-zuid	475	725	52	2	NSS	yes
lmq_NSASR_1070	Nieuw Rhijngeest-zuid	475	725	2	1	NSS	yes
lmq_NSASR_1071	Nieuw Rhijngeest-zuid	475	725	3880	49	NSS	yes
lmq_NSASR_1072	Nieuw Rhijngeest-zuid	475	725	1404	61	NSS	yes
lmq_NSASR_1073	Minderbroederskloosterr	1175	1228	202	3	NSS	yes
lmq_NSASR_1074	Minderbroederskloosterr	1350	1450	1511	9	NSS	yes
lmq_NSASR_1075	Minderbroederskloosterr	1400	1500	1560	6	NSS	yes
lmq_NSASR_1076	Kasteel Voorst	1283	1362	83	4	NSS	yes
lmq_NSASR_1077	Dorestad	725	899	21	1	NSS	yes
lmq_NSASR_1078	Dorestad	725	899	815	6	NSS	yes
lmq_NSASR_1079	Dorestad	725	899	148	20	NSS	yes

lmq_NSASR_1080	Dorestad	725	899	342	7	NSS	yes
lmq_NSASR_1081	Tjitsma-Foarryp	550	750	2070	10	NSS	yes
lmq_NSASR_1082	Tjitsma-Foarryp	750	850	936	6	NSS	yes
lmq_NSASR_1083	Tjitsma-Foarryp	850	950	961	2	NSS	yes
lmq_NSASR_1084	Huis Malburg	900	1049	110	1	NSS	yes
lmq_NSASR_1085	Stenen Kamer/Linge	900	1050	166	3	NSS	yes
lmq_NSASR_1086	Bethlehemstraat - Voogdijstraat	1400	1600	134	28	NSS	yes
lmq_NSASR_1087	Bethlehemstraat - Voogdijstraat	1350	1450	12	1	NSS	yes
lmq_NSASR_1088	Langestraat 3-5	1418	1500	381	1	NSS	yes
lmq_NSASR_1089	Burseplein	1400	1600	2236	20	NSS	yes
lmq_NSASR_1090	Oude en nieuwe Gasthuis	1400	1450	690	1	NSS	yes
lmq_NSASR_1091	Stenen Kamer/Linge	725	900	54	1	NSS	yes
lmq_NSASR_1092	Nieuwendijk 1979	1225	1325	725	1	NSS	yes
lmq_NSASR_1093	Scalloway	300	900	501	3	NSS	yes
lmq_NSASR_1094	Scalloway	300	900	53	3	NSS	yes
lmq_NSASR_1095	Scalloway	300	900	83	8	NSS	yes
lmq_NSASR_1096	Scalloway	300	1000	245	2	NSS	yes
lmq_NSASR_1097	Earl's Bu	880	1160	623	1	NSS	yes
lmq_NSASR_1098	Earl's Bu	1000	1200	2390	2	NSS	yes
lmq_NSASR_1099	Mine Howe	0	1900	411	4	NSS	yes
lmq_NSASR_1100	Kirk Ness	400	700	6	3	NSS	yes
lmq_NSASR_1101	Quoygrew	800	1900	502	1	NSS	yes
lmq_NSASR_1102	Tuquoy	1050	1250	165	2	NSS	yes
lmq_NSASR_1103	Tuquoy	1200	1400	2690	1	NSS	yes
lmq_NSASR_1104	Tuquoy	1200	1600	430	1	NSS	yes
lmq_NSASR_1105	Brough Road	800	1300	1928	1	NSS	yes
lmq_NSASR_1106	Brough Road	800	1100	2022	3	NSS	yes
lmq_NSASR_1107	Beachview Burnside	1020	1320	466	7	NSS	yes
lmq_NSASR_1108	Beachview Burnside	1020	1280	848	3	NSS	yes
lmq_NSASR_1109	Beachview Burnside	1020	1280	299	1	NSS	yes
lmq_NSASR_1110	Beachview Burnside	1020	1280	2242	2	NSS	yes
lmq_NSASR_1111	Beachview Studio	1030	1280	157	1	NSS	yes
lmq_NSASR_1112	Beachview Studio	990	1220	930	4	NSS	yes
lmq_NSASR_1113	Beachview Studio	990	1210	1124	4	NSS	yes
lmq_NSASR_1114	Buckquoy	750	1050	29	1	NSS	yes
lmq_NSASR_1115	Saevar Howe	750	950	541	1	NSS	yes
lmq_NSASR_1116	Earl's Bu	890	1160	320	1	NSS	yes
lmq_NSASR_1117	Earl's Bu	750	1200	654	2	NSS	yes
lmq_NSASR_1118	Earl's Bu	1000	1200	894	1	NSS	yes
lmq_NSASR_1119	Earl's Bu	990	1190	4141	28	NSS	yes
lmq_NSASR_1120	Earl's Bu	890	1160	8150	23	NSS	yes
lmq_NSASR_1121	Earl's Bu	750	1200	1505	20	NSS	yes
lmq_NSASR_1122	Earl's Bu	1000	1200	280	1	NSS	yes
lmq_NSASR_1123	Freswick Inland	300	1600	1460	3	NSS	yes
lmq_NSASR_1124	Freswick Inland	1093	1603	202	1	NSS	yes
lmq_NSASR_1125	Bon Accord	1200	1400	1502	1	NSS	yes
lmq_NSASR_1126	Bon Accord	1200	1400	126	1	NSS	yes
lmq_NSASR_1127	Perth High Street	800	1150	31	1	NSS	yes
lmq_NSASR_1128	Perth High Street	1200	1250	82	3	NSS	yes
lmq_NSASR_1129	Perth High Street	1250	1300	420	1	NSS	yes
lmq_NSASR_1130	Perth High Street	800	1900	88	2	NSS	yes
lmq_NSASR_1131	Perth High Street	1150	1200	4	1	NSS	yes
lmq_NSASR_1132	Perth High Street	1250	1300	103	1	NSS	yes
lmq_NSASR_1133	Perth High Street	1300	1350	100	2	NSS	yes
lmq_NSASR_1134	Perth High Street	800	1900	13	1	NSS	yes
lmq_NSASR_1135	Howe	300	900	1207	8	NSS	yes
lmq_NSASR_1136	Howe	800	1900	24	3	NSS	yes
lmq_NSASR_1137	Holyrood	1300	1500	103	1	NSS	yes
lmq_NSASR_1138	Arbroath Abbey Visitor Centre	1300	1500	1189	5	NSS	yes
lmq_NSASR_1139	Portmahomack	500	1100	6	2	NSS	yes
lmq_NSASR_1140	Portmahomack	500	1100	2	1	NSS	yes
lmq_NSASR_1141	Portmahomack	500	1100	5	2	NSS	yes
lmq_NSASR_1142	Portmahomack	500	1100	5	1	NSS	yes
lmq_NSASR_1143	St Ethernan's Monastery	400	1300	215	1	NSS	yes
lmq_NSASR_1144	Mindets tomt	1125	1225	2	2	NSS	yes
lmq_NSASR_1145	Mindets tomt	1125	1350	2	2	NSS	yes
lmq_NSASR_1146	Søndre Felt	1350	1500	2	2	NSS	yes
lmq_NSASR_1147	Kaupang	805	810	9	9	NSS	yes
lmq_NSASR_1148	Ipswich Stoke Quay	700	850	10516	1	NSS	yes
lmq_NSASR_1149	Ipswich Stoke Quay	850	1099	10516	1	NSS	yes
lmq_NSASR_1150	Ipswich Stoke Quay	1075	1199	10516	1	NSS	yes
lmq_NSASR_1151	Ipswich Stoke Quay	700	850	10516	13	NSS	yes

lmq_NSASR_1152	Ipswich Stoke Quay	700	850	10516	1	NSS	yes
lmq_NSASR_1153	Ipswich Stoke Quay	1075	1199	10516	1	NSS	yes
lmq_NSASR_1154	Ipswich Stoke Quay	700	850	10516	1	NSS	yes
lmq_NSASR_1155	Ipswich Stoke Quay	700	850	10516	1	NSS	yes
lmq_NSASR_1156	Oxford Castle	911	1071	2357	1	NSS	yes
lmq_NSASR_1157	Oxford Castle	911	1071	2357	2	NSS	yes
lmq_NSASR_1158	Oxford Castle	911	1071	2357	1	NSS	yes
lmq_NSASR_1159	Oxford Merton College	1375	1550	2157	1	NSS	yes
lmq_NSASR_1160	Oxford Merton College	1375	1550	2157	1	NSS	yes
lmq_NSASR_1161	Tradescent Lane Canterbury	1125	1350	1496	1	NSS	yes
lmq_NSASR_1162	Tradescent Lane Canterbury	1125	1350	1496	1	NSS	yes
lmq_NSASR_1163	Tradescent Lane Canterbury	1125	1350	1496	1	NSS	yes
lmq_NSASR_1164	Tradescent Lane Canterbury	1125	1350	1496	1	NSS	yes
lmq_NSASR_1165	Tradescent Lane Canterbury	1125	1350	1496	1	NSS	yes
lmq_NSASR_1166	Tradescent Lane Canterbury	1125	1350	1496	1	NSS	yes
lmq_NSASR_1167	Carisbrooke Castle	1100	1200	505	9	NSS	yes
lmq_NSASR_1168	Greyfriars	850	1075	8823	2	NSS	yes
lmq_NSASR_1169	Greyfriars	1100	1225	8823	5	NSS	yes
lmq_NSASR_1170	Greyfriars	1400	1550	8823	3	NSS	yes
lmq_NSASR_1171	Townwall Street	1150	1250	87591	2	NSS	yes
lmq_NSASR_1172	Townwall Street	1150	1250	87591	1	NSS	yes
lmq_NSASR_1173	Southhampton French Quarter	900	1750	7413	24	NSS	yes
lmq_NSASR_1174	Canterbury Whitefriars	750	1538	14278	12	NSS	yes
lmq_NSASR_1175	Oxford Ashmolean	1200	1600	4184	11	NSS	yes
lmq_NSASR_1176	Oxford Classics Centre	1100	1700	188	1	NSS	yes
lmq_NSASR_1177	Winchester Staple Gardens	850	1500	20287	42	NSS	yes
lmq_NSASR_1178	113-119 High St	1100	1200	36	4	Holmes 2017	yes
lmq_NSASR_1179	21-22 Maiden La, London	650	800	2953	22	Holmes 2017	yes
lmq_NSASR_1180	Battle Bridge Lane	1300	1500	0	0	Holmes 2017	yes
lmq_NSASR_1181	Bishopstone	700	900	2335	1	Holmes 2017	yes
lmq_NSASR_1182	Church St, Romsey	1400	1600	162	1	Holmes 2017	yes
lmq_NSASR_1183	Oxford Classics Centre	1200	1300	35	1	Holmes 2017	yes
lmq_NSASR_1184	Oxford Dominican Priory	1250	1300	0	0	Holmes 2017	yes
lmq_NSASR_1185	Dorter Undercroft, Westminster Abbey	1050	1070	9535	81	Holmes 2017	yes
lmq_NSASR_1186	Southhampton French Quarter	800	1100	332	6	Holmes 2017	yes
lmq_NSASR_1187	Southhampton French Quarter	1100	1250	2744	10	Holmes 2017	yes
lmq_NSASR_1188	Southhampton French Quarter	1250	1400	1333	2	Holmes 2017	yes
lmq_NSASR_1189	Southhampton French Quarter	1400	1500	1055	1	Holmes 2017	yes
lmq_NSASR_1190	Oxford Hinxey Hall	1400	1500	146	1	Holmes 2017	yes
lmq_NSASR_1191	Hospital of St. Mary of Ospringe	1470	1550	89	1	Holmes 2017	yes
lmq_NSASR_1192	Jubilee Hall, London	650	850	118	1	Holmes 2017	yes
lmq_NSASR_1193	Lewes Castle	1000	1200	0	0	Holmes 2017	yes
lmq_NSASR_1194	Lewes House	1100	1175	0	0	Holmes 2017	yes
lmq_NSASR_1195	Lewes Priory	900	1066	913	5	Holmes 2017	yes
lmq_NSASR_1196	Oxford Lincoln College	1050	1100	397	4	Holmes 2017	yes
lmq_NSASR_1197	Oxford Lincoln College	1400	1500	425	10	Holmes 2017	yes
lmq_NSASR_1198	Little Pickle, Bletchingley	1500	1550	1193	6	Holmes 2017	yes
lmq_NSASR_1199	Melbourne St, Southampton	650	800	712	2	Holmes 2017	yes
lmq_NSASR_1200	Minster, Isle of Sheppey	750	800	824	0	Holmes 2017	yes
lmq_NSASR_1201	Northfleet	400	650	0	0	Holmes 2017	yes
lmq_NSASR_1202	Phoenix Brewery	1200	1300	0	0	Holmes 2017	yes
lmq_NSASR_1203	Oxford Queen's College	1300	1725	1314	9	Holmes 2017	yes
lmq_NSASR_1204	Sandtun, West Hythe	700	800	0	0	Holmes 2017	yes
lmq_NSASR_1205	St Mary's Stadium, Southampton	700	800	0	0	Holmes 2017	yes
lmq_NSASR_1206	St Saviour	1400	1550	936	3	Holmes 2017	yes
lmq_NSASR_1207	Townwall Street	1175	1300	91504	3	Holmes 2017	yes
lmq_NSASR_1208	West Quay, Southampton	650	800	4755	1	Holmes 2017	yes
lmq_NSASR_1209	Wickham Glebe	1200	1400	507	3	Holmes 2017	yes
lmq_NSASR_1210	Austin Friars 73-8b	500	1500	104	1	Albarella & Pirnie	yes
lmq_NSASR_1211	Castle Mall AML 85/97	1400	1500	878	0	Albarella & Pirnie	yes
lmq_NSASR_1212	Castle Mall AML 85/97	1000	1100	346	0	Albarella & Pirnie	yes
lmq_NSASR_1213	Castle Mall AML 85/97	1100	1300	37	0	Albarella & Pirnie	yes
lmq_NSASR_1214	Castle Mall AML 85/97	1400	1500	1297	0	Albarella & Pirnie	yes
lmq_NSASR_1215	Castle Mall AML 85/97	1100	1300	576	0	Albarella & Pirnie	yes
lmq_NSASR_1216	Castle Mall AML 85/97	1000	1100	853	0	Albarella & Pirnie	yes
lmq_NSASR_1217	Castle Mall AML 85/97	800	1100	1516	0	Albarella & Pirnie	yes
lmq_NSASR_1218	Dragon Hall, King Street 97-98	1350	1550	88	0	Albarella & Pirnie	yes
lmq_NSASR_1219	Ipswich AML 4578	500	1500	857	0	Albarella & Pirnie	yes
lmq_NSASR_1220	Ipswich AML 4578	650	850	1835	0	Albarella & Pirnie	yes
lmq_NSASR_1221	Lincoln sites (bones)	800	1100	518	0	Albarella & Pirnie	yes
lmq_NSASR_1222	Northampton AML 4589	1400	1500	139	2	Albarella & Pirnie	yes
lmq_NSASR_1223	Park St 76	1250	1400	1	0	Albarella & Pirnie	yes

lmq_NSASR_1224	St Martin-at-Palace Plain 81	1200	1500	133	1	Albarella & Pirnie	yes
lmq_NSASR_1225	St Martin-at-Palace Plain 81	1150	1250	92	2	Albarella & Pirnie	yes
lmq_NSASR_1226	St Martin-at-Palace Plain 81	1000	1100	401	4	Albarella & Pirnie	yes
lmq_NSASR_1227	The Shires 88 AML 56/92 Little Ln	1250	1400	3	1	Albarella & Pirnie	yes
lmq_NSASR_1228	The Shires 88 AML 56/92 Little Ln	1250	1400	88	1	Albarella & Pirnie	yes
lmq_NSASR_1229	The Shires 88 AML 56/92 St Peter's	1250	1400	59	2	Albarella & Pirnie	yes
lmq_NSASR_1230	The Shires 88 AML 56/92 St Peter's	1250	1400	11	2	Albarella & Pirnie	yes
lmq_NSASR_1231	West Parade 70-72	1000	1200	30	1	Albarella & Pirnie	yes
lmq_NSASR_1232	Whittlesea Mere 76-77	1200	1400	9	8	Albarella & Pirnie	yes
lmq_NSASR_1233	Woolmonger St 94-7 (St Peters Walk)	800	1100	592	0	Albarella & Pirnie	yes
lmq_NSASR_1234	1-5 Aldwark	1400	1600	537	1	LMQ	yes
lmq_NSASR_1235	Barnard Castle	1130	1630	2332	116	LMQ	yes
lmq_NSASR_1236	Milk Street	1150	1200	251	2	LMQ	yes
lmq_NSASR_1237	6-8 Pavement	876	1066	492	2	LMQ	yes
lmq_NSASR_1238	Half Moon Yard	1100	1300	143	3	LMQ	yes
lmq_NSASR_1239	Lindisfarne - Manor House	500	1500	161	2	LMQ	yes
lmq_NSASR_1240	Mount Grace Priory	1398	1539	3126	29	LMQ	yes
lmq_NSASR_1241	Scarborough Castle	1200	1500	63	1	LMQ	yes
lmq_NSASR_1242	St. Giles Hospital	1150	1500	32	5	LMQ	yes
lmq_NSASR_1243	Berwick Workspace	1200	1500	578	4	LMQ	yes
lmq_NSASR_1244	16-22 Coppergate	400	1720	31187	260	LMQ	yes
lmq_NSASR_1245	Blue Bridge Lane	675	1525	11914	6	LMQ	yes
lmq_NSASR_1246	Closegate	1400	1500	1291	9	LMQ	yes
lmq_NSASR_1247	24-30 Tanner Row	1100	1250	2644	10	LMQ	yes
lmq_NSASR_1248	41 Piccadilly	1400	1500	410	0	LMQ	yes
lmq_NSASR_1249	North Bridge, Context 2052	1200	1300	14	2	LMQ	yes
lmq_NSASR_1250	Orchard Lane, Huntingdon	900	1150	0	1	LMQ	yes
lmq_NSASR_1251	Cour Carree, Louvre	1500	1600	153	1	Clavel 2001	yes
lmq_NSASR_1252	Amiens Rank Xeros	1300	1600	281	3	Clavel 2001	yes
lmq_NSASR_1253	Amiens St. Germain	900	1100	755	0	Clavel 2001	yes
lmq_NSASR_1254	Lille - chateau de Courtrai	1300	1400	2495	7	Clavel 2001	yes
lmq_NSASR_1255	Vincennes - Capetian Manor	1300	1400	963	15	Clavel 2001	yes
lmq_NSASR_1256	Paris Saint-Michel	1300	1500	667	1	Clavel 2001	yes
lmq_NSASR_1257	Ribe - ASR 9 - Posthuset	700	1200	3071	200	Enghoff 2000	yes
lmq_NSASR_1258	Duisburg	900	1200	0	1	Enghoff 2000	yes
lmq_NSASR_1259	Bodenteich Castle	1200	1600	0	5	Enghoff 2000	yes
lmq_NSASR_1260	Ribe - ASR 13 - Lindegården	1200	1300	245	2	LMQ	yes
lmq_NSASR_1261	Ribe - ASR 2090 - von Støckens Plads	1000	1200	203	4	LMQ	yes
lmq_NSASR_1262	Oslo - Kanslergt 10	1200	1400	1107	27	Enghoff 1999	yes
lmq_NSASR_1263	Hitzacker	800	1100	260	2	Enghoff 1999	yes
lmq_NSASR_1264	Haithabu	900	1100	13842	129	Enghoff 1999	yes
lmq_NSASR_1265	Fishergate (York)	650	1800	14339	78	LMQ	yes
lmq_NSASR_1266	Ribe - Kunstmuseet	700	800	16	0	Enghoff 2000	no
lmq_NSASR_1267	Aggersborg	700	980	482	0	Enghoff 2000	no
lmq_NSASR_1268	Schleswig	1000	1350	1064	3	Enghoff 2000	yes
lmq_NSASR_1269	Freyenstein	1200	1300	69	0	Enghoff 2000	no
lmq_NSASR_1270	Kiel	1200	1300	144	0	Enghoff 2000	no
lmq_NSASR_1271	Huize van den Kasteele	1000	1100	125	0	LMQ	no
lmq_NSASR_1272	Huize van den Kasteele	1000	1100	190	1	LMQ	yes

B Bulk Stable Isotope Data

Sample ID	Site	Taxa	δ13C	δ15N	CN Ratio
comps_001	Nieuw Rhijngeest-zuid (2009-10, 2014)	Perca fluviatilis	-19.21	12.42	3.13
comps_004	Nieuw Rhijngeest-zuid (2009-10, 2014)	Perca fluviatilis	-23.71	8.43	3.14
comps_006	Minderbroedersklooster	Esox lucius	-22.62	13.63	3.32
comps_008	Minderbroedersklooster	Esox lucius	-25.51	13.28	3.31
comps_009	Minderbroedersklooster	Esox lucius	-23.79	13.99	3.28
comps_012	Minderbroedersklooster	Cyprinidae	-23.42	12.73	3.3
comps_014	Minderbroedersklooster	Cyprinidae	-22.65	11.97	3.18
comps_017	Minderbroedersklooster	Coregoninae	-23.53	14.51	3.31
comps_019	Minderbroedersklooster	Coregoninae	-23.9	14.56	3.32
comps_020	Minderbroedersklooster	Coregoninae	-23.81	14.53	3.31
comps_021	Minderbroedersklooster	Coregoninae	-23.31	14.46	3.29
comps_022	Minderbroedersklooster	Coregoninae	-23.53	14.5	3.33
comps_023	Minderbroedersklooster	Melanogrammus aeglefinus	-13.37	14.19	3.17
comps_024	Minderbroedersklooster	Melanogrammus aeglefinus	-13.81	14.12	3.24
comps_026	Minderbroedersklooster	Melanogrammus aeglefinus	-13.42	14.02	3.13
comps_029	Minderbroedersklooster	Melanogrammus aeglefinus	-13.08	15.03	3.19
comps_030	Minderbroedersklooster	Melanogrammus aeglefinus	-13.02	14.92	3.23
comps_031	Minderbroedersklooster	Melanogrammus aeglefinus	-13.15	14.01	3.08
comps_032	Minderbroedersklooster	Melanogrammus aeglefinus	-13.25	14.2	3.11
comps_034	Minderbroedersklooster	Esox lucius	-20.71	12.4	3.3
comps_037	Minderbroedersklooster	Esox lucius	-20.82	12.95	3.32
comps_040	Minderbroedersklooster	Esox lucius	-20.39	12.47	3.31
comps_041	Minderbroedersklooster	Melanogrammus aeglefinus	-13.93	14.31	3.25
comps_042	Minderbroedersklooster	Melanogrammus aeglefinus	-13.21	14.37	3.18
comps_050	Nieuw Rhijngeest-zuid (2009-10, 2014)	Coregoninae	-13.77	12.93	3.23
comps_053	Nieuw Rhijngeest-zuid (2009-10, 2014)	Anguilla anguilla	-20.01	11.3	3.26
comps_056	Nieuw Rhijngeest-zuid (2009-10, 2014)	Abramis brama	-21.96	7.58	3.1
comps_057	Nieuw Rhijngeest-zuid (2009-10, 2014)	Alosa fallax	-14.07	12.03	3.19
COP225	16-22 Coppergate	Gadidae	-12.18	15.59	3.16
COP245	16-22 Coppergate	Gadus morhua	-14.94	14.35	3.31
COP277	16-22 Coppergate	Gadus morhua	-11.84	17.47	3.11
COP298	16-22 Coppergate	Melanogrammus aeglefinus	-12.4	15.14	3.17
COP319	16-22 Coppergate	Gadus morhua	-13.51	16.41	3.23
COP325	16-22 Coppergate	Esox lucius	-25.11	12.7	3.22
COP340	16-22 Coppergate	Anguilla anguilla	-14.67	11.61	3.13
COP341	16-22 Coppergate	Anguilla anguilla	-13.82	13.45	3.17
COP342	16-22 Coppergate	Anguilla anguilla	-13.59	13.19	3.16
COP343	16-22 Coppergate	Anguilla anguilla	-13.83	12.98	3.2
COP344	16-22 Coppergate	Anguilla anguilla	-25.46	16.43	3.18
COP345	16-22 Coppergate	Anguilla anguilla	-24.52	12.98	3.1
COP346	16-22 Coppergate	Anguilla anguilla	-24.59	13.74	3.13
DK_002	ASR 9 Posthuset	Liza ramada	-9.84	9.2	3.04
DK_003	ASR 9 Posthuset	Cyprinidae	-21.38	7.54	3.17
DK_007	ASR 9 Posthuset	Melanogrammus aeglefinus	-13.88	13.83	3.05
DK_016	ASR 9 Posthuset	Abramis brama	-17.09	6.2	3.2
DK_017	ASR 9 Posthuset	Abramis brama	-17.44	5.83	3.32
DK_018	ASR 9 Posthuset	Abramis brama	-16.24	5.3	3.19
DK_021	ASR 9 Posthuset	Melanogrammus aeglefinus	-14.53	13.32	3.16
DK_029	ASR 9 Posthuset	Liza ramada	-7.57	8.34	3.13
DK_033	ASR 9 Posthuset	Salmo trutta	-15.64	11.75	3.18
DK_045	ASR 9 Posthuset	Abramis brama	-16.28	5.22	3.19
DK_046	ASR 9 Posthuset	Anguilla anguilla	-11.34	14.82	3.17
DK_047	ASR 9 Posthuset	Pleuronectiformes	-12.83	12.09	3.22
DK_049	ASR 9 Posthuset	Liza ramada	-11.46	11.91	3.2
DK_050	ASR 9 Posthuset	Salmo trutta	-15.57	11.16	3.33
DK_066	ASR 9 Posthuset	Abramis brama	-15.77	5.24	3.15
DK_068	ASR 9 Posthuset	Liza ramada	-25.07	8.91	3.29

DK_076	ASR 9 Posthuset	Salmo trutta	-14.85	10.29	3.18
DK_095	ASR 9 Posthuset	Pleuronectiformes	-11.05	13.11	3.18
DK_096	ASR 9 Posthuset	Liza ramada	-10.13	11.14	3.19
DK_104	ASR 9 Posthuset	Pleuronectiformes	-13.85	12.28	3.21
DK_109	ASR 9 Posthuset	Esox lucius	-19.93	13.34	3.26
DK_110	ASR 9 Posthuset	Salmo trutta	-15.04	10.24	3.09
DK_113	ASR 9 Posthuset	Salmo trutta	-14.83	11.23	3.15
DK_114	ASR 9 Posthuset	Salmo trutta	-16.31	12.03	3.27
DK_125	ASR 9 Posthuset	Liza ramada	-21.21	11.77	3.26
DK_126	ASR 9 Posthuset	Salmo trutta	-14.61	12	3.27
DK_127	ASR 9 Posthuset	Salmo sp.	-14.44	12.18	3.19
DK_130	ASR 9 Posthuset	Pleuronectiformes	-14.04	11.12	3.3
DK_140	ASR 13 Lindegården	Salmo trutta	-14.58	10.7	3.16
DK_141	ASR 13 Lindegården	Salmo trutta	-14.88	10.52	3.21
DK_142	ASR 2090 von Støckens Plads	Salmo trutta	-13.81	12.32	3.13
DK_143	ASR 2090 von Støckens Plads	Salmo trutta	-13.4	15.5	3.06
DK_144	ASR 2090 von Støckens Plads	Salmo trutta	-13.64	15.4	3.11
DK_145	ASR 2090 von Støckens Plads	Salmo trutta	-13.46	15.4	3.09
DK_146	ASR 13 Lindegården	Melanogrammus aeglefinus	-13.58	14.64	3.09
DK_164	ASR 2090 von Støckens Plads	Melanogrammus aeglefinus	-14.76	13.65	3.2
DK_168	ASR 2090 von Støckens Plads	Melanogrammus aeglefinus	-13.73	13.88	3.07
DK_171	ASR 2090 von Støckens Plads	Abramis brama	-20.3	9.55	3.32
DK_172	ASR 2090 von Støckens Plads	Abramis brama	-19.64	8.72	3.17
DK_206	ASR 2090 von Støckens Plads	Melanogrammus aeglefinus	-13.82	13.79	3.04
EB_001	Earl's Bu	Salmo sp.	-14.39	9.15	3.25
EB_002	Earl's Bu	Melanogrammus aeglefinus	-13.67	13.48	3.27
EB_003	Earl's Bu	Salmo salar	-15.76	9.03	3.3
EB_004	Earl's Bu	Anguilla anguilla	-16.14	13.38	3.16
EB_005	Earl's Bu	Salmo trutta	-13.94	12.93	3.23
EB_007	Earl's Bu	Melanogrammus aeglefinus	-12.64	12.56	3.18
EB_008	Earl's Bu	Gadidae	-12.3	13.76	3.21
EB_011	Earl's Bu	Salmo salar	-15.38	9.09	3.22
EB_012	Earl's Bu	Gadidae	-11.55	14.08	3.11
EB_014	Earl's Bu	Salmo sp.	-12.49	12.9	3.18
EB_015	Earl's Bu	Melanogrammus aeglefinus	-13.74	14.11	3.11
EB_019	Earl's Bu	Salmo salar	-14.75	8.63	3.14
EB_020	Earl's Bu	Melanogrammus aeglefinus	-12.02	13.83	3.1
EB_021	Earl's Bu	Salmo salar	-14.2	7.9	3.1
EB_023	Earl's Bu	Melanogrammus aeglefinus	-12.67	14.55	3.26
EB_029	Earl's Bu	Salmo salar	-14.55	9.15	3.14
EB_030	Earl's Bu	Gadidae	-12.51	14.19	3.25
EB_031	Earl's Bu	Salmo trutta	-14.59	13.9	3.12
EB_032	Earl's Bu	Salmo trutta	-12.02	13.03	3.13
EB_037	Earl's Bu	Pleuronectiformes	-14.42	11.58	3.15
EB_038	Earl's Bu	Salmo trutta	-17.19	10.51	3.2
EB_040	Earl's Bu	Melanogrammus aeglefinus	-12.97	13.59	3.33
EB_044	Earl's Bu	Anguilla anguilla	-19.76	9.62	3.15
EB_045	Earl's Bu	Raja clavata	-11.56	12.03	3.18
EB_046	Earl's Bu	Melanogrammus aeglefinus	-12.55	13.44	3.13
EB_047	Earl's Bu	Melanogrammus aeglefinus	-12.44	13.53	3.11
EB_048	Earl's Bu	Salmo trutta	-11.85	13.84	3.11
EB_049	Earl's Bu	Salmo trutta	-11.41	13.97	3.05
EB_052	Earl's Bu	Gadus morhua	-13.2	14.63	3.27
EB_055	Earl's Bu	Salmo trutta	-12.76	14.05	3.15
EB_057	Earl's Bu	Salmo trutta	-12.36	13.34	3.18
EB_059	Earl's Bu	Anguilla anguilla	-19.72	9.51	3.13
EB_060	Earl's Bu	Melanogrammus aeglefinus	-12.4	13.47	3.11
EB_061	Earl's Bu	Gadus morhua	-11.78	13.5	3.13

EB_062	Earl's Bu	Salmo salar	-15.22	9.38	3.26
EB_063	Earl's Bu	Melanogrammus aeglefinus	-13.25	13.76	3.15
LMQ014	16-22 Coppergate	Salmo salar	-14.06	10.23	3.18
LMQ016D	16-22 Coppergate	Salmo salar	-14.53	11.75	3.15
LMQ020	16-22 Coppergate	Salmo salar	-14.58	10.61	3.06
LMQ021	16-22 Coppergate	Salmo salar	-14.75	9.59	3.21
LMQ022	16-22 Coppergate	Salmo salar	-13.69	9.69	3.18
LMQ024D	16-22 Coppergate	Salmo salar	-14.57	10.73	3.21
LMQ025	16-22 Coppergate	Salmo salar	-15.25	8.53	3.19
LMQ027	16-22 Coppergate	Salmo salar	-13.44	9.03	3.15
LMQ028	16-22 Coppergate	Salmo salar	-13.91	9.85	3.07
LMQ030	16-22 Coppergate	Esox lucius	-22.46	13.55	3.21
LMQ031D	16-22 Coppergate	Salmo salar	-14.27	11.47	3.14
LMQ032	16-22 Coppergate	Salmo salar	-14.9	10.51	3.33
LMQ037	16-22 Coppergate	Salmo trutta	-15.21	10.77	3.27
LMQ043	16-22 Coppergate	Gadus morhua	-15.83	14.4	3.32
LMQ048	16-22 Coppergate	Salmo salar	-14.49	9.03	3.19
LMQ052	16-22 Coppergate	Salmo salar	-14.91	8.92	3.17
LMQ053	16-22 Coppergate	Salmo sp.	-13.91	10.11	3.1
LMQ061	16-22 Coppergate	Salmo salar	-14.89	9.87	3.15
LMQ062	16-22 Coppergate	Salmo sp.	-14.6	10.1	3.09
LMQ067	16-22 Coppergate	Salmo salar	-15.17	9.4	3.29
LMQ073	16-22 Coppergate	Salmo salar	-14.19	9.3	3.15
LMQ075	16-22 Coppergate	Salmo salar	-14.66	9.54	3.17
LMQ076	16-22 Coppergate	Salmo salar	-14.68	9.26	3.12
LMQ083	16-22 Coppergate	Salmo salar	-14.26	9.4	3.19
LMQ087	16-22 Coppergate	Salmo trutta	-12.68	14.64	3.24
LMQ089	16-22 Coppergate	Salmo salar	-14.22	10.24	3.15
LMQ094	16-22 Coppergate	Salmo salar	-14.45	7.88	3.19
LMQ095	16-22 Coppergate	Salmo salar	-14.54	10.34	3.22
LMQ102D	16-22 Coppergate	Salmo salar	-14.79	10.18	3.14
LMQ110	16-22 Coppergate	Salmo salar	-14.12 ev		3.06
LMQ112	16-22 Coppergate	Salmo salar	-14.91	9.64	3.29
LMQ116	16-22 Coppergate	Salmo trutta	-13.51	14.87	3.2
LMQ129	16-22 Coppergate	Salmo salar	-13.84	11.68	3.14
LMQ130	16-22 Coppergate	Salmo salar	-14.07	8.83	3.17
LMQ132	16-22 Coppergate	Salmo salar	-14.25	10.33	3.17
LMQ138	16-22 Coppergate	Salmo salar	-15.59	9.95	3.27
LMQ139	16-22 Coppergate	Salmo salar	-13.64	10.35	3.16
LMQ141	16-22 Coppergate	Salmo salar	-14.4	10.05	3.2
LMQ145	16-22 Coppergate	Salmo salar	-14.79	10.03	3.18
LMQ148	16-22 Coppergate	Salmo salar	-13.88	10.28	3.13
LMQ149	16-22 Coppergate	Salmo salar	-14.94	9.41	3.14
LMQ153	16-22 Coppergate	Salmo salar	-14.22	10.66	3.26
LMQ154	16-22 Coppergate	Salmo salar	-14.72	9.59	3.15
LMQ156	16-22 Coppergate	Salmo salar	-14.91	9.34	3.15
LMQ158	16-22 Coppergate	Salmo salar	-14.53	9	3.18
LMQ167	16-22 Coppergate	Salmo salar	-15.41	9.01	3.2
LMQ172	16-22 Coppergate	Salmo salar	-15.41	9.13	3.14
LMQ176	16-22 Coppergate	Salmo trutta	-14.61	13.93	3.28
LMQ180	16-22 Coppergate	Salmo sp.	-14.81	9.11	3.23
LMQ190	16-22 Coppergate	Salmo salar	-14.6	10.45	3.31
LMQ192	16-22 Coppergate	Salmo salar	-14.15	9.19	3.22
LMQ193	16-22 Coppergate	Salmo salar	-15.26	9.81	3.27
LMQ200	16-22 Coppergate	Salmo salar	-14.43	8.49	3.2
salmo_001	Oude en nieuwe Gasthuis	Salmo trutta	-22.02	11.58	3.28
salmo_002	Oude en nieuwe Gasthuis	Salmo salar	-14.53	9.89	3.17
salmo_011	In den Struys' Veere	Salmo salar	-15.53	9.88	3.24

salmo_015	In den Struys' Veere	Salmo salar	-14.1	8.74	3.09
salmo_016	In den Struys' Veere	Salmo salar	-16.07	10.25	3.25
salmo_020	In den Struys' Veere	Pleuronectiformes	-12.8	12.86	3.05
salmo_029	Nieuw Rhijngeest-zuid (2009-10, 2014)	Salmo sp.	-12.98	14.39	3.18
salmo_037	Plantage Leiderdorp	Esox lucius	-21.92	12.11	3.24
salmo_039	Plantage Leiderdorp	Salmo salar	-15.13	9.91	3.21
salmo_047	Kasteel Voorst Zwolle	Salmo sp.	-26.29	9.2	3.26
salmo_057	Nieuw Rhijngeest-zuid (2009-10, 2014)	Salmo salar	-14.53	10.28	3.24
salmo_064	Minderbroedersklooster	Salmo salar	-15.38	10.48	3.33
salmo_078	Minderbroedersklooster	Salmo salar	-15.19	8.73	3.26
salmo_098	Tjitsma Foarryp Wijnaldum	Salmo salar	-15.15	8.63	3.27
salmo_102	Tjitsma Foarryp Wijnaldum	Salmo salar	-16.16	18.78	3.16
salmo_107	Tjitsma Foarryp Wijnaldum	Salmo trutta	-14.34	15.13	3.27
salmo_111	Stadhuis Zutphen	Salmo salar	-15.37	12.58	3.27
salmo_112	Huize van den Kasteele	Esox lucius	-20.19	11.37	3.2
salmo_115	Nieuw Rhijngeest-zuid (2009-10, 2014)	Salmo salar	-15.96	11.24	3.26
salmo_117	Nieuw Rhijngeest-zuid (2009-10, 2014)	Salmo salar	-15.1	12.25	3.25
DK_001	ASR 9 Posthuset	Salmo trutta	-16.43	10.04	3.34
DK_008	ASR 9 Posthuset	Salmo salar	-16.08	11.57	3.4
DK_011	ASR 9 Posthuset	Salmo trutta	-16.53	12.54	3.48
DK_012	ASR 9 Posthuset	Salmo trutta	-17	12.08	3.56
DK_025	ASR 9 Posthuset	Salmo trutta	-17.14	10.85	3.53
DK_034	ASR 9 Posthuset	Salmo trutta	-16.49	12.53	3.48
DK_050	ASR 9 Posthuset	Salmo trutta	-15.57	11.16	3.33
DK_056	ASR 9 Posthuset	Salmo salar	-16.62	11.82	3.47
DK_075	ASR 9 Posthuset	Salmo salar	-16.43	11.48	3.56
DK_099	ASR 9 Posthuset	Salmo trutta	-15.94	12.24	3.49
EB_010	Earl's Bu	Salmo salar	-16.09	8.93	3.44
LMQ032	16-22 Coppergate	Salmo salar	-14.9	10.51	3.33
LMQ039	16-22 Coppergate	Salmo salar	-15.12	9.61	3.38
LMQ050	16-22 Coppergate	Salmo salar	-15.76	9.05	3.39
LMQ084D	16-22 Coppergate	Salmo salar	-16.12	11.04	3.43
LMQ106	16-22 Coppergate	Salmo salar	-16.31	9.02	3.5
LMQ140	16-22 Coppergate	Salmo salar	-14.92	10.05	3.4
LMQ190	16-22 Coppergate	Salmo salar	-14.6	10.45	3.31
salmo_048	Kasteel Voorst Zwolle	Salmo sp.	-27.72	11.11	3.39
salmo_064	Minderbroedersklooster	Salmo salar	-15.38	10.48	3.33
salmo_069	Minderbroedersklooster	Salmo sp.	-15.47	11.02	3.4
salmo_079	Minderbroedersklooster	Salmo salar	-15.76	9.95	3.56
salmo_081	Minderbroedersklooster	Salmo salar	-16.9	10.67	3.6
salmo_084	Minderbroedersklooster	Salmo salar	-15.16	10.98	3.37
salmo_087	Minderbroedersklooster	Salmo salar	-16.27	10.56	3.53
salmo_089	Heveskesklooster	Salmo salar	-18.35	11.18	3.59

C ZooMS Data

Sample	ZooMS ID	COL1α1 520 - 531	COL1α3 746 - 762
		α1 520	α3 746
Salmon markers		1026	1397.0
Trout markers		996	1422.0
DK01	Salmo trutta	996.52	1397.76/1421.78
DK08	Salmo salar	1026.554362	1421.8
DK09	Salmo trutta	996.51	
DK10	Salmo trutta	996.16	1421.6
DK11	Salmo trutta	996.56	1397.77/1421.78
DK12	Salmo trutta	996.52	1397.76/1421.77
DK19	Salmo salar	1026.551145	1396.73/1421.77
DK22	Salmo trutta	996.54	
DK23	Salmo trutta	996.5680426	
DK24	Salmo trutta	996.52	1397.8
DK25	Salmo trutta	996.52	1421.8
DK33	Salmo trutta	996.53	1421.7
DK34	Salmo trutta	996.58	1397.81/1421.81
DK36	Salmo trutta	996.53	
DK37	Salmo trutta	996.54	
DK50	Salmo trutta	996.55	1397.8/1421.78
DK55	Salmo trutta	996.5263158	1397.84/1421.8459
DK56	Salmo salar	1026.567249	1397.8
DK61	Salmo trutta	996.52	
DK62	Salmo salar	1026.55	1397.7
DK64	Salmo trutta	996.54	
DK65	Salmo salar	1026.51	
DK75	Salmo salar	1026.531579	1397.823/1421.81
DK76	Salmo trutta	996.46	1397.76/1421.75
DK77	Salmo trutta	996.5	
DK79	Salmo trutta	996.52	
DK80	Salmo trutta	996.54	
DK81	Salmo trutta	996.51	
DK82	Salmo salar	1026.53	
DK83	Salmo trutta	996.52	
DK85	Salmo trutta	996.51	
DK86	Salmo trutta	996.52	
DK97	Salmo trutta	996.48	1397.74/1421.75
DK99	Salmo trutta	996.49	1397.72/1421.74
DK106	Salmo trutta	996.6812092	1397.94/1421.96
DK107	Salmo trutta	996.51	
DK108	Salmo trutta	996.64	1397.92/1421.91
DK110	Salmo trutta	996.5	1421.7
DK113	Salmo trutta	996.53	1421.8
DK114	Salmo salar	1026.58	1396.8/1421.82
DK117	Salmo salar		
DK120	Salmo salar	1026.52	1397.76/1421.75

DK124	Salmo trutta	996.5	1421.7
DK126	Salmo trutta	996.52	1397.78/1421.71
DK131	Salmo salar		1396.71/1421.75
DK140	Salmo trutta	996.5308938	1421.8
DK141	Salmo trutta	996.52	1397.68/1421.72
DK142	Salmo trutta	996.55	1397.79/1421.81
DK143	Salmo trutta	996.56	1421.9
DK144	Salmo trutta	996.77	1397.69/1421.74
DK145	Salmo trutta	996.4865728	1397.73/1421.77
EB03	Salmo salar		1421.7
EB05	Salmo trutta	996.5452064	1421.7
EB06	Salmo trutta	996.5	1397.8
EB09	Salmo trutta	996.5	
EB10	Salmo salar	1026.56	1421.8
EB11	Salmo salar	1026.573281	1421.7
EB19	Salmo salar	1026.55	1396.77/1421.77
EB21	Salmo salar	1026.55	1396.76/1421.77
EB25	Salmo salar	1026.54	
EB31	Salmo trutta	996.5390509	1421.7
EB32	Salmo trutta	996.53	1397.79/1421.73
EB33	Salmo trutta	996.52	1396.7
EB34	Salmo salar	1026.53	
EB35	Salmo trutta	996.5	1421.7
EB38	Salmo trutta	996.5	1421.7
EB48	Salmo trutta	996.52	1421.7
EB49	Salmo trutta	996.5358295	1421.7
EB51	Salmo trutta	996.526086	
EB55	Salmo trutta	996.6622919	1397.94/1421.75
EB56	Salmo trutta	996.5354734	1397.7591/1421.73
EB57	Salmo trutta	996.53	1421.7
EB62	Salmo salar	1026.58	1396.78/1421.8
LMQ014	Salmo salar	1026.55	1421.8
LMQ016	Salmo salar	1026.5	1396.67/1421.69
LMQ020	Salmo salar	1026.541649	1421.7
LMQ021	Salmo salar	1026.52	1421.7
LMQ022	Salmo salar	1026.53	1421.7
LMQ024	Salmo salar	1026.535578	1421.7
LMQ025	Salmo salar	1026.52	1421.7
LMQ027	Salmo salar	1026.52	1421.7
LMQ028	Salmo salar	1026.45	1421.7
LMQ029	Salmo salar	1026.562539	1397.81/1421.77
LMQ031	Salmo salar	1026.51	1421.7
LMQ032	Salmo salar	1026.52	1421.7
LMQ037	Salmo trutta	996.74	1397.7
LMQ039	Salmo salar	1026.55	1397.8/1421.83
LMQ048	Salmo salar	1026.6	1421.8

LMQ050	Salmo salar	1026.5	1421.7
LMQ052	Salmo salar	1026.55	1421.7
LMQ061	Salmo salar	1026.519991	1421.7
LMQ067	Salmo salar	1026.93	1422.6
LMQ073	Salmo salar	1026.54	1421.7
LMQ075	Salmo salar	1026.5	1421.7
LMQ076	Salmo salar	1026.51	
LMQ083	Salmo salar	1026.51	1421.7
LMQ084DF	Salmo salar	1026.541825	1421.7
LMQ087	Salmo trutta	996.5	1397.77/1421.7
LMQ089	Salmo salar	1026.52	1421.7
LMQ094	Salmo salar	1026.57	1421.8
LMQ095	Salmo salar	1026.51	1396.66/1421.69
LMQ102	Salmo salar	1026.53	1421.7
LMQ104	Salmo salar	1026.555335	1397.73/1421.74
LMQ106	Salmo salar	1026.587496	1397.84/1421.73
LMQ109	Salmo salar		1397.82/1421.82
LMQ110	Salmo salar	1026.508254	1421.7
LMQ112	Salmo salar	1026.49	1421.7
LMQ116	Salmo trutta	996.4903188	1421.7
LMQ129	Salmo salar	1026.51	1421.7
LMQ130	Salmo salar	1026.535681	
LMQ132	Salmo salar	1026.48	1421.7
LMQ138	Salmo salar	1026.53	1421.7
LMQ139	Salmo salar	1026.520282	1421.7
LMQ140	Salmo salar	1026.49	1421.7
LMQ141	Salmo salar	1026.52	1396.7/1421.71
LMQ145	Salmo salar	1026.49	1421.7
LMQ148	Salmo salar	1026.51	1421.8
LMQ149	Salmo salar	1026.52	1421.7
LMQ154	Salmo salar	1026.504807	1421.7
LMQ156	Salmo salar	1026.51	1421.7
LMQ158	Salmo salar	1026.52	1421.7
LMQ163	Salmo salar	1026.5	
LMQ167	Salmo salar	1026.54	1421.7
LMQ172	Salmo salar	1026.49	1421.7
LMQ176	Salmo trutta	996.65	1421.9
LMQ186	Salmo salar	1026.539079	1421.7
LMQ190	Salmo salar	1026.53	1421.7
LMQ192	Salmo salar	1026.49	1421.7
LMQ193	Salmo salar	1026.54	1421.7
LMQ200	Salmo salar	1026.51	1396.68/1421.7
S001	Salmo trutta	996.6630941	1421.6
S002	Salmo salar	1026.557668	1397.78/1421.74
S003	Salmo salar	1026.52	1421.7
S09	Salmo salar	1026.53	1421.8

S10	Salmo salar	1026.573527	1397.78/1421.72
S108	Salmo trutta	996.54	1397.8
S11	Salmo salar	1026.51	1421.7
S15	Salmo salar	1026.52	1421.8
S16	Salmo salar	1026.52	1421.7
S39	Salmo salar	1026.54	1421.8
S49	Salmo salar	1026.605524	1397.85/1421.68
S50	Salmo salar	1026.642522	1421.5
S53	Salmo salar	1026.522822	1397.7
S54	Salmo salar	1026.56	1421.9
S55	Salmo salar	1026.59	1397.88/1421.85
S57	Salmo salar	1026.545981	1397.76/1421.77
S58	Salmo salar	1026.547792	1421.8
S59	Salmo salar	1026.533517	1397.75/1421.78
S60	Salmo salar	1026.51	1397.72/1421.74
S63	Salmo salar	1026.53	1397.74/1421.73
S64	Salmo salar	1026.54	1421.8
S65	Salmo salar	1026.6	1421.7
S66	Salmo salar	1026.536984	1397.77/1421.75
S68	Salmo salar	1026.623781	1397.73/1421.71
S71	Salmo salar	1026.53	1421.8
S72	Salmo salar	1026.54	1421.8
S73	Salmo salar	1026.53	1421.7
S74	Salmo salar	1026.52	1396.67/1421.7
S75	Salmo salar	1026.51	1421.7
S76	Salmo salar	1026.52	1421.7
S78	Salmo salar	1026.57	
S79	Salmo salar	1026.48	1421.7
S81	Salmo salar	1026.52	1397.76/1421.79
S82	Salmo salar	1026.52	1421.7
S84	Salmo salar	1026.56492	1421.7
S85	Salmo salar	1026.527111	1397.71/1421.7
S86	Salmo salar	1026.518872	1397.7/1421.71
S87	Salmo salar	1026.547073	1397.80/1421.76
S89	Salmo salar	1026.56	1421.8
S90	Salmo salar		
S95	Salmo salar		
S98	Salmo salar	1026.56492	1421.7
S111	Salmo salar	1026.546008	1421.7
S113	Salmo salar	1026.648205	1397.48/1422.49
S114	Salmo salar	1026.528935	1421.7
S115	Salmo salar	1026.548767	1397.78/1421.79
S117	Salmo salar	1026.55793	1421.8
S118	Salmo salar	1026.52	1421.7
S119	Salmo salar	1026.57	1397.81/1421.81
S120	Salmo salar	1026.54	1421.8

D Documentary Records Data

Word/Phrase	Date	Municipality	Unit	Approx. Modern Price/Tax	Number (if known)	Price Per Unit (if applicable)
salmon	1327	Leicester	whole fish	£123.38	1	£123.38
salmon	1327	Leicester	UNK	£464.27		NA
salmon	1327	Leicester	whole fish	£146.28	1	£146.28
salmon	1327	Leicester	whole fish	NA	1	NA
salmon	1327	Leicester	whole fish	£901.84	2	£450.92
salmon	1327	Leicester	UNK	£361.24		NA
salmon	1327	Leicester	whole fish	£1,082.46	5	£216.49
salmon	1327	Leicester	UNK	£134.83		NA
salmon	1327	Leicester	UNK	£653.80		NA
salmon	1327	Leicester	NA	NA		NA
salmon	1327	Leicester	UNK	£155.18		NA
salmon	1327	Leicester	UNK	£234.05		NA
salmon	1327	Leicester	UNK	£13.99		NA
salmon	1327	Leicester	UNK	£13.99		NA
salmon	1327	Leicester	UNK	£19.08		NA
salmon	1327	Leicester	whole fish	£117.02	1	£117.02
salmon	1327	Leicester	UNK	£73.78		NA
salmon	1327	Leicester	UNK	£7.63		NA
salmon	1327	Leicester	UNK	£16.54		NA
salmon	1327	Leicester	UNK	£19.08		NA
salmon	1327	Leicester	whole fish	£16.54	1	£16.54
salmon-fee	1327	Leicester	NA	NA		NA
salmon	1327	Leicester	NA	NA		NA
salmon	1327	Leicester	NA	£159.00		NA
salmon	1327	Leicester		NA		NA
salmon	1327	Leicester	whole fish	£2,115.31	12	£176.28
pike	1327	Leicester	whole fish	£2,358.26	12	£196.52
bream	1327	Leicester	whole fish	£1,044.30	12	£87.03
eels	1327	Leicester	whole fish	£2,287.03	12	£190.59
lampreys	1327	Leicester	whole fish	£4,795.38	12	£399.62
salmon	1327	Leicester	UNK	£396.86		NA
quilibet salmon	1228	Torksey	All salmon	NA		NA
salmonis	1421	London		£6,270.88		NA
salmonis	1421	London		£12,950.07		NA
salmonis	1421	London	barrels	£6,504.93	12	£542.08
allecis	1421	London	barrels	£122.11	4	£30.53
salmonis	1467	Lynn	barrels	£8,330.22	12	£694.19
salmonis	1467	Lynn	barrels	£872.58	2	£436.29
salmonis	1467	Lynn	barrels	£653.80	1	£653.80
salmonis	1467	Lynn	barrels	£1,308.87	3	£436.29
salmonis	1467	Lynn	barrels	£1,308.87	3	£436.29
salmonis	1467	Lynn	barrels	£5,234.21	12	£436.18
salmonis	1467	Lynn	barrels	£36,636.95	84	£436.15
salmonis	1467	Lynn	barrels	£26,169.80	72	£363.47
salmonis	1467	Lynn	barrels	£20,440.78	60	£340.68
salmonis	1467	Lynn	barrels	£436.29	1	£436.29
salmonis	1467	Lynn	barrels	£10,468.43	36	£290.79
allecis	1467	Lynn	barrels	£1,745.16	12	£145.43
salmonis	1467	Lynn	barrels	£42,743.75	98	£436.16
salmonis	1467	Lynn	barrels	£5,234.21	12	£436.18
allecis alba	1467	Lynn	barrels	£3,925.34	36	£109.04
allecis	1467	Lynn	barrels	£5,234.21	36	£145.39
salmonis	1467	Lynn	barrels	£1,308.87	3	£436.29
salmonis	1444	Southampton	barrels	£27,390.90	36	£760.86
salmonis	1444	Southampton	barrels	£1,745.16	3	£581.72
ffysch	1350	Winchester		NA		NA
ffysch	1350	Winchester		£0.96		NA
fysh	1350	Winchester		£1.91		NA
fysh	1350	Winchester		£9.55		NA
ffysh	1350	Winchester		£5.73		NA
fysh	1350	Winchester		£1.91		NA
samowne	1350	Winchester		£11.45		NA
samowne	1350	Winchester		£7.63		NA

samowne	1350	Winchester		£3.82		NA
salmon.	1308	Durham	whole fish	£213.69	2	£106.85
salmon. calver	1342	Durham	prepared fish	£99.21	1	£99.21
salso salmon.	1343	Durham	prepared fish	£27.98	1	£27.98
salmon. stopp.	1343	Durham	prepared fish	£190.80	2	£95.40
salmon. calver	1343	Durham	prepared fish	£142.46	3	£47.49
salmon. stopp.	1343	Durham	prepared fish	£190.80	2	£95.40
salmon. calver	1343	Durham	prepared fish	£286.20	4	£71.55
Stopedsalmon	1343	Durham	prepared fish	£78.86	1	£78.86
Salmon. Troutys	1388	Durham	whole fish	£41.98	5	£8.40
salmon. poudrt	1389	Durham	prepared fish	£119.57	2	£59.79
salmon. sals.	1416	Durham	prepared fish	£156.45	4	£39.11
salmon. poudred	1417	Durham	prepared fish	£109.39	1	£109.39
salmon.	1442	Durham	whole fish	£20.35	1	£20.35
dogdraves	1442	Durham	whole fish	£95.40	2	£47.70
salmon. poudred	1442	Durham	prepared fish	£203.52	5	£40.70
anguilla sals.	1442	Durham	whole fish	£127.20	5	£25.44
trutes sals et trutes rec.	1442	Durham	whole fish	£150.09	20	£7.50
poudred salmon.	1449	Durham	prepared fish	£95.40	7	£13.63
salmon.	1449	Durham	whole fish	£78.86	4	£19.72
salmon.	1449	Durham	prepared fish	£145.01	11	£13.18
salmonibus	1308	Durham	whole fish	£47,390.30	23	£2,060.45
salmonibus	1308	Durham	whole fish	£3,041.31	23	£132.23
dogdr.	1308	Durham	whole fish	£27,371.82	1748	£15.66
salmonibus	1330	Durham	whole fish	£357.43	9	£39.71
salmonibus salsis	1334	Durham	whole fish	£253.12	2	£126.56
salmonibus recentibus	1334	Durham	whole fish	£214.97	2	£107.49
allec. rub.	1334	Durham	whole fish	£351.07	1000	£0.35
salmonibus	1334	Durham	whole fish	£200.97	2	£100.49
allec.	1334	Durham	whole fish	£493.53	1500	£0.33
salmonibus	1334	Durham	whole fish	£822.97	10	£82.30
salmonibus	1334	Durham	whole fish	£2,837.80	41	£69.21
salmonibus	1334	Durham	whole fish	£618.18	11	£56.20
salmonibus	1334	Durham	whole fish	£194.61	7	£27.80
turbot	1334	Durham	whole fish	£83.95	1	£83.95
salmonibus	1334	Durham	whole fish	£513.88	12	£42.82
salmonibus	1334	Durham	whole fish	£1,013.77	28	£36.21
salmonibus	1334	Durham	whole fish	£1,020.13	18	£56.67
Rayes	1334	Durham	whole fish	£113.21	6	£18.87
allec. recent.	1334	Durham	whole fish	£279.84	700	£0.40
salmonibus	1334	Durham	whole fish	£643.62	15	£42.91
allec.	1334	Durham	whole fish	£793.72	1000	£0.79
salmonibus	1334	Durham	whole fish	£188.25	7	£26.89
summis alb. pisc.	1334	Durham	whole fish	£1,960.13	11	£178.19
salmonibus	1334	Durham	whole fish	£150.09	6	£25.02
allec. recent.	1334	Durham	whole fish	£432.47	1500	£0.29
medietate porpays	1334	Durham	whole fish	£139.92	1	£139.92
summis alb. pisc.	1334	Durham	whole fish	£1,452.61	13	£111.74
salmonibus	1334	Durham	whole fish	£831.88	31	£26.83
salmonibus	1334	Durham	whole fish	£624.54	24	£26.02
salmonibus	1334	Durham	whole fish	£1,312.69	32	£41.02
Coungres	1334	Durham	whole fish	£64.87	3	£21.62
salmonibus	1334	Durham	whole fish	£394.32	14	£28.17
allec. recent.	1334	Durham	whole fish	£480.81	1300	£0.37
salmonibus	1334	Durham	whole fish	£393.04	17	£23.12
summis alb. p.	1334	Durham	whole fish	£796.26	7	£113.75
salmonibus	1334	Durham	whole fish	£83.95	4	£20.99
allec.	1334	Durham	whole fish	£449.01	1900	£0.24
summis alb. p.	1334	Durham	whole fish	£649.98	6	£108.33
salmonibus	1334	Durham	whole fish	£273.48	15	£18.23
allec. recent.	1334	Durham	whole fish	£484.63	1400	£0.35
salmonibus	1334	Durham	whole fish	£129.74	6	£21.62
salmonibus	1334	Durham	whole fish	£175.53	11	£15.96
salmonibus	1338	Durham	whole fish	£190.80	6	£31.80

turbot magnis	1338	Durham	whole fish	£634.72	7	£90.67
Rowndelet de Sturgeown	1388	Durham	prepared fish	£295.10	2	£147.55
salmonibus pulv'	1388	Durham	prepared fish	£97.94	2	£48.97
allec. alb.	1389	Durham	barrels	£379.05	1	£379.05
salmonibus pulv'	1403	Durham	prepared fish	£104.30	2	£52.15
salmonibus pulv'	1403	Durham	prepared fish	£22.90	7	£3.27
salmonibus salsis	1403	Durham	prepared fish	£156.45	4	£39.11
salmonibus salsis	1403	Durham	prepared fish	£104.30		NA
salmon.	1299	Durham	barrels	£5,238.03	1	£5,238.03
salmon.	1311	Durham	whole fish	£1,938.50	12	£161.54
salmone	1311	Durham		£857.32		NA
salmon.	1311	Durham		£601.65		NA
salmon.	1340	Durham		£3,599.71		NA
salmonibus	1474	Durham		£166.63		NA
salmon. sals. et pouder'.	1409	Durham	prepared fish	£601.65	15	£40.11
stockfysh	1409	Durham	prepared fish	£417.21	50	£8.34
dogdrafe	1409	Durham	whole fish	£6,031.75	109	£55.34
dogdrafe	1524	Durham	whole fish	£2,315.01	166	£13.95
drycodlyng	1524	Durham	prepared fish	£1,824.02	1846	£0.99
allec. alb.	1524	Durham	barrels	£2,976.44	8	£372.06
salmonum salt	1524	Durham	barrels	£6,945.03	8	£868.13
seyme salmon. salt	1524	Durham	prepared fish	£2,645.73	8	£330.72
piscibus recent.	1524	Durham		£1,509.84		NA

E Statistical Analysis and Data Visualization Code

Quinlan Salmo sp. PhD Code

Introduction

This RMarkdown document contains a record of all statistical and data visualization code used in the PhD thesis entitled “The Medieval Ichthyoarchaeology and Historical Ecology of Salmo sp. Fishes Across the North Sea Basin”, submitted to the Archaeology Department of the University of York by Liz M. Quinlan.

The intention behind making this document public is threefold– first to act as a reference of previous successful code for my own continued research, second to participate in and encourage open data sharing within the world of archaeological science, and third to help demystify analytical processes for other early career researchers who, like I did, had no coding experience prior to commencing a PhD or other degree.

The code included in this document may not always be the most elegant, but it has worked for my purposes. I am happy to receive any feedback on code used or decisions made, and actively welcome discussion about best practices in archaeological science data analysis using R.

The following document is broken down by chapter, with all code in order. All produced figures have been included, and annotations explaining the decision making process are include in certain circumstances. Chapters 1, 3 and 4 do not include any figures or analysis produced or conducted in R, and are omitted from this document.

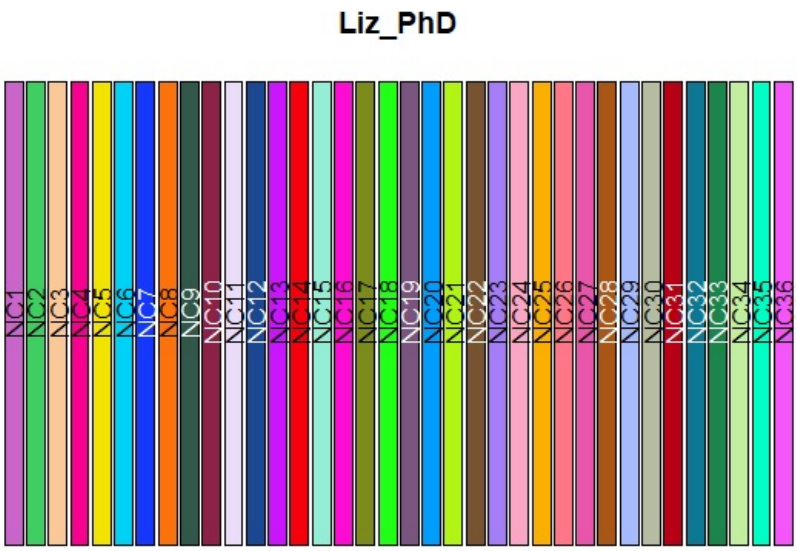
General Thesis Code

```
library(broom)
library(cowplot)
library(ggplot2)
library(DiagrammeR)
library(dplyr)
library(ggdist)
library(ggExtra)
library(ggforce)
library(ggmap)
library(ggplot2)
library(ggpmisc)
library(ggpubr)
library(ggrepel)
library(ggsn)
library(grid)
library(gridExtra)
library(magick)
library(mapdata)
library(maps)
library(maptools)
library(MASS)
library(palmerpenguins)
library(plyr)
library(rcartocolor)
library(Rcpp)
library(readr)
library(reshape)
library(reshape2)
library(rgdal)
library(rgeos)
library(rKIN)
library(rnaturalearth)
library(rnaturalearthdata)
library(scales)
library(sf)
library(spData)
library(stringr)
library(tidyverse)
```

```
library(viridis)
library(qqplotr)
library(wesanderson)
```

The custom palette for this thesis data is below, using the polychrome package. There are other color palettes used throughout the thesis, but this one is used when more than 5 colors are required.

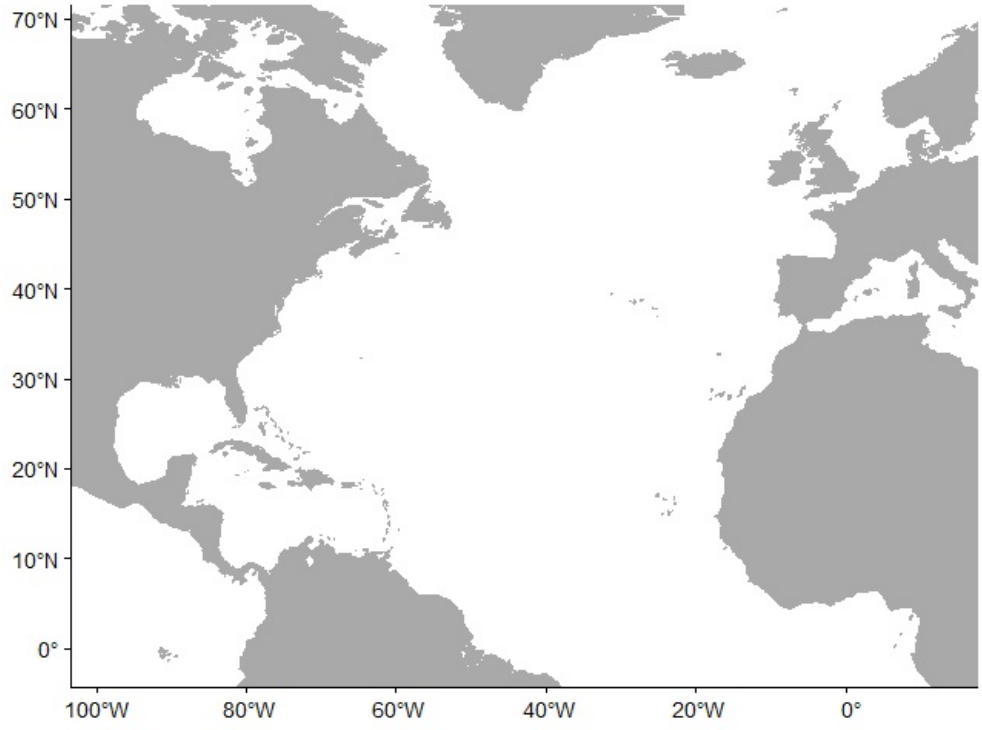
```
library(Polychrome)
Liz_PhD <- createPalette(36, c("#CC66CC", "#33CC66", "#FAC898", "#FF1493", "#FFEF00"))
swatch(Liz_PhD)
```



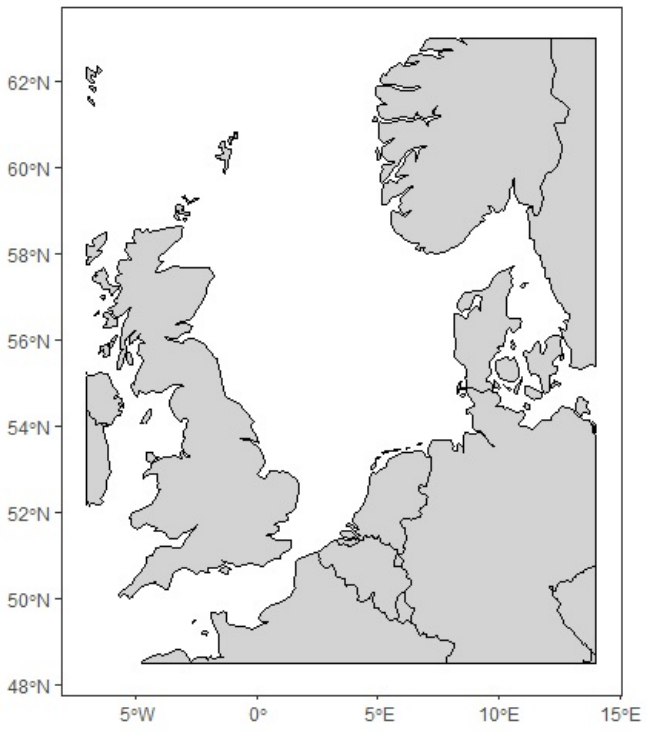

```
names(Liz_PhD) <-NULL
```

The base map for the North Sea study area, including major rivers and lakes

```
#Map of all sites with rivers
sf::sf_use_s2(FALSE)
world <- ne_countries(scale = "medium", returnclass = "sf")
world_map<-ggplot(data=world) + geom_sf(color="darkgrey", fill="darkgrey")+ theme(plot.margin=unit(c(0,0
world_map
```



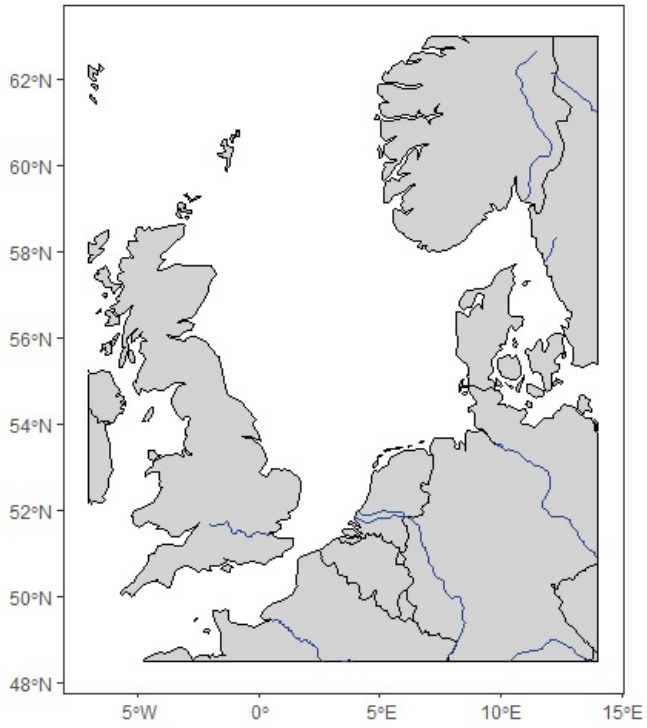

```
NWEU_crop <- st_crop(world, xmin= -7, xmax= 14,
                     ymin= 48.5, ymax=63)
Europe_crop <- ggplot(data=NWEU_crop) + geom_sf(color="black", fill="lightgrey") +theme_bw() + theme(pan
Europe_crop
```




```
utils::download.file(file.path('https://www.naturalearthdata.com/http//www.naturalearthdata.com/download
rivers50 <- ne_download(scale = 50, type = 'rivers_lake_centerlines', category = 'physical', returnclass
rivers_cropped <- st_crop(st_as_sf(rivers50), xmin= -7, xmax= 14,
                          ymin= 48.5, ymax=63)

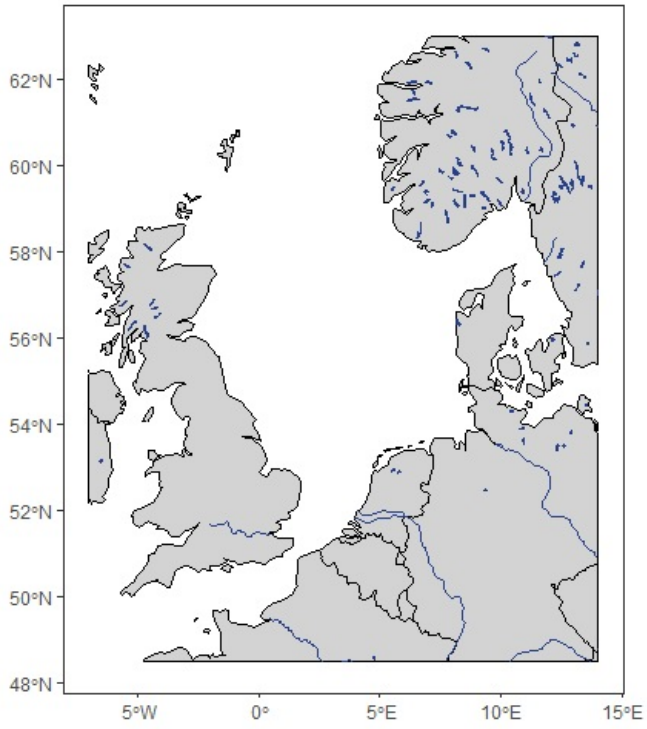
NorthSea_Rivers <- st_crop(st_as_sf(rivers50), xmin= -7, xmax= 14,
                           ymin= 48.5, ymax=63)

StudyArea <- Europe_crop + geom_sf(data=NorthSea_Rivers, col= "royalblue4")
StudyArea
```




```
europe_rivers <- ne_download(scale = 10, type = 'lakes_europe', category = 'physical', returnclass = "sf
EURivers_cropped <- st_crop(st_as_sf(europe_rivers), xmin= -7, xmax= 14,ymin= 48.5, ymax=63)

StudyArea_2<- StudyArea + geom_sf(data= EURivers_cropped, col= "royalblue4")
NS_Map<- StudyArea_2 + coord_sf(xlim= c(-7, 14), ylim= c(48.5,63))
NS_Map
```



Chapter 2 - Archaeological Background and Materials

Code

Figure 2.1 - Biomolecular Types Map

```
BM_Locations<- read.csv("BM_Locations.csv")
```

```
BM_Map <- Europe_crop + geom_point(data= BM_Locations, aes(x=lat, y= long, color= Biomolecular_Data), si
BM_Map
```

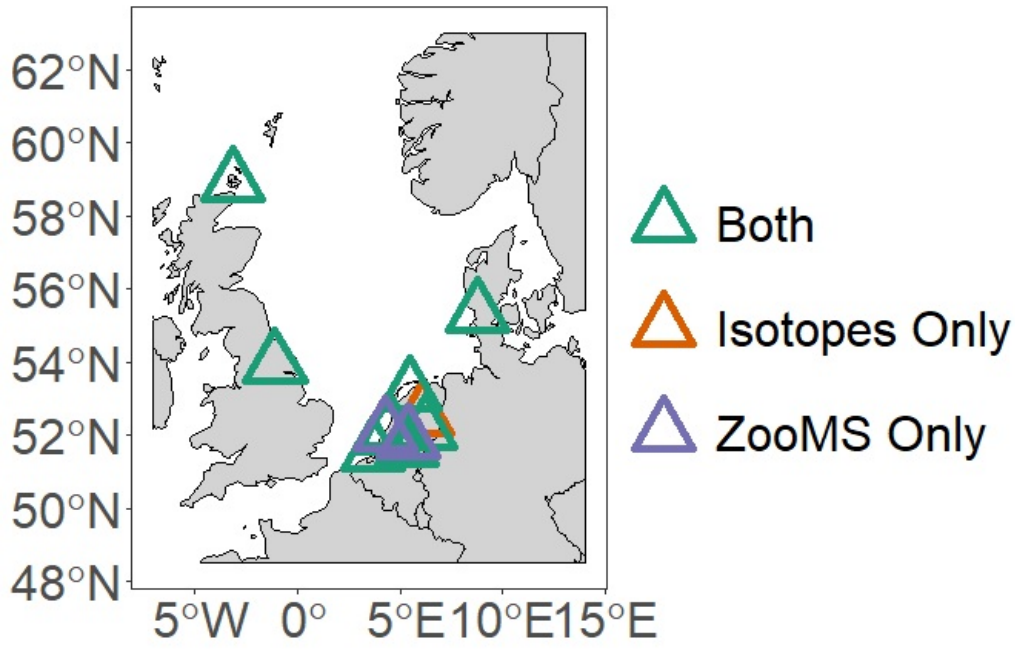
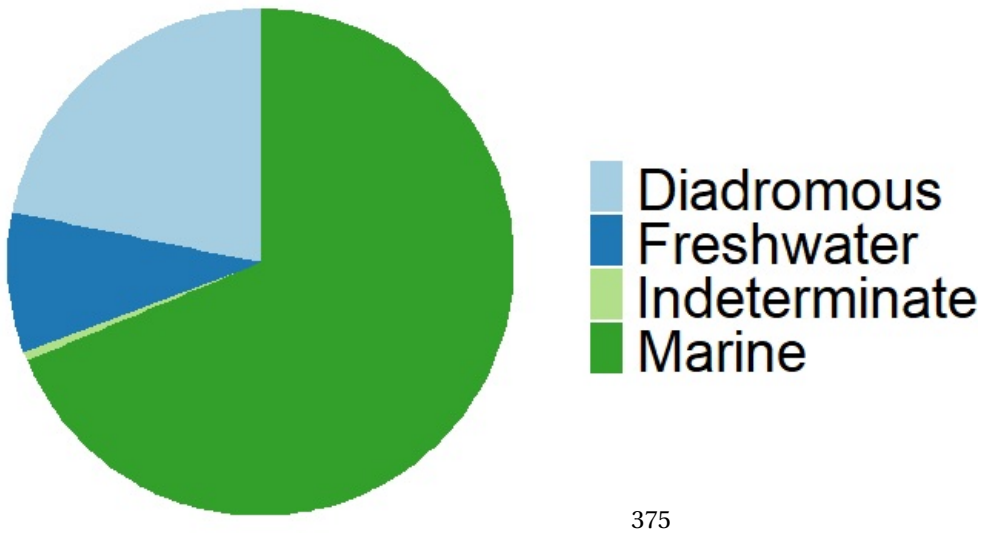


Figure 2.2 - Coppergate NISP Proportions

```
category <- c("Freshwater", "Marine", "Diadromous", "Indeterminate")
NISP <- c(1323, 10136, 3218, 83)
prop <- c("9.0%", "68.7%", "21.8", "0.5%")
COP_Props <- data.frame(category, NISP, prop)

COP_Pie <-  ggplot(COP_Props, aes(x = 1, y = NISP, fill = category)) + geom_bar(stat = "identity")
COP_Pie2 <- COP_Pie + coord_polar(theta = 'y') +theme_void() + labs(fill=NULL) + scale_fill_brewer(palet
COP_Pie2
```



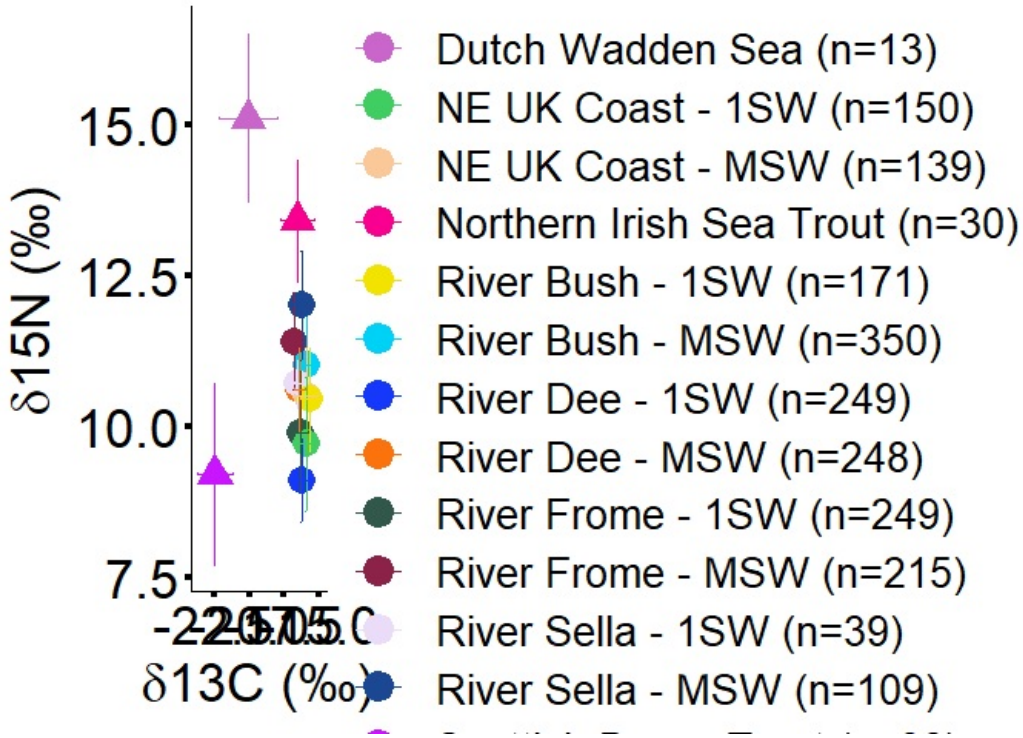
Chapter 5 - Salmo sp. Ecology

Code

Figure 5.4 - Modern Isotope Baselines

```
Modern_Baselines <- read.csv("Salmo_Modern_Baselines.csv")

p <- ggplot(Modern_Baselines, aes(x=D13C, y=D15N, color=Sample, shape= Species)) + geom_point(size=5, st
Mean_Error_Plot <- p+theme(legend.text=element_text(size=20), legend.key.size = unit(1, "cm"),legend.tit
Mean_Error_Plot
```



Chapter 6 - North Sea Archaeological Salmo sp. Review

Code

Dataset formation and cleaning

```
#Data uploading and subsetting
#subsets of groups
NSASR_Master <-read.csv("NSASR_Master.csv")
NSASR_salmonids <- subset(NSASR_Master, salmonid.site == "yes")
NSASR_non_salmonids <-subset(NSASR_Master, salmonid.site =="no")
NSASR_Master[NSASR_Master == "Albarella & Pirnie"] <- "Albarella & Pirnie 2008"
#Subsets of countries
NSASR_England <- subset(NSASR_salmonids, country == "England")
NSASR_Scotland <- subset(NSASR_salmonids, country == "Scotland")
NSASR_Norway <- subset(NSASR_salmonids, country == "Norway")
NSASR_Netherlands <- subset(NSASR_salmonids, country == "Netherlands")
NSASR_France <- subset(NSASR_salmonids, country == "France")
NSASR_Denmark <- subset(NSASR_salmonids, country == "Denmark")
NSASR_Germany <- subset(NSASR_salmonids, country == "Germany")
NSASR_Belgium <- subset(NSASR_salmonids, country == "Belgium")
```



```
#Subsets of sources
NSASR_NSS <- subset(NSASR_Master, source == "NSS")
NSASR_Albarella <- subset(NSASR_Master, source == "Albarella & Pirnie")
NSASR_Holmes <- subset(NSASR_Master, source == "Holmes 2017")
NSASR_LMQ <- subset(NSASR_Master, source == "LMQ")
NSASR_Clavel <- subset(NSASR_Master, source == "Clavel 2001")
```

```
NSASR_Enghoff_1999 <- subset(NSASR_Master, source == "Enghoff 1999")
NSASR_Enghoff_2000 <- subset(NSASR_Master, source == "Enghoff 2000")

#Dataset with Coppergate  and La Roche en Ardenne removed
NSASR_Coppergate_Removed <- subset(NSASR_Master, site_name !="16-22 Coppergate")
NSASR_LaRenA_Removed <- subset(NSASR_Coppergate_Removed, site_name != "Chateau La Roche en Ardenne")

str(NSASR_Master)
```

```
## 'data.frame':    1270 obs. of  37 variables:
##  $ lmq_NSASR_number        : chr  "lmq_NSASR_0001" "lmq_NSASR_0002" "lmq_NSASR_0003" "lmq_NSASR_0004"
##  $ site_name               : chr  "Mindets tomt" "Mindets tomt" "Mindets tomt" "Søndre Felt" ...
##  $ phase_description       : chr  "Mindets tomt, osteological period I" "Mindets tomt, osteological p
##  $ municipality_or_region  : chr  "Oslo" "Oslo" "Oslo" "Oslo" ...
##  $ country                 : chr  "Norway" "Norway" "Norway" "Norway" ...
##  $ site_type               : chr  "Settlement " "Settlement " "Settlement " "Settlement " ...
##  $ context_type            : chr  "" "" "" "" ...
##  $ cultural_period         : chr  "1025-1125/50 AD" "1225-1350 AD" "1350-1624 AD" "Late Middle Ages"
##  $ date_start              : int  1025 1225 1350 1350 1170 1300 1332 800 840 800 ...
##  $ date_end                : chr  "1125-1150" "1350" "1624" "1500" ...
##  $ midpoint                : num  1088 1288 1487 1425 1235 ...
##  $ lat                     : num  59.9 59.9 59.9 59.9 60.4 ...
##  $ long                    : num  10.77 10.77 10.77 10.77 5.32 ...
##  $ collection_method       : chr  "Hand Collected" "Hand Collected" "Hand Collected" "Sieved" ...
##  $ cm_group                : chr  "Hand Collected" "Hand Collected" "Hand Collected" "Sieved" ...
##  $ report_date             : chr  "1988" "1988" "1988" "1988" ...
##  $ indeterminate_NISP      : chr  "98" "405" "0" "71" ...
##  $ fish_NISP               : int  1035 3382 98 281 100 196 140 23 250 46 ...
##  $ freshwater_nisp         : chr  "0" "0" "0" "0" ...
##  $ marine_NISP             : chr  "1035" "3382" "98" "281" ...
##  $ diadromous              : chr  "0" "0" "0" "0" ...
##  $ unknown                 : chr  "0" "0" "0" "0" ...
##  $ salmo                   : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_salar             : chr  "0" "0" "0" "0" ...
##  $ salmo_cf_salar          : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_salar_salmo_trutta: int  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_trutta            : chr  "0" "0" "0" "0" ...
##  $ salmo_cf_trutta         : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmonid                : chr  "0" "0" "0" "0" ...
##  $ salmonidae              : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ total_context_salmonids : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ reference               : chr  "Lie, R.W., 1988. F. Animal Bones, in: Schia, E. (Ed.), \"Mindets t
##  $ analyst                 : chr  "Rolf W. Lie" "Rolf W. Lie" "Rolf W. Lie" "Rolf W. Lie" ...
##  $ salmonid.site           : chr  "no" "no" "no" "no" ...
##  $ source                  : chr  "NSS" "NSS" "NSS" "NSS" ...
##  $ midpoint_era            : chr  "1050-1200" "1200-1350" "1350-1500" "1350-1500" ...
##  $ report_decade           : chr  "1980s" "1980s" "1980s" "1980s" ...
```

```
#Mutating columns to read as numeric or characters


NSASR_Master <- NSASR_Master %>%
  mutate(date_start = as.character(date_start),
         date_end = as.character(date_end),
         report_date = as.numeric(report_date),
         indeterminate_NISP = as.numeric(indeterminate_NISP),
         fish_NISP = as.numeric(fish_NISP),
         freshwater_nisp = as.numeric(freshwater_nisp),
         marine_NISP = as.numeric(marine_NISP),
         diadromous = as.numeric(diadromous),
         unknown = as.numeric(unknown),
         salmo = as.numeric(salmo),
         salmo_salar = as.numeric(salmo_salar),
         salmo_cf_salar = as.numeric(salmo_cf_salar),
         salmo_salar_salmo_trutta = as.numeric(salmo_salar_salmo_trutta),
         salmo_trutta = as.numeric(salmo_trutta),
         salmo_cf_trutta = as.numeric(salmo_cf_trutta),
```

```
         salmonid = as.numeric(salmonid),
         salmonidae = as.numeric(salmonidae),
         total_context_salmonids = as.numeric(total_context_salmonids))
```

```
## Warning in eval(cols[[col]], .data, parent.frame()): NAs introduced by coercion

## Warning in eval(cols[[col]], .data, parent.frame()): NAs introduced by coercion

## Warning in eval(cols[[col]], .data, parent.frame()): NAs introduced by coercion

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## Warning in eval(cols[[col]], .data, parent.frame()): NAs introduced by coercion

## Warning in eval(cols[[col]], .data, parent.frame()): NAs introduced by coercion
```

```
warnings()
str(NSASR_Master)
```

```
## 'data.frame':    1270 obs. of  37 variables:
##  $ lmq_NSASR_number        : chr  "lmq_NSASR_0001" "lmq_NSASR_0002" "lmq_NSASR_0003" "lmq_NSASR_0004"
##  $ site_name               : chr  "Mindets tomt" "Mindets tomt" "Mindets tomt" "Søndre Felt" ...
##  $ phase_description       : chr  "Mindets tomt, osteological period I" "Mindets tomt, osteological p
##  $ municipality_or_region  : chr  "Oslo" "Oslo" "Oslo" "Oslo" ...
##  $ country                 : chr  "Norway" "Norway" "Norway" "Norway" ...
##  $ site_type               : chr  "Settlement " "Settlement " "Settlement " "Settlement " ...
##  $ context_type            : chr  "" "" "" "" ...
##  $ cultural_period         : chr  "1025-1125/50 AD" "1225-1350 AD" "1350-1624 AD" "Late Middle Ages"
##  $ date_start              : chr  "1025" "1225" "1350" "1350" ...
##  $ date_end                : chr  "1125-1150" "1350" "1624" "1500" ...
##  $ midpoint                : num  1088 1288 1487 1425 1235 ...
##  $ lat                     : num  59.9 59.9 59.9 59.9 60.4 ...
##  $ long                    : num  10.77 10.77 10.77 10.77 5.32 ...
##  $ collection_method       : chr  "Hand Collected" "Hand Collected" "Hand Collected" "Sieved" ...
##  $ cm_group                : chr  "Hand Collected" "Hand Collected" "Hand Collected" "Sieved" ...
##  $ report_date             : num  1988 1988 1988 1988 1985 ...
##  $ indeterminate_NISP      : num  98 405 0 71 193 172 68 0 0 0 ...
##  $ fish_NISP               : num  1035 3382 98 281 100 ...
##  $ freshwater_nisp         : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ marine_NISP             : num  1035 3382 98 281 99 ...
##  $ diadromous              : num  0 0 0 0 1 0 0 0 0 0 ...
##  $ unknown                 : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo                   : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_salar             : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_cf_salar          : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_salar_salmo_trutta: num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_trutta            : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_cf_trutta         : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmonid                : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmonidae              : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ total_context_salmonids : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ reference               : chr  "Lie, R.W., 1988. F. Animal Bones, in: Schia, E. (Ed.), \"Mindets t
##  $ analyst                 : chr  "Rolf W. Lie" "Rolf W. Lie" "Rolf W. Lie" "Rolf W. Lie" ...
##  $ salmonid.site           : chr  "no" "no" "no" "no" ...
##  $ source                  : chr  "NSS" "NSS" "NSS" "NSS" ...
##  $ midpoint_era            : chr  "1050-1200" "1200-1350" "1350-1500" "1350-1500" ...
##  $ report_decade           : chr  "1980s" "1980s" "1980s" "1980s" ...
```

```
#Changing the forced NAs to 0 values for the columns which deal with NISP and other element values
```

```
NSASR_Master[['salmo']][is.na(NSASR_Master[['salmo']])] <- 0
NSASR_Master[['salmo_salar']][is.na(NSASR_Master[['salmo_salar']])] <- 0
NSASR_Master[['salmo_cf_salar']][is.na(NSASR_Master[['salmo_cf_salar']])] <- 0
NSASR_Master[['salmo_salar_salmo_trutta']][is.na(NSASR_Master[['salmo_salar_salmo_trutta']])] <- 0
NSASR_Master[['salmo_trutta']][is.na(NSASR_Master[['salmo_trutta']])] <- 0
NSASR_Master[['salmo_cf_trutta']][is.na(NSASR_Master[['salmo_cf_trutta']])] <- 0
NSASR_Master[['salmonid']][is.na(NSASR_Master[['salmonid']])] <- 0
NSASR_Master[['fish_NISP']][is.na(NSASR_Master[['fish_NISP']])] <- 0
NSASR_Master[['freshwater_nisp']][is.na(NSASR_Master[['freshwater_nisp']])] <- 0
NSASR_Master[['marine_NISP']][is.na(NSASR_Master[['marine_NISP']])] <- 0
NSASR_Master[['diadromous']][is.na(NSASR_Master[['diadromous']])] <- 0
NSASR_Master[['unknown']][is.na(NSASR_Master[['unknown']])] <- 0
NSASR_Master[['salmonidae']][is.na(NSASR_Master[['salmonidae']])] <- 0
NSASR_Master[['indeterminate_NISP']][is.na(NSASR_Master[['indeterminate_NISP']])] <- 0
NSASR_Master[['total_context_salmonids']][is.na(NSASR_Master[['total_context_salmonids']])] <- 0

str(NSASR_Master)
```

```
## 'data.frame':    1270 obs. of  37 variables:
##  $ lmq_NSASR_number        : chr  "lmq_NSASR_0001" "lmq_NSASR_0002" "lmq_NSASR_0003" "lmq_NSASR_0004"
##  $ site_name               : chr  "Mindets tomt" "Mindets tomt" "Mindets tomt" "Søndre Felt" ...
##  $ phase_description       : chr  "Mindets tomt, osteological period I" "Mindets tomt, osteological p
##  $ municipality_or_region  : chr  "Oslo" "Oslo" "Oslo" "Oslo" ...
##  $ country                 : chr  "Norway" "Norway" "Norway" "Norway" ...
##  $ site_type               : chr  "Settlement " "Settlement " "Settlement " "Settlement " ...
##  $ context_type            : chr  "" "" "" "" ...
##  $ cultural_period         : chr  "1025-1125/50 AD" "1225-1350 AD" "1350-1624 AD" "Late Middle Ages"
##  $ date_start              : chr  "1025" "1225" "1350" "1350" ...
##  $ date_end                : chr  "1125-1150" "1350" "1624" "1500" ...
##  $ midpoint                : num  1088 1288 1487 1425 1235 ...
##  $ lat                     : num  59.9 59.9 59.9 59.9 60.4 ...
##  $ long                    : num  10.77 10.77 10.77 10.77 5.32 ...
##  $ collection_method       : chr  "Hand Collected" "Hand Collected" "Hand Collected" "Sieved" ...
##  $ cm_group                : chr  "Hand Collected" "Hand Collected" "Hand Collected" "Sieved" ...
##  $ report_date             : num  1988 1988 1988 1988 1985 ...
##  $ indeterminate_NISP      : num  98 405 0 71 193 172 68 0 0 0 ...
##  $ fish_NISP               : num  1035 3382 98 281 100 ...
##  $ freshwater_nisp         : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ marine_NISP             : num  1035 3382 98 281 99 ...
##  $ diadromous              : num  0 0 0 0 1 0 0 0 0 0 ...
##  $ unknown                 : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo                   : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_salar             : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_cf_salar          : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_salar_salmo_trutta: num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_trutta            : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmo_cf_trutta         : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmonid                : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ salmonidae              : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ total_context_salmonids : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ reference               : chr  "Lie, R.W., 1988. F. Animal Bones, in: Schia, E. (Ed.), \"Mindets t
##  $ analyst                 : chr  "Rolf W. Lie" "Rolf W. Lie" "Rolf W. Lie" "Rolf W. Lie" ...
##  $ salmonid.site           : chr  "no" "no" "no" "no" ...
##  $ source                  : chr  "NSS" "NSS" "NSS" "NSS" ...
##  $ midpoint_era            : chr  "1050-1200" "1200-1350" "1350-1500" "1350-1500" ...
##  $ report_decade           : chr  "1980s" "1980s" "1980s" "1980s" ...
```

```
NSASR_midpoint_subset <- NSASR_Master %>%
  group_by(midpoint) %>%
  summarise(total_context_salmonids = sum(total_context_salmonids))


#Adding Salmon,Trout and Salmonid columns from sum of relevant taxa columns

NSASR_Master$Salmon=rowSums(cbind(NSASR_Master$salmo_salar,NSASR_Master$salmo_cf_salar))
NSASR_Master$Trout=rowSums(cbind(NSASR_Master$salmo_trutta,NSASR_Master$salmo_cf_trutta))
```

```
NSASR_Master$Salmonids=rowSums(cbind(NSASR_Master$salmo,NSASR_Master$salmonid, NSASR_Master$salmo_salar_

#Defining decades and creating report_decade column
b<-c(1969, 1979, 1989, 1999, 2009, 2019, 2029)
names<-c("1970s","1980s", "1990s", "2000s", "2010s", "2020s")
NSASR_Master$report_date <- as.numeric(as.character(NSASR_Master$report_date)) #adjusting report_date to
NSASR_Master$report_decade <- cut(NSASR_Master$report_date, breaks=b, label=names) #assign to master dat


#Defining 150-year periods
b<-c(450, 600, 750, 900, 1050, 1200,1350, 1500, 1650)
names<-c("450-\n600", "600-\n750", "750-\n900", "900-\n1050", "1050-\n1200", "1200-\n1350", "1350-\n1500
NSASR_Master$midpoint <- as.numeric(as.character(NSASR_Master$midpoint)) #adjusting midpoint date to onl
NSASR_Master$midpoint_era <- cut(NSASR_Master$midpoint, breaks=b, label=names) #assign to master datafra
```

Figure 6.1

```
grViz("digraph a_nice_graph{
      graph [overlap = true]
      node [fontname = Helvetica, shape = rectangle, width = 4, style = filled, color = plum, fillcolor =
      edge [color = darkgray]

      a [label = 'Chosen Data Source
      (NSS 2016-Present, LMQ 2019-2021,
      Clavel 2001, Enghoff 1999, Enghoff 2000,
      Albarella & Pirni 2008, Holmes 2017']

      node [fontname = Helvetica, shape = oval, width = 4, style = filled, color= WhiteSmoke, fillcolor =
      edge [color = DarkGray]

      b [label = 'Narrow by Date Range'];
      e [label = 'Narrow by
      Geographic Location'];
      h [label = 'Narrow by
      Taxa Identification']

      node [fontname = Helvetica, shape = oval, width = 4, style = filled, color = YellowGreen, fillcolo
      edge [color= DarkGray]

      c [label = 'Midpoint between 500-1500CE'];
      f [label = 'Site in North Sea Basin'];
      i [label = 'Site with Salmonidae Presence']

      node [fontname = Helvetica, shape = oval, width = 4, style = filled, color = Salmon, fillcolor = Sa
      edge [color= DarkGray]

      d [label = 'Midpoint Outside Range'];
      g [label = 'Site Outside North Sea Basin']

      node [fontname = Helvetica, shape = oval, width = 4, style = filled, color = LightSteelBlue, fillc
      edge [color= DarkGray]

      j [label = 'Sites with
      no recorded salmonidae']

      a-> b
      b-> c
      b-> d
      c-> e
      e-> f
      e-> g
      f-> h
      h-> i
      h-> j
}
")
```

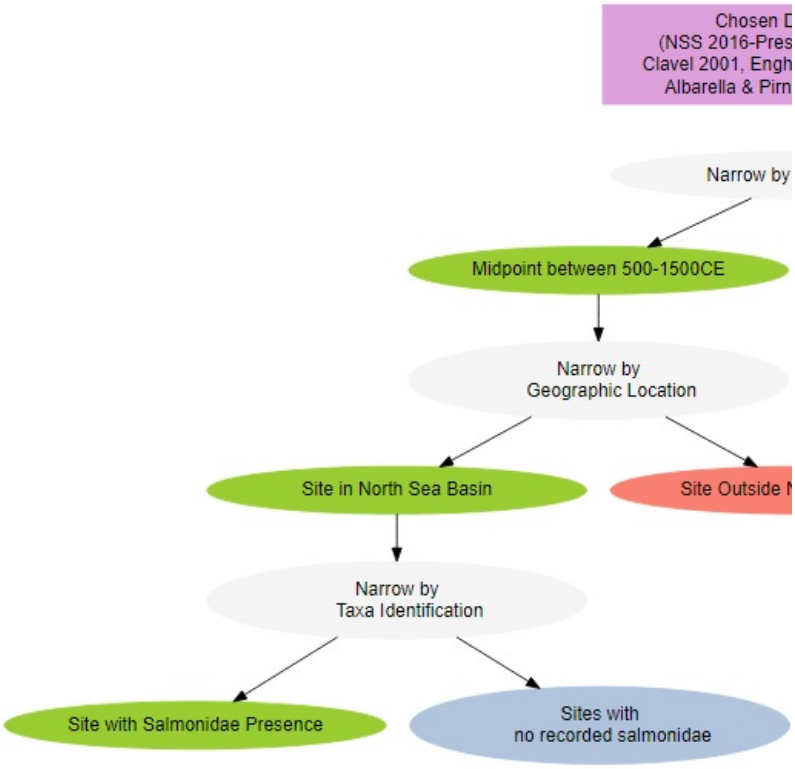
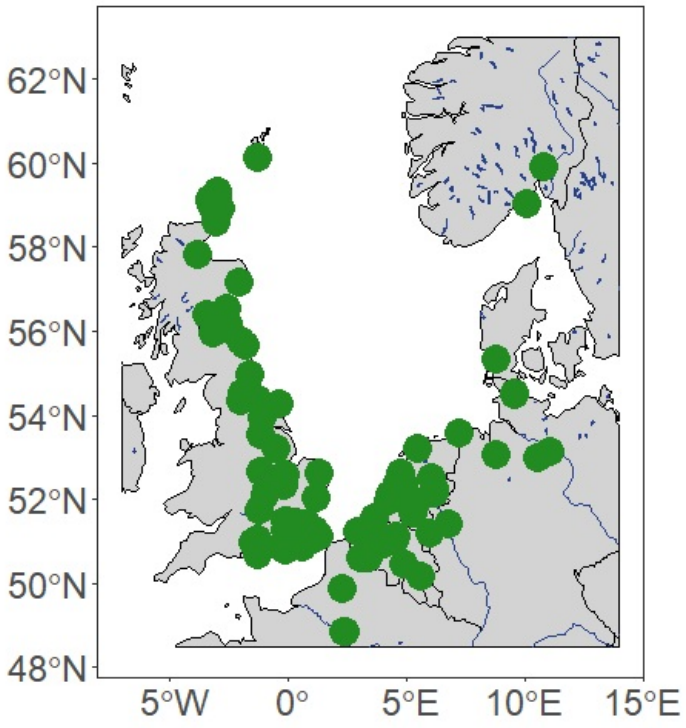


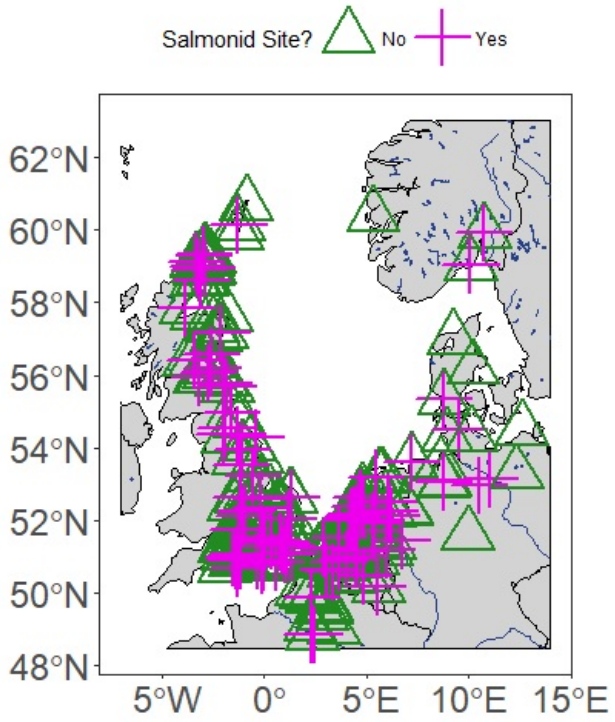
Figure 6.2

```
#map of all salmonid sites with rivers
Salmon_Sites<- NS_Map + geom_point(data=NSASR_salmonids, aes(x= long, y= lat), color= "forestgreen", sha
Salmon_Sites
```




```
#map of yes/no salmonid sites

All_Sites<-NS_Map + geom_point(data=NSASR_Master, aes(x= long, y= lat, color=salmonid.site, shape=salmon
All_Sites
```




```
ggarrange(All_Sites, Salmon_Sites, nrow = 1, labels= "AUTO")
```

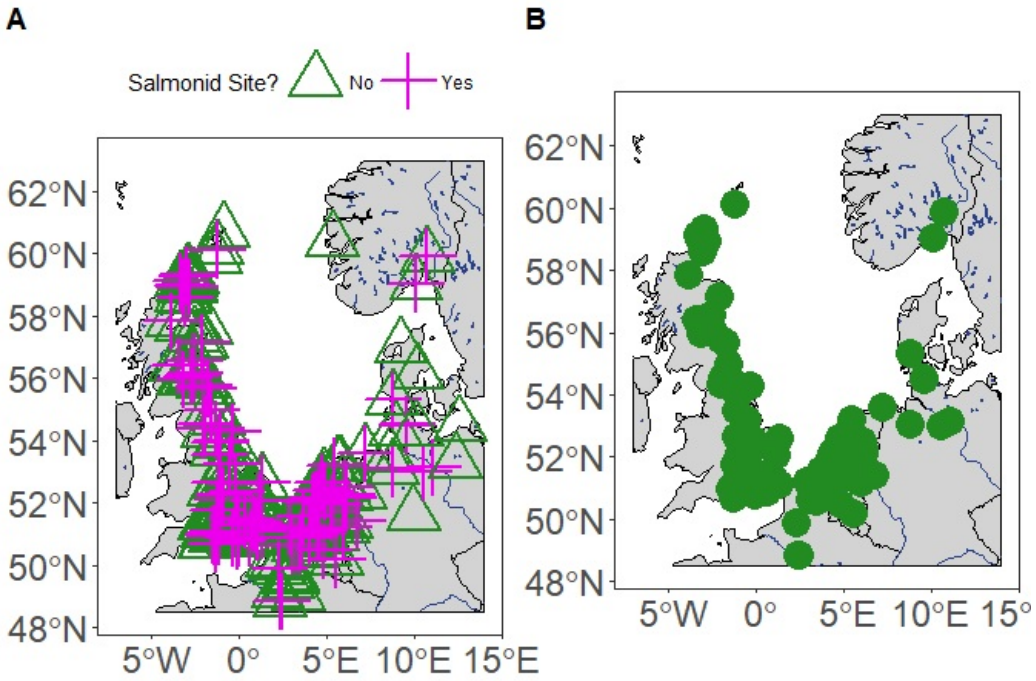


Figure 6.3

```
#Pie chart of all fish proportions
Values <- c(726363, 59942, 138685, 47641)
Type <- c("Marine", "Freshwater", "Diadromous", "Unknown")
Prop <- c(74.7,6.2,14.2,4.9)
NISP_Proportions <- data.frame(Values, Type, Prop)

NISP_Prop <-  ggplot(NISP_Proportions, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity"
NISP_Prop <- NISP_Prop + coord_polar(theta = 'y') + theme(legend.text=element_text(size=16)) + theme_voi
NISP_Prop <- NISP_Prop + theme(legend.title = element_blank())
NISP_Prop
```

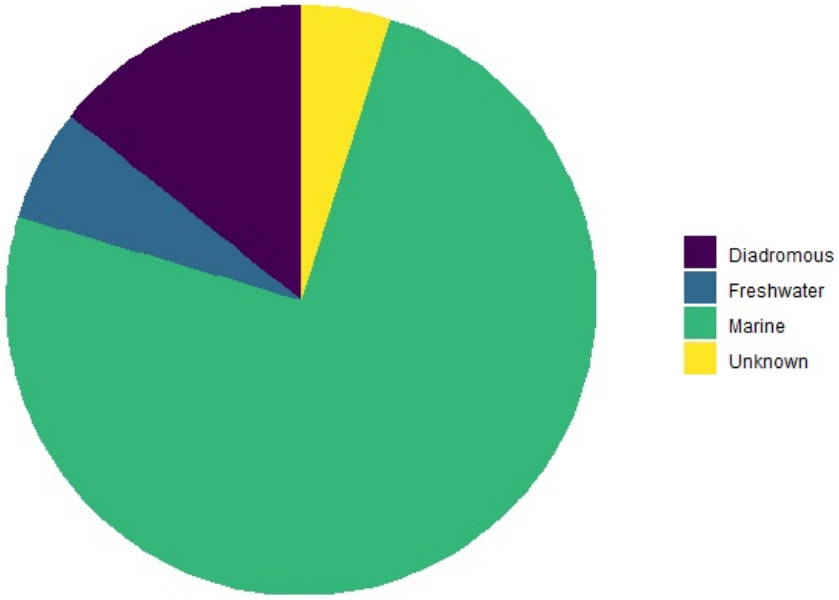
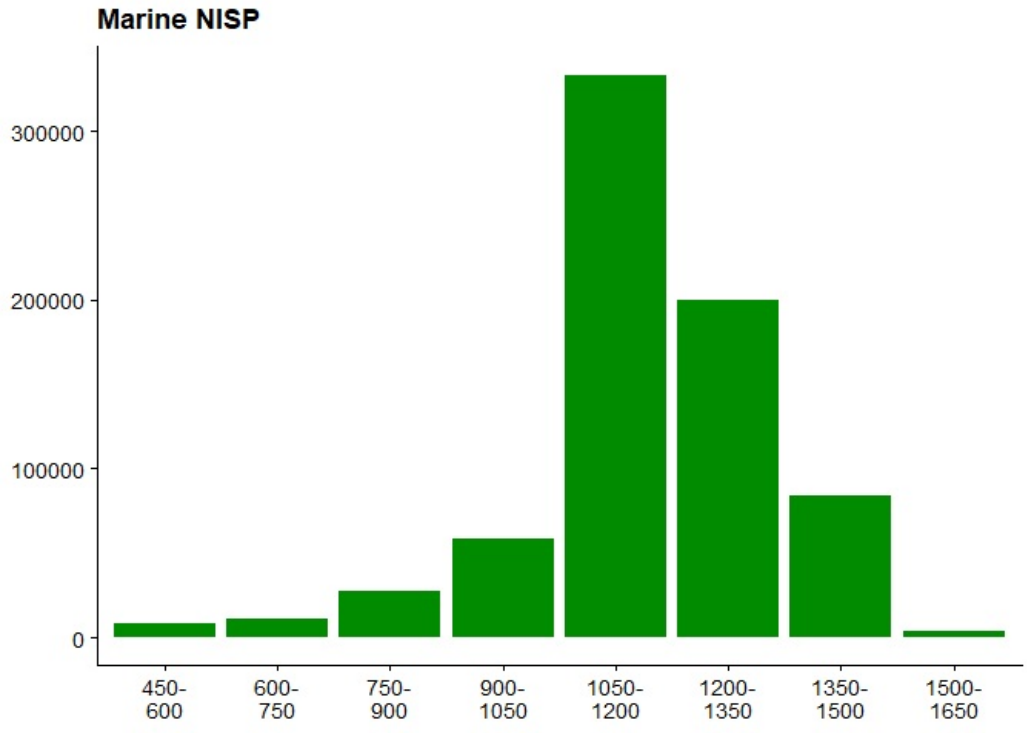


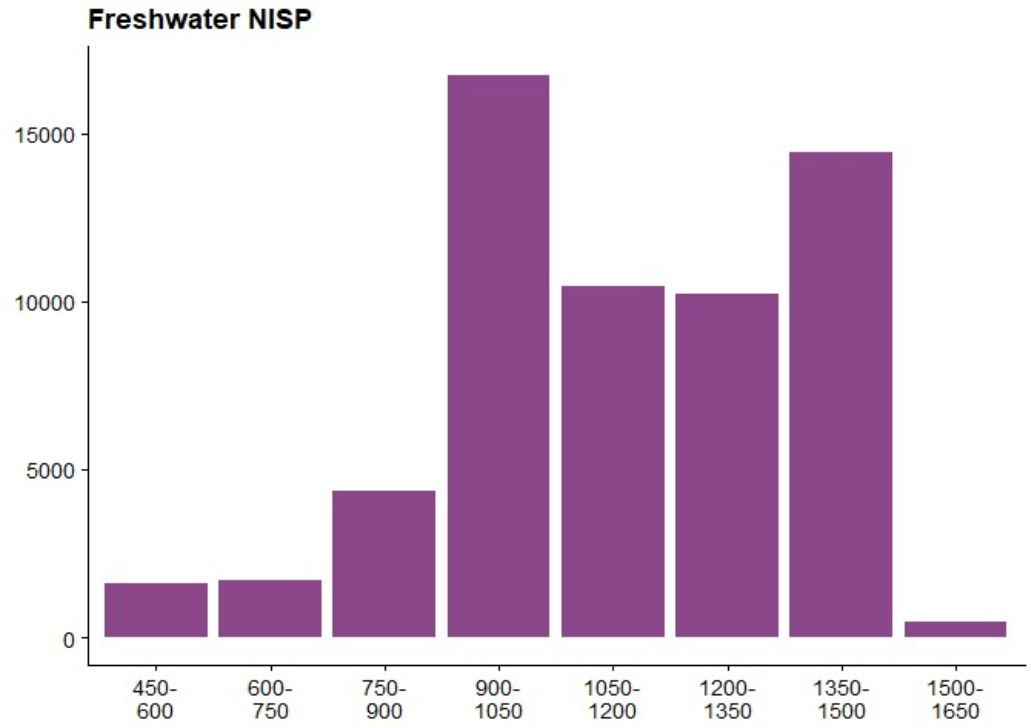
Figure 6.4

```
#Stacked chart for fish types over time for the entire NSASR dataset
#NISP over the years Marine

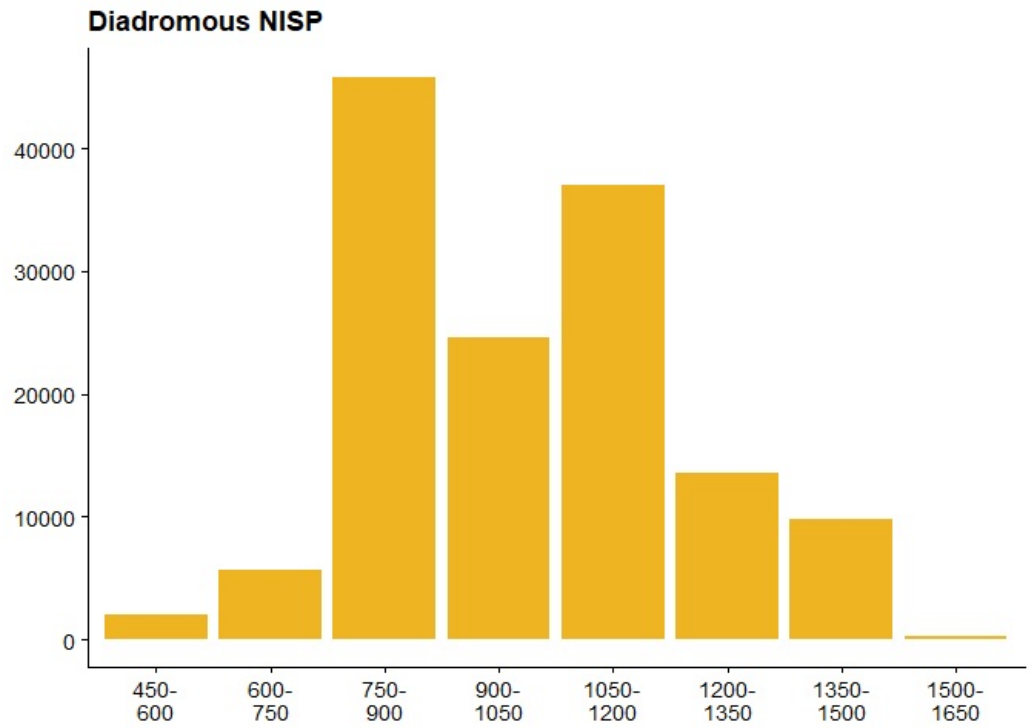
NSASR_Marine <- NSASR_Master %>% dplyr::select(marine_NISP,midpoint_era)
NSASR_Marine <- subset(NSASR_Marine, !is.na(midpoint_era))
Marine_plot <- ggplot(NSASR_Marine, aes(x=midpoint_era, y= marine_NISP)) + geom_col(fill = "green4") + la
Marine_plot <- Marine_plot +  theme(legend.position = "none")+ theme(axis.title.y = element_blank())+ th
Marine_plot
```



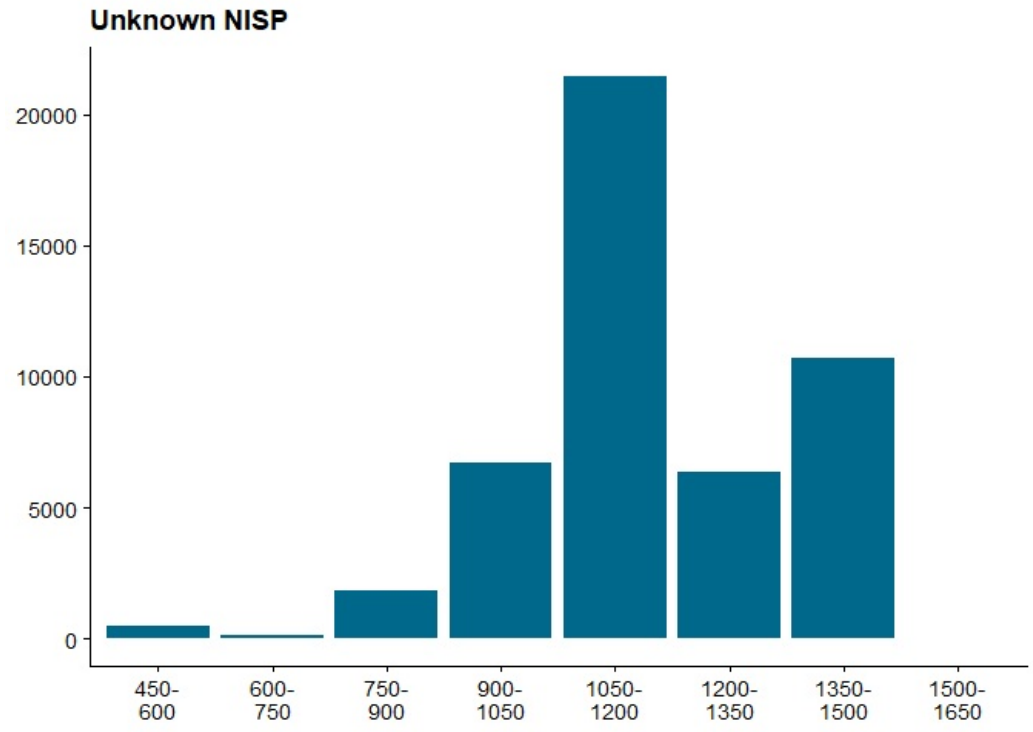

```
#Repeated the above for Freshwater sites
NSASR_Freshwater <- NSASR_Master %>% dplyr::select(freshwater_nisp,midpoint_era)
NSASR_Freshwater <- subset(NSASR_Freshwater, !is.na(midpoint_era))
Freshwater_plot <- ggplot(NSASR_Freshwater, aes(x=midpoint_era, y= freshwater_nisp)) + geom_col(fill = "
Freshwater_plot <- Freshwater_plot +  theme(legend.position = "none")+ theme(axis.title.y = element_blan
Freshwater_plot
```




```
#Same for Diadromous
NSASR_Diadromous <- NSASR_Master %>% dplyr::select(diadromous,midpoint_era)
NSASR_Diadromous <- subset(NSASR_Diadromous, !is.na(midpoint_era))
Diadromous_plot <- ggplot(NSASR_Diadromous, aes(x=midpoint_era, y= diadromous)) + geom_col(fill = "golde
Diadromous_plot <- Diadromous_plot +  theme(legend.position = "none")+ theme(axis.title.y = element_blan
Diadromous_plot
```




```
#Same for Unknown
NSASR_Unknown <- NSASR_Master %>% dplyr::select(unknown,midpoint_era)
NSASR_Unknown <- subset(NSASR_Unknown, !is.na(midpoint_era))
Unknown_plot <- ggplot(NSASR_Unknown, aes(x=midpoint_era, y= unknown)) + geom_col(fill = "deepskyblue4")
Unknown_plot <- Unknown_plot +  theme(legend.position = "none")+ theme(axis.title.y = element_blank())+
Unknown_plot
```




```
#Arranging
grid.arrange(Marine_plot,Freshwater_plot,Diadromous_plot,Unknown_plot)
```

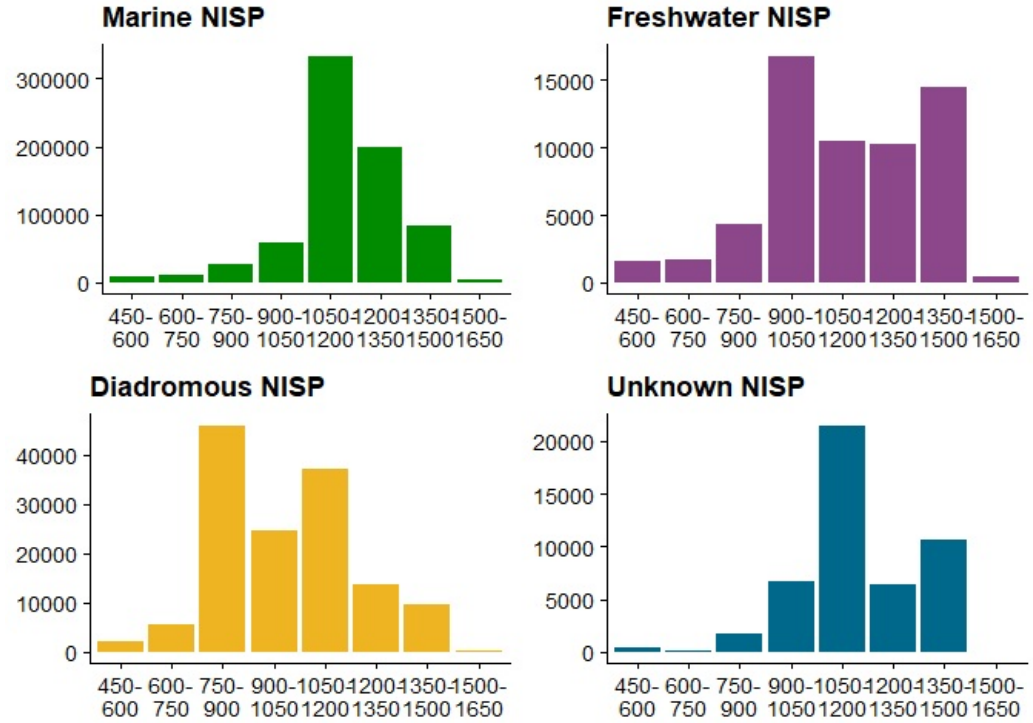


Figure 6.5

```
BE_Sites<- NS_Map + geom_point(data=NSASR_Belgium, aes(x= long, y= lat), color= "goldenrod", shape=1, si
BE_Map <- BE_Sites+ coord_sf(xlim= c(2.5, 6.5), ylim= c(49.5,51.8))
```

```
## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.
```



```
BE_Map+ geom_label_repel(data=NSASR_Belgium, aes(x= long, y= lat, label= site_name), stat= "unique", max
```

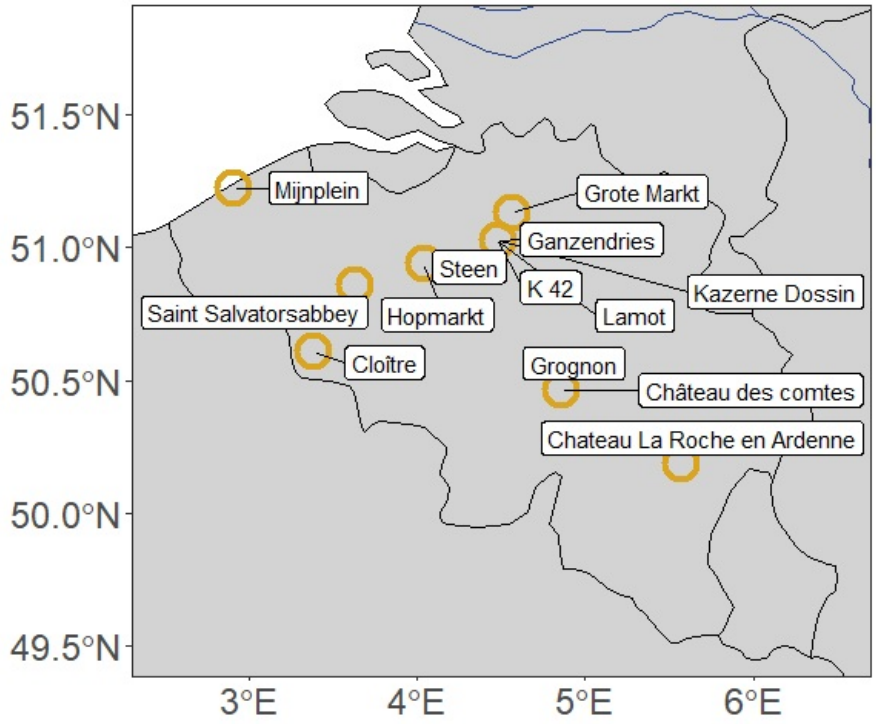


Figure 6.6

```
DK_Sites<- NS_Map + geom_point(data=NSASR_Denmark, aes(x= long, y= lat), color= "dodgerblue3", shape=1, 
DK_Map <- DK_Sites+ coord_sf(xlim= c(7, 13), ylim= c(54.5,57.5))
```

```
## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.
```

```
DK_Map + geom_label_repel(data=NSASR_Denmark, aes(x= long, y= lat, label= site_name), stat= "unique", ma
```

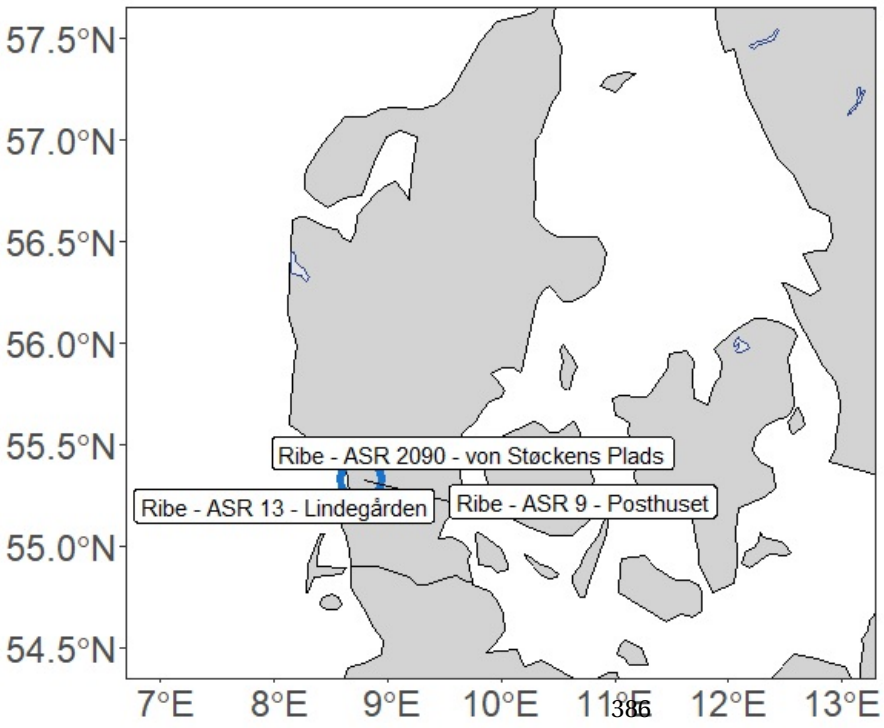


Figure 6.7

```
ENG_Sites<- NS_Map + geom_point(data=NSASR_England, aes(x= long, y= lat), color= "forestgreen", shape=1,
ENG_Map <- ENG_Sites+ coord_sf(xlim= c(-7, 2.5), ylim= c(50,57))
```

```
## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.
```

```
ENG_Map
```

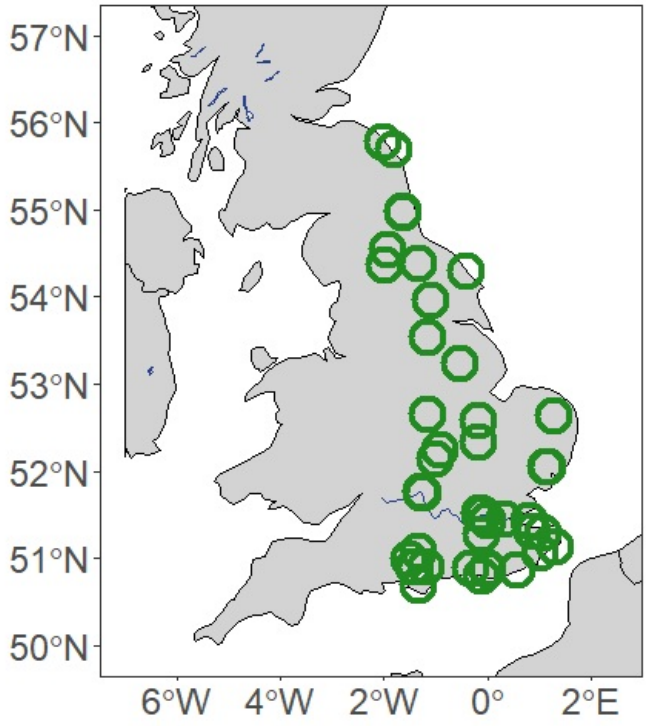


Figure 6.8

```
FR_Sites<- NS_Map + geom_point(data=NSASR_France, aes(x= long, y= lat), color= "chocolate4", shape=1, si
FR_Map <- FR_Sites+ coord_sf(xlim= c(0, 6), ylim= c(48.5,52))
```

```
## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.
```

```
FR_Map+ geom_label_repel(data=NSASR_France, aes(x= long, y= lat, label= site_name), stat= "unique", max.
```

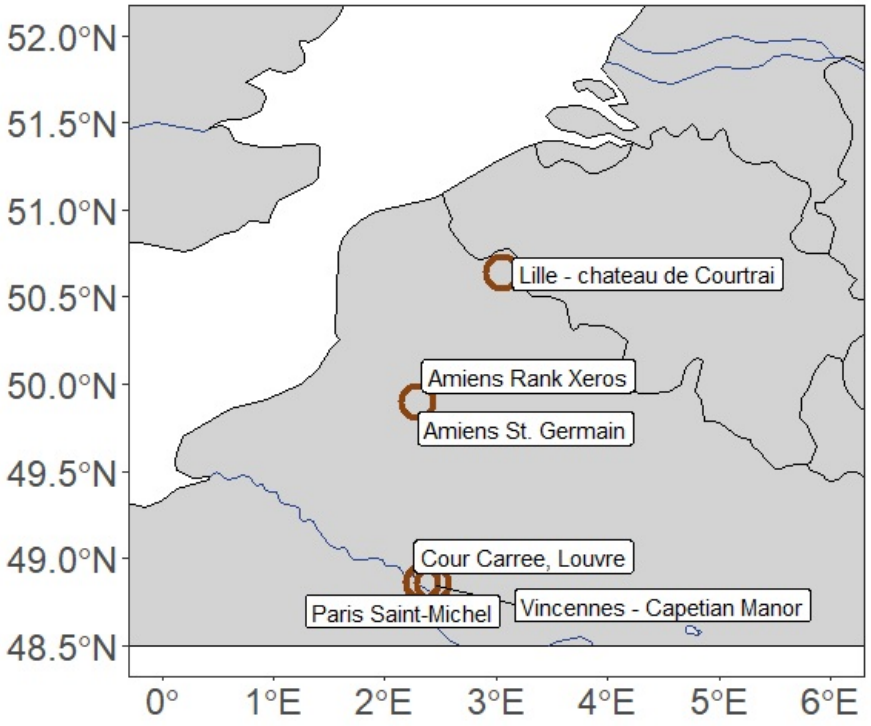


Figure 6.9

```
GE_Sites<- NS_Map + geom_point(data=NSASR_Germany, aes(x= long, y= lat), color= "deeppink3", shape=1, si
GE_Map <- GE_Sites+ coord_sf(xlim= c(4, 13), ylim= c(51,56))
```

```
## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.
```

```
GE_Map+ geom_label_repel(data=NSASR_Germany, aes(x= long, y= lat, label= site_name), stat= "unique", max
```

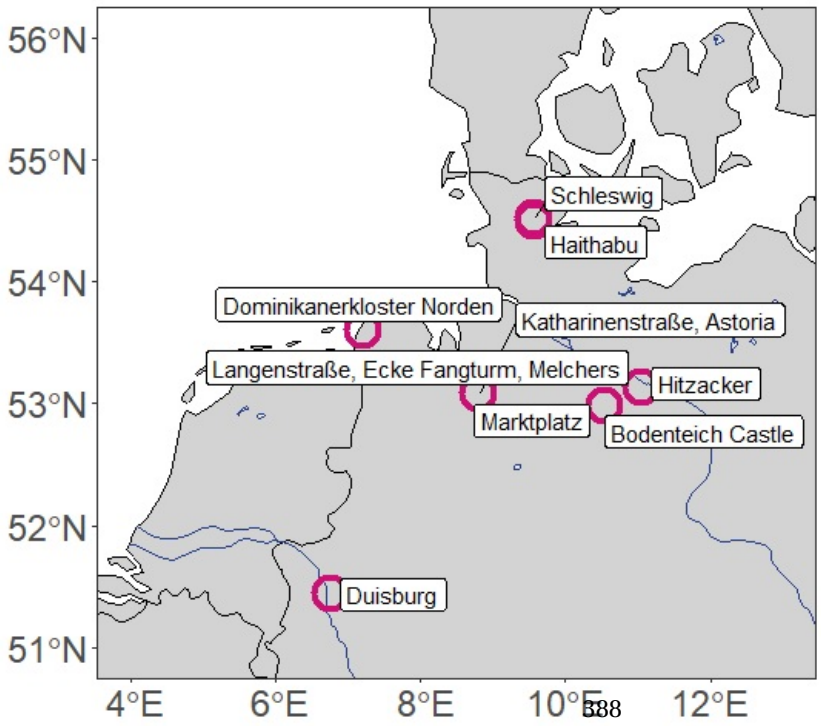


Figure 6.10

```
NL_Sites<- NS_Map + geom_point(data=NSASR_Netherlands, aes(x= long, y= lat), color= "orange", shape=1, s
NL_Map <- NL_Sites+ coord_sf(xlim= c(3.5, 7.5), ylim= c(50.8,53.8))
```

```
## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.
```

```
NL_Map + geom_label_repel(data=NSASR_Netherlands, aes(x= long, y= lat, label= site_name), stat= "unique",
```

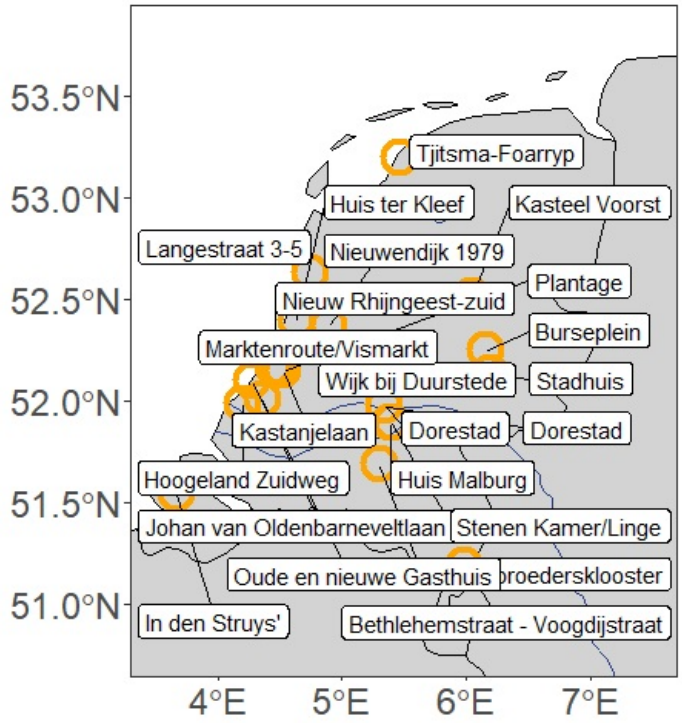


Figure 6.11

```
NOR_Sites<- NS_Map + geom_point(data=NSASR_Norway, aes(x= long, y= lat), color= "red", shape=1, size=6,
NOR_Map <- NOR_Sites+ coord_sf(xlim= c(4, 13.5), ylim= c(58,62))
```

```
## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.
```

```
NOR_Map + geom_label_repel(data=NSASR_Norway, aes(x= long, y= lat, label= site_name), stat= "unique", ma
```

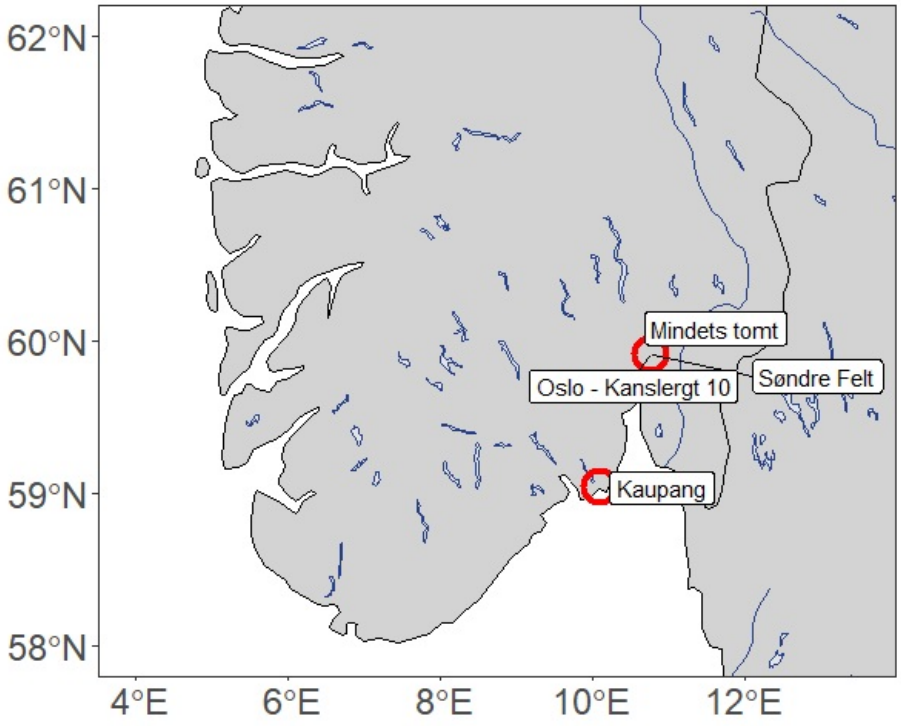


Figure 6.12

```
SCOT_Sites<- NS_Map + geom_point(data=NSASR_Scotland, aes(x= long, y= lat), color= "darkorchid2", shape=
SCOT_Map <- SCOT_Sites+ coord_sf(xlim= c(-7.5, 0), ylim= c(55,61))
```

```
## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.
```

```
SCOT_Map + geom_label_repel(data=NSASR_Scotland, aes(x= long, y= lat, label= site_name), stat= "unique",
```

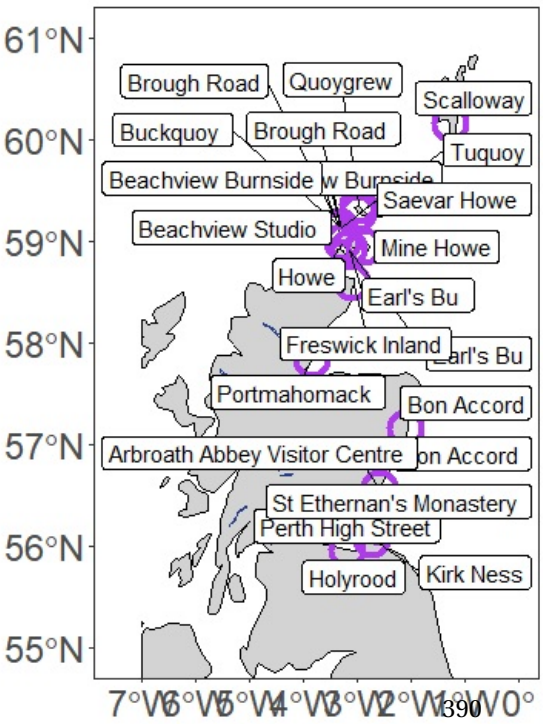
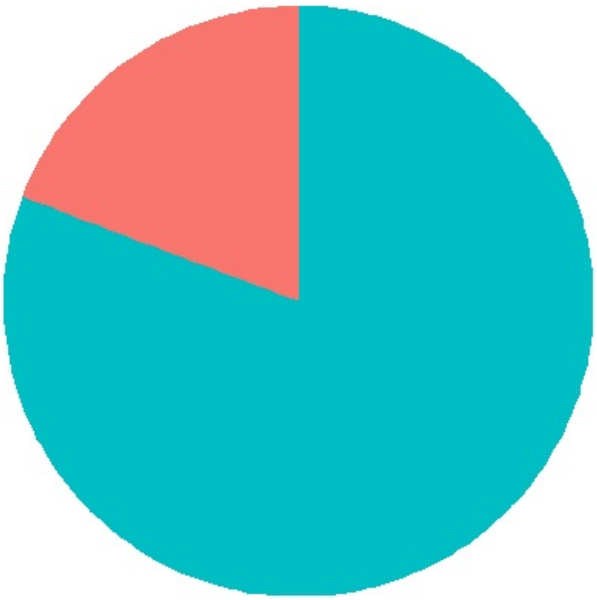


Figure 6.13

```
#Ribe sites (ASR 9, ASR 2090, ASR 13)
Values <- c(10,42)
```

```
Type <- c("Salmo salar","Salmo trutta")
Prop <- c(19.2, 80.8 )
Ribe_Pie <- data.frame(Values, Type, Prop)

Ribe_piechart <-  ggplot(Ribe_Pie, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity")
Ribe_piechart <- Ribe_piechart + coord_polar(theta = 'y') + theme_void() + theme(legend.position = "none
Ribe_piechart
```

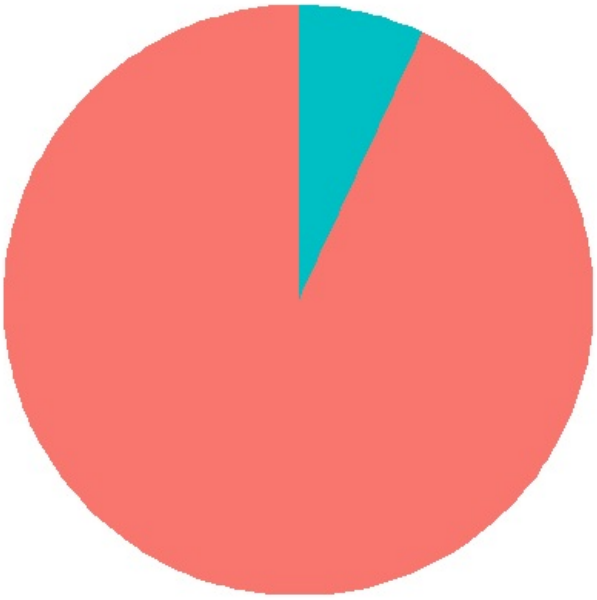


```
ggsave("Ribe_ZooMS_Pie.png", Ribe_piechart, bg = "transparent")
```

```
## Saving 7 x 5 in image
```

```
#Coppergate pie chart
Values <- c(54,4)
Type <- c("Salmo salar","Salmo trutta")
Prop <- c(93.1, 6.9)
Coppergate_Pie <- data.frame(Values, Type, Prop)

Coppergate_piechart <-  ggplot(Coppergate_Pie, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "i
Coppergate_piechart <- Coppergate_piechart + coord_polar(theta = 'y') + theme_void() + theme(legend.posi
Coppergate_piechart
```

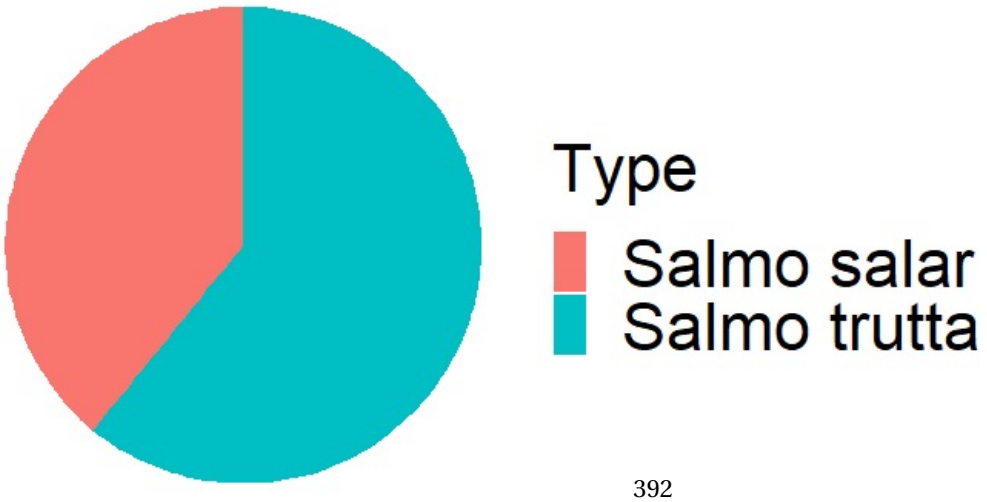


```
ggsave("Coppergate_ZooMS_Pie.png", Coppergate_piechart, bg = "transparent")
```

```
## Saving 7 x 5 in image
```

```
#Orkney pie chart
Values <- c(9, 14)
Type <- c("Salmo salar","Salmo trutta")
Prop <- c(39.1, 60.9)
Orkney_Pie <- data.frame(Values, Type, Prop)

Orkney_piechart <-  ggplot(Orkney_Pie, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity"
Orkney_piechart <- Orkney_piechart + coord_polar(theta = 'y') + theme_void() + theme(legend.text = eleme
Orkney_piechart
```

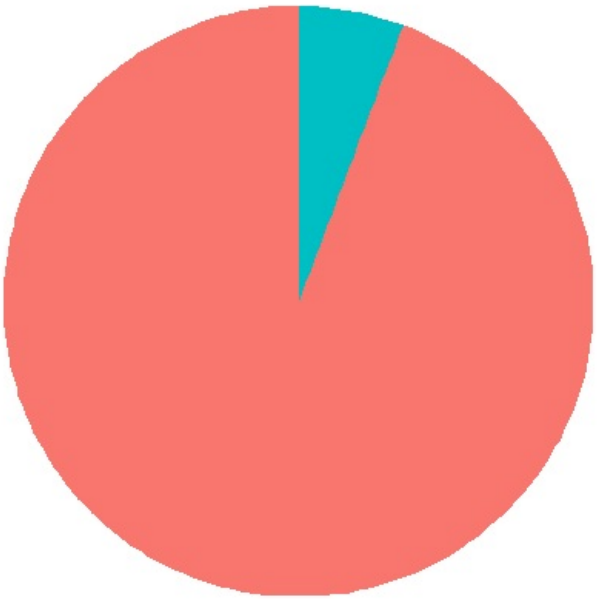



```
ggsave("Orkney_ZooMS_Pie.png", Orkney_piechart, bg = "transparent")
```

```
## Saving 7 x 5 in image
```

```
#Dutch pie chart
Values <- c(49,3)
Type <- c("Salmo salar","Salmo trutta")
Prop <- c(94.2, 5.8)
Dutch_Pie <- data.frame(Values, Type, Prop)

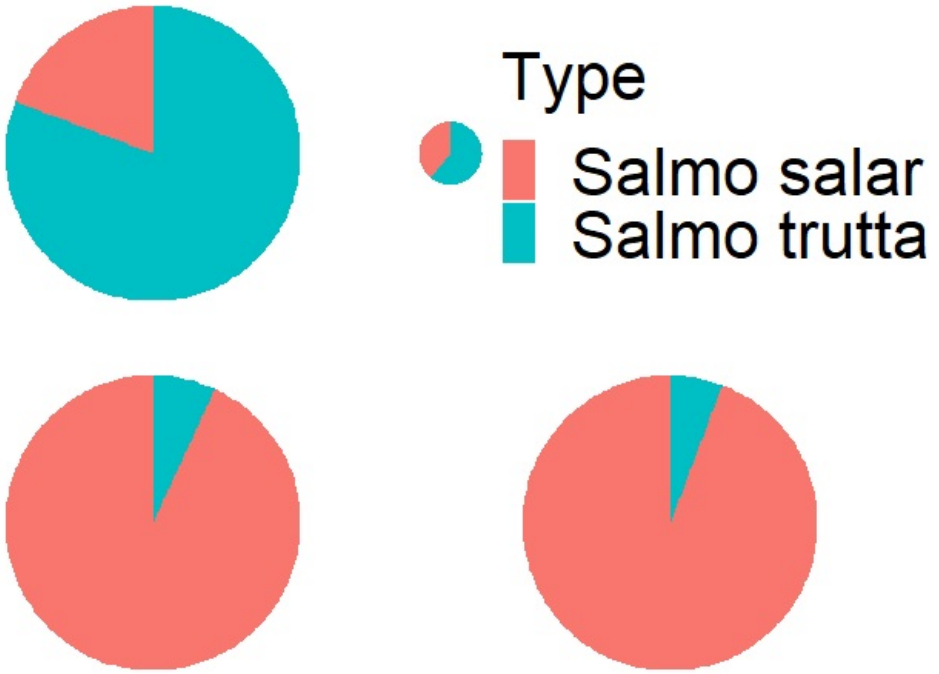
Dutch_piechart <-  ggplot(Dutch_Pie, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity")
Dutch_piechart <- Dutch_piechart + coord_polar(theta = 'y') + theme_void() + theme(legend.position = "no
Dutch_piechart
```



```
ggsave("Dutch_ZooMS_Pie.png", Dutch_piechart, bg = "transparent")
```

```
## Saving 7 x 5 in image
```

```
grid.arrange(Ribe_piechart, Orkney_piechart, Coppergate_piechart, Dutch_piechart)
```



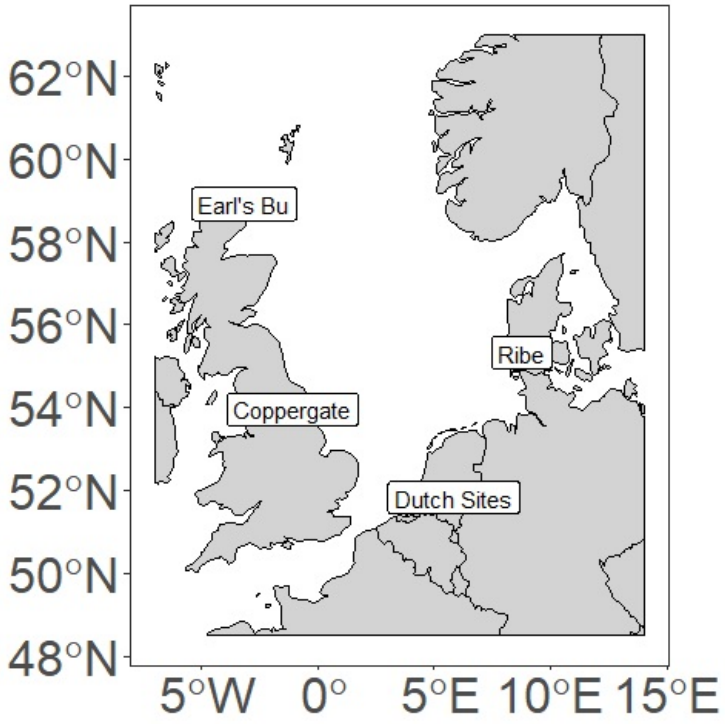

```
RibePie = image_read("C:\\Users\\Liz Quinlan\\Documents\\Thesis_Figures_To_Edit\\Ribe_ZooMS_Pie.png")
OrkneyPie = image_read("C:\\Users\\Liz Quinlan\\Documents\\Thesis_Figures_To_Edit\\Orkney_ZooMS_Pie.png"
CoppergatePie =image_read("C:\\Users\\Liz Quinlan\\Documents\\Thesis_Figures_To_Edit\\Coppergate_ZooMS_P
DutchPie =image_read("C:\\Users\\Liz Quinlan\\Documents\\Thesis_Figures_To_Edit\\Dutch_ZooMS_Pie.png")
#Making study area map

site <- c("Coppergate", "Earl's Bu", "Ribe", "Dutch Sites")
lat <- c(53.95766,58.92262, 55.33011, 51.827905)
long <- c(-1.080860, -3.156919, 8.766400, 5.836145)
short_sites <- data.frame(site, lat, long)

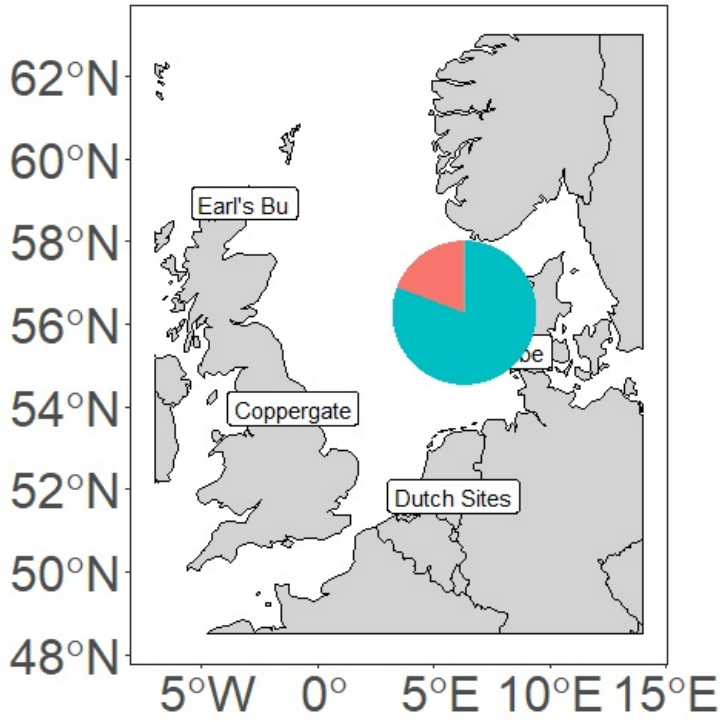
NS_Map <- Europe_crop + geom_label(data=short_sites, aes(x= long, y= lat, label= site, label.size= 0.5))
```

```
## Warning in geom_label(data = short_sites, aes(x = long, y = lat, label = site,
## : Ignoring unknown aesthetics: label.size
```

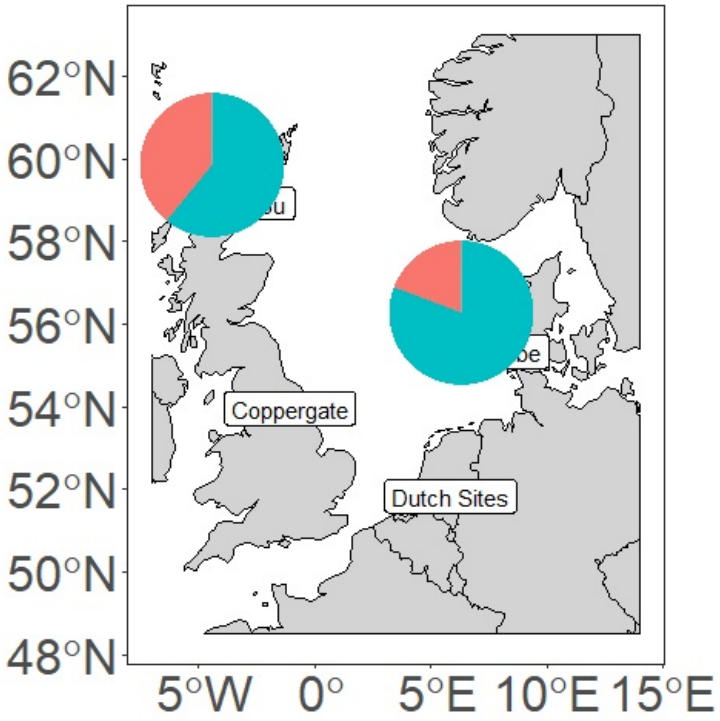
```
NS_Map
```



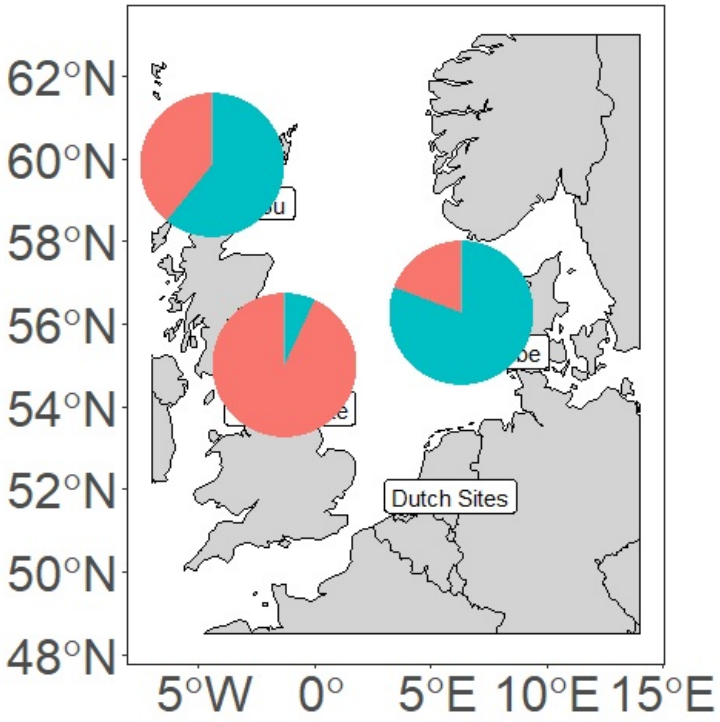

```
Pie_Map <- ggdraw() + draw_plot(NS_Map) + draw_image(RibePie, x= 0.12, y= 0.07, scale= .25)
Pie_Map
```




```
Pie_Map2 <- ggdraw() + draw_plot(Pie_Map) + draw_image(OrkneyPie, x= -.12, y= 0.27, scale= .25)
Pie_Map2
```




```
Pie_Map3 <- ggdraw() + draw_plot(Pie_Map2) + draw_image(CoppergatePie, x= -0.05, y= 0.00, scale= .25)
Pie_Map3
```




```
Pie_Map4 <- ggdraw() + draw_plot(Pie_Map3) + draw_image(DutchPie, x= 0.23, y= -0.27, scale= .25)
Pie_Map4
```

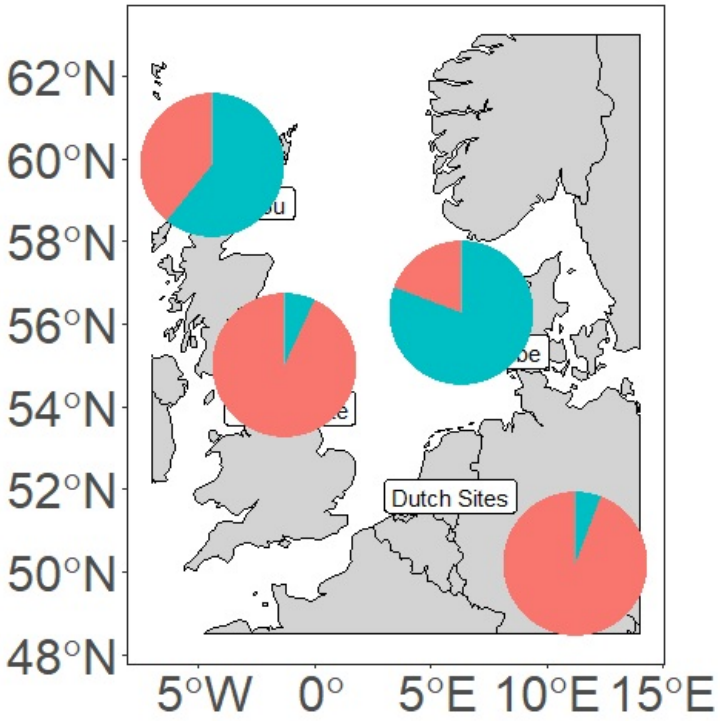
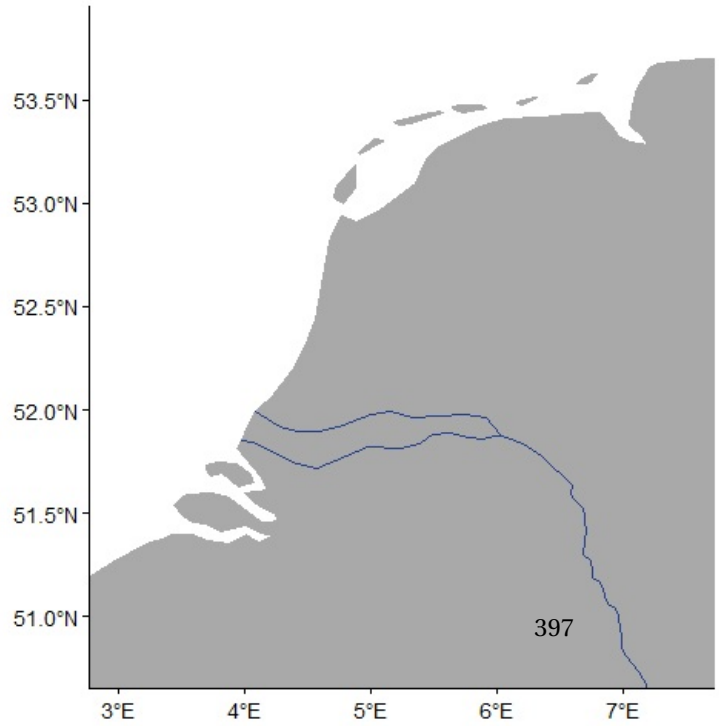


Figure 6.14

```
#reading in Dutch data
dutch_locations <- subset(BM_Locations, Country=="Netherlands")
dutch_ZooMS <- read.csv("Dutch_Sites.csv")
#creating map of the Netherlands
NL_map <- world_map + geom_sf(data=rivers_cropped, col = 'royalblue4')
```

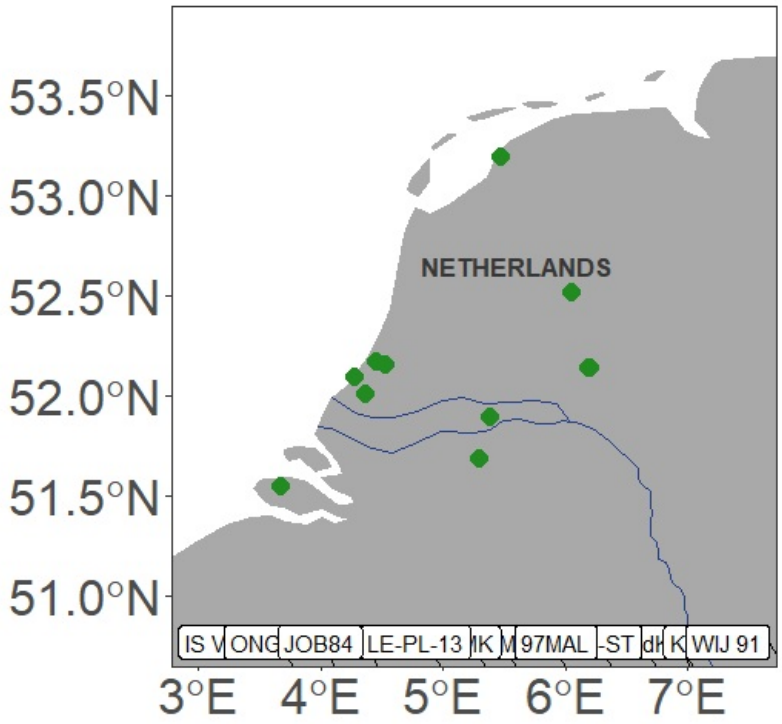
```
## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.
```

```
NL_map2<-NL_map + coord_sf(xlim= c(3, 7.5), ylim= c(50.8,53.8))
NL_map2
```



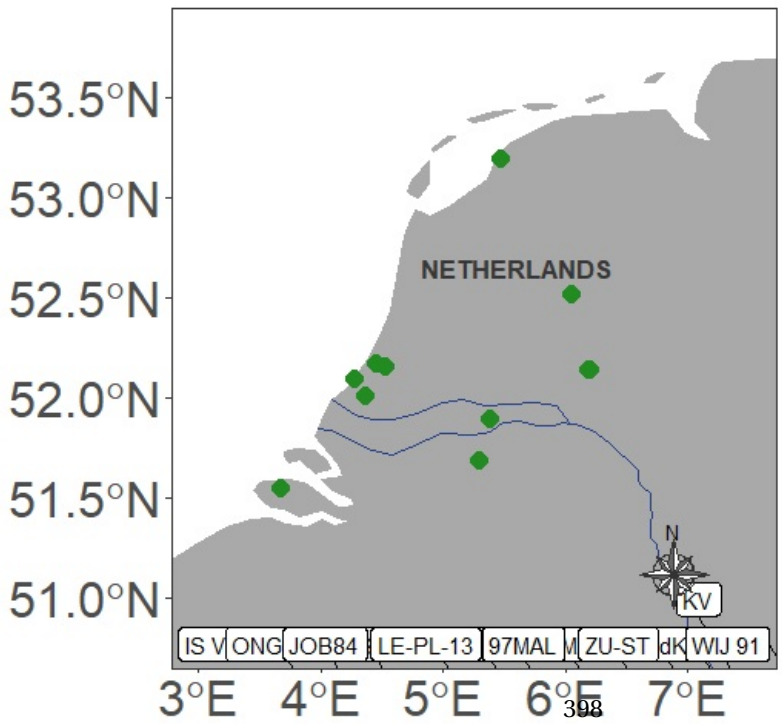

```
NL_Map3 <- NL_map2 + theme_bw() + theme(panel.background = element_rect(fill="white"), panel.grid.major =
```

```
NL_Map3
```




```
library(ggspatial)
NL_Map4<- NL_Map3 +
  ggspatial::annotation_north_arrow(
    location = "br", which_north = "true",
    pad_x = unit(0.4, "in"), pad_y = unit(0.4, "in"),
    style = ggspatial::north_arrow_nautical(
      fill = c("grey40", "white"),
      line_col = "grey20"))

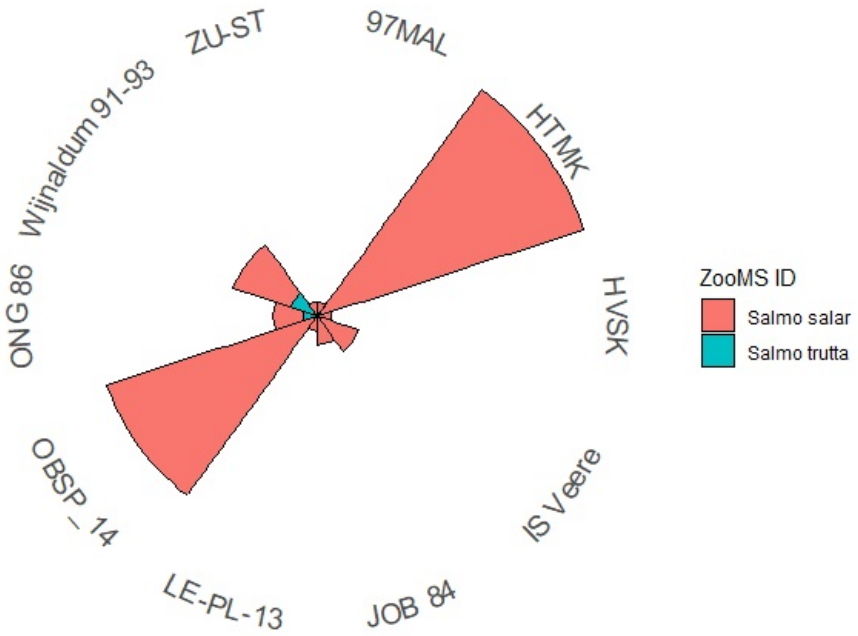
NL_Map4
```




```
#Making visual representation of species representation for larger dutch assemblages, using a polar wind

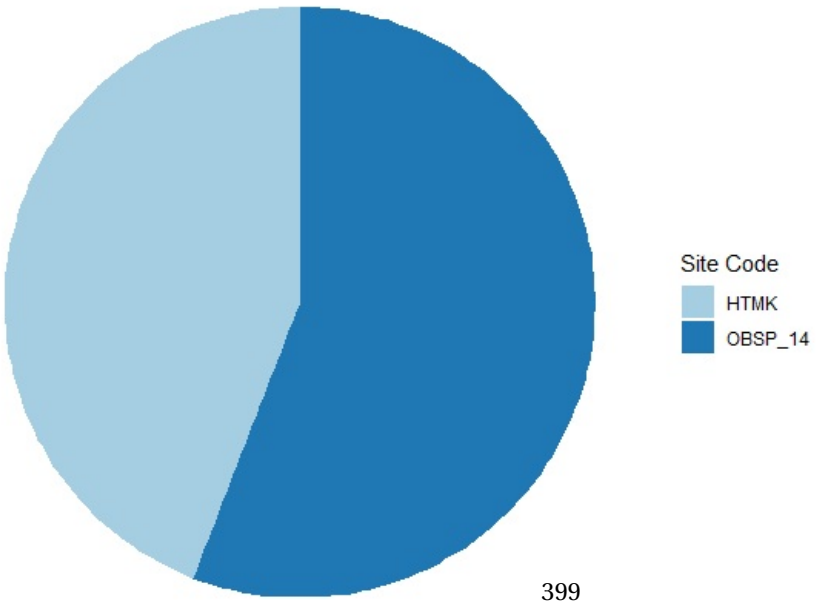
#polar plot first
base <- ggplot(dutch_ZooMS, aes(x = site_code, fill = ZooMS_ID))
```

```
library(geomtextpath)
Dutch_Polar <-base+geom_bar(width = 1) + coord_curvedpolar() +geom_bar(width = 1, colour = "black") + la
Dutch_Polar
```




```
#pie chart now
sitename <- c("OBSP_14", "HTMK")
salmon_NISP <- c(19, 15)
label <- c("19 samples", "15 samples")
Major_Dutch <- data.frame(sitename, salmon_NISP, label)

Major_Dutch_Pie <-  ggplot(Major_Dutch, aes(x = 1, y = salmon_NISP, fill = sitename)) + geom_bar(stat = 
Majors_Pie <- Major_Dutch_Pie + coord_polar(theta = 'y') +theme_void() + labs(fill= "Site Code") + scale_
Majors_Pie
```




```
#Arranging them together
```

```
ggarrange(NL_Map4, ggarrange(Dutch_Polar,Majors_Pie, ncol = 1, labels = c("B", "C")), nrow = 1, labels =
```

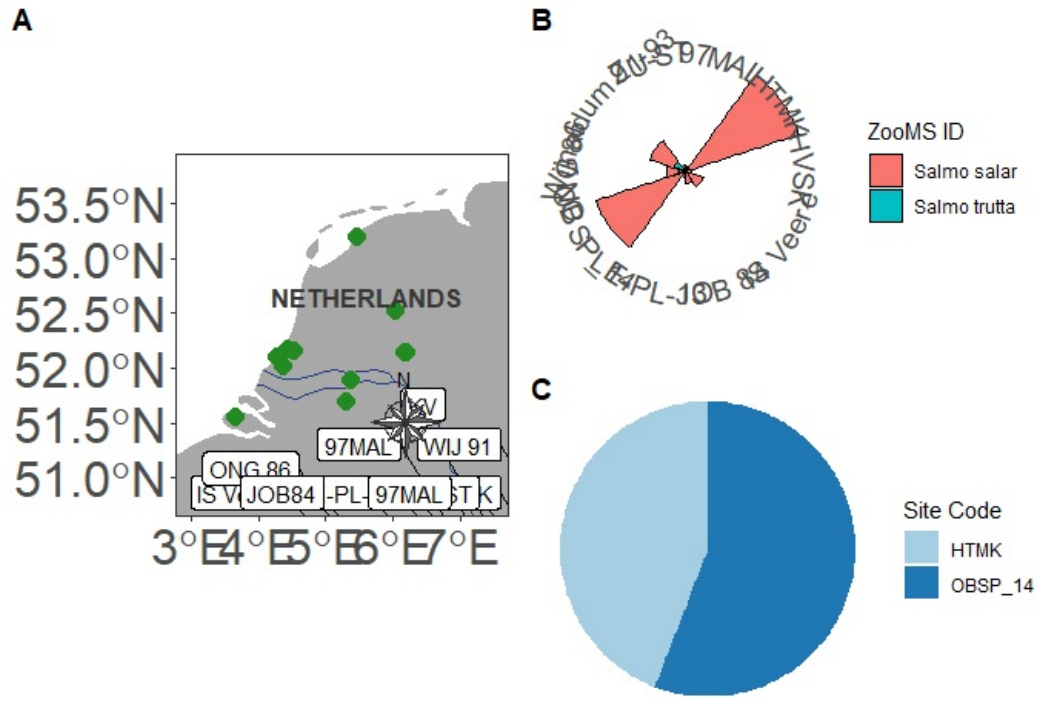


Figure 6.15

```
Period_Fish_Data <- read.csv("Period_Fish_Data.csv")

#Renamed columns
colnames(Period_Fish_Data)
```

```
## [1] "Period"        "Number.Sites"  "Fish.NISP"     "Salmonid.NISP"
```

```
names(Period_Fish_Data) [1] <- "Period"
names(Period_Fish_Data) [2] <- "Number_Sites"
names(Period_Fish_Data) [3] <- "Fish_NISP"
names(Period_Fish_Data) [4] <- "Salmonid_NISP"

colnames(Period_Fish_Data)
```

```
## [1] "Period"        "Number_Sites"  "Fish_NISP"     "Salmonid_NISP"
```

```
Period_Fish_Data$Period <- c("450-600", "600-750", "750-900", "900-1050", "1050-1200", "1200-1350", "135

scaleFactor <- max(Period_Fish_Data$Fish_NISP) / max(Period_Fish_Data$Salmonid_NISP)
#options(scipen=10000) removes scientific notation
options(scipen=10000)

ggplot(Period_Fish_Data, aes(x=Period,  width=.4)) +
  geom_col(aes(y=Fish_NISP), fill="seagreen4", position = position_nudge(x = -.4)) +
  geom_col(aes(y=Salmonid_NISP * scaleFactor), fill="salmon") +
  scale_y_continuous(name="Fish NISP", sec.axis=sec_axis(~./scaleFactor, name="Salmonid NISP"))  + scale
  theme(
    axis.title.y.left=element_text(color="seagreen4", size=30, face="bold", vjust= 10.5),
    axis.text.y.left=element_text(color="black", size=18),
    axis.title.y.right=element_text(color="salmon", size=30, face="bold", vjust= 10.5),
    axis.text.y.right=element_text(color="black", size=18),
    axis.text.x.bottom = element_text(color= "black", size=18),
    axis.title.x.bottom = element_text(color = "black", size=30, face= "bold", vjust= -3.5),
  ) + theme(panel.background = element_blank()) + theme(plot.margin = unit(c(2,2,2,2), "cm"))
```

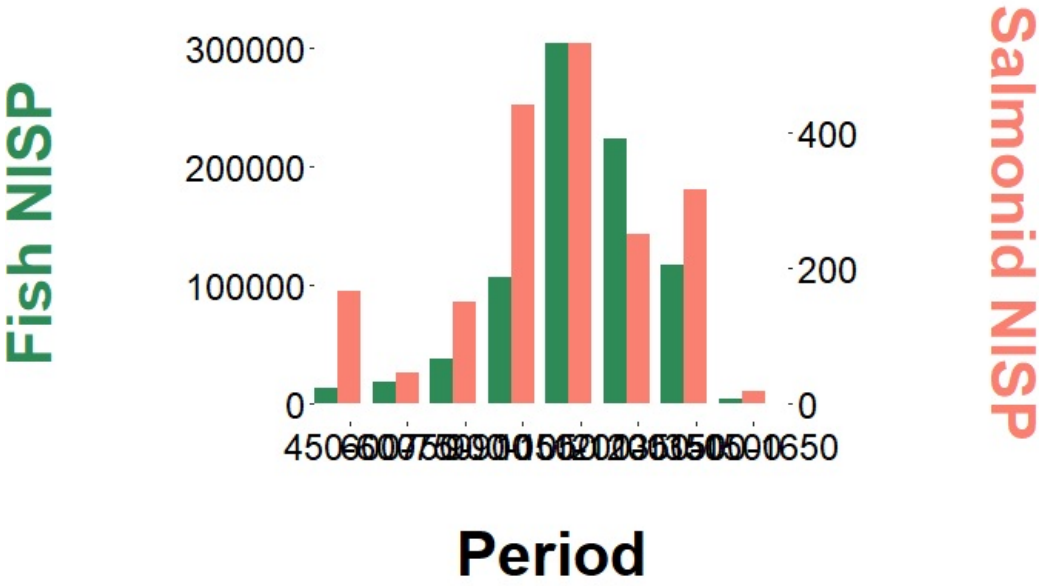


Figure 6.16

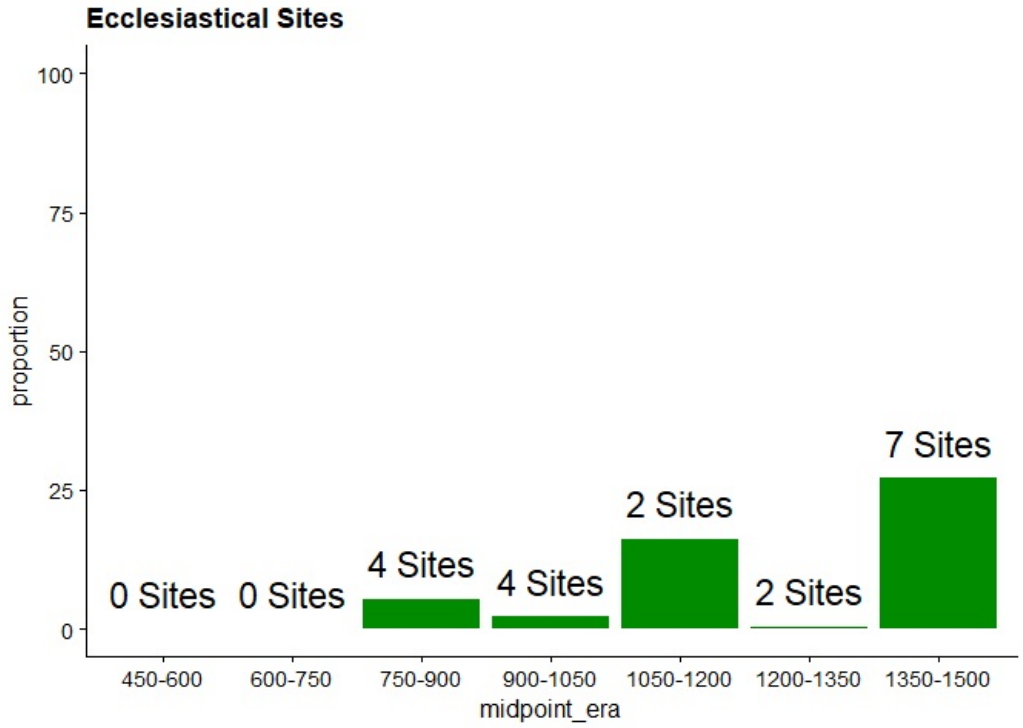
```
Ecc_Sites <- read.csv("Ecc_Prop.csv")
High_Sites <- read.csv("HS_Prop.csv")
Urban_Sites <- read.csv("Urban_Prop.csv")

Sites_E <- c("0 Sites", "0 Sites", "4 Sites", "4 Sites", "2 Sites", "2 Sites", "7 Sites", "1 site")
Sites_H <- c("0 Sites", "0 Sites", "0 Sites", "4 Sites", "4 Sites", "8 Sites", "4 Sites", "1 site")
Sites_U <- c("1 Site", "7 Sites", "4 Sites", "15 Sites", "19 Sites", "23 Sites", "26 Sites", "1 site")


eccles_prop <- ggplot(Ecc_Sites, aes(x=midpoint_era, y= proportion)) + geom_col(fill="green4")+ scale_x_
eccles_prop
```

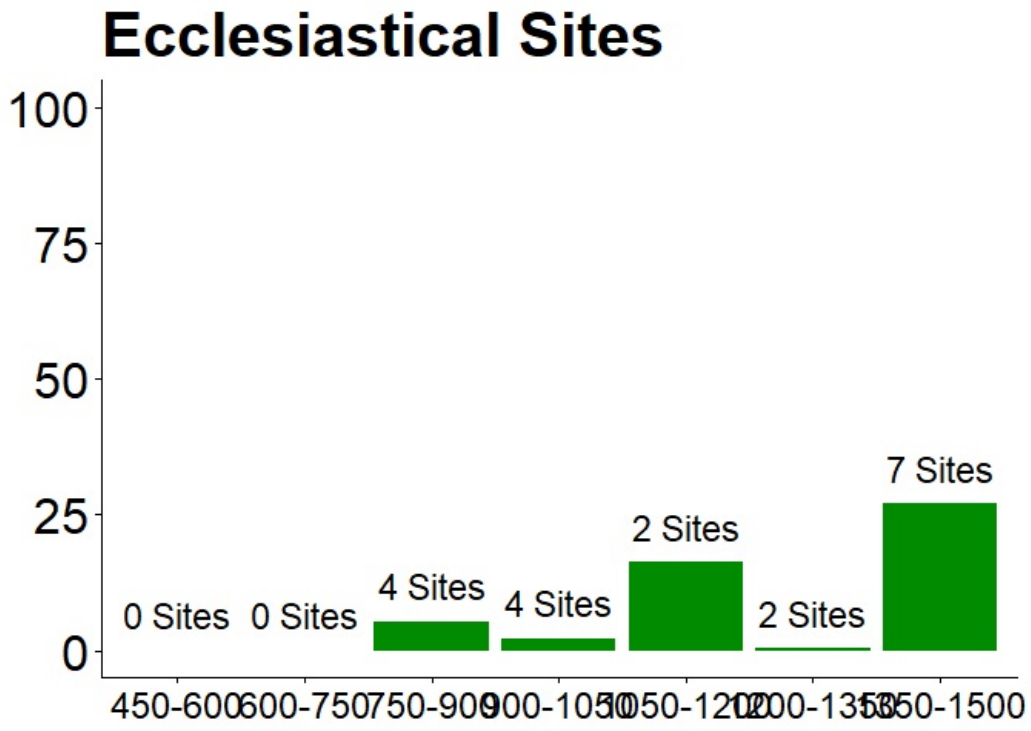
```
## Warning: Removed 1 rows containing missing values (`position_stack()`).

## Warning: Removed 1 rows containing missing values (`geom_text()`).
```




```
Eprop <- eccles_prop +  theme(legend.position = "none")+ theme(axis.title.y = element_blank())+ theme(ax
Eprop
```

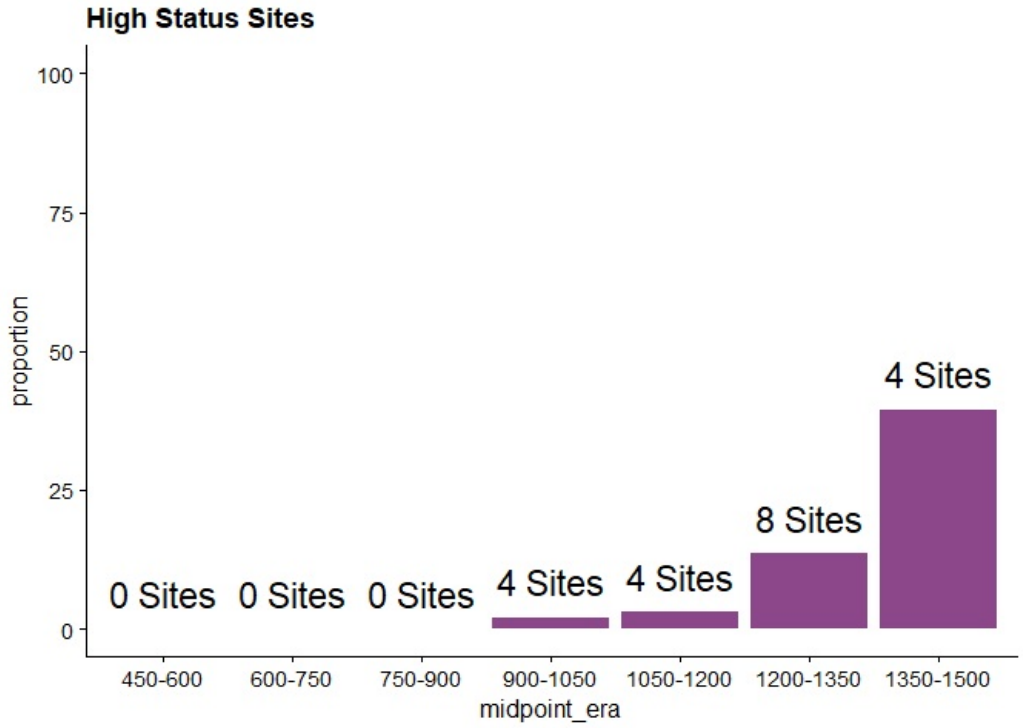
```
## Warning: Removed 1 rows containing missing values (`position_stack()`).
## Removed 1 rows containing missing values (`geom_text()`).
```




```
HS_prop <- ggplot(High_Sites, aes(x=midpoint_era, y=proportion)) + geom_col(fill="orchid4")+ scale_x_dis
HS_prop
```

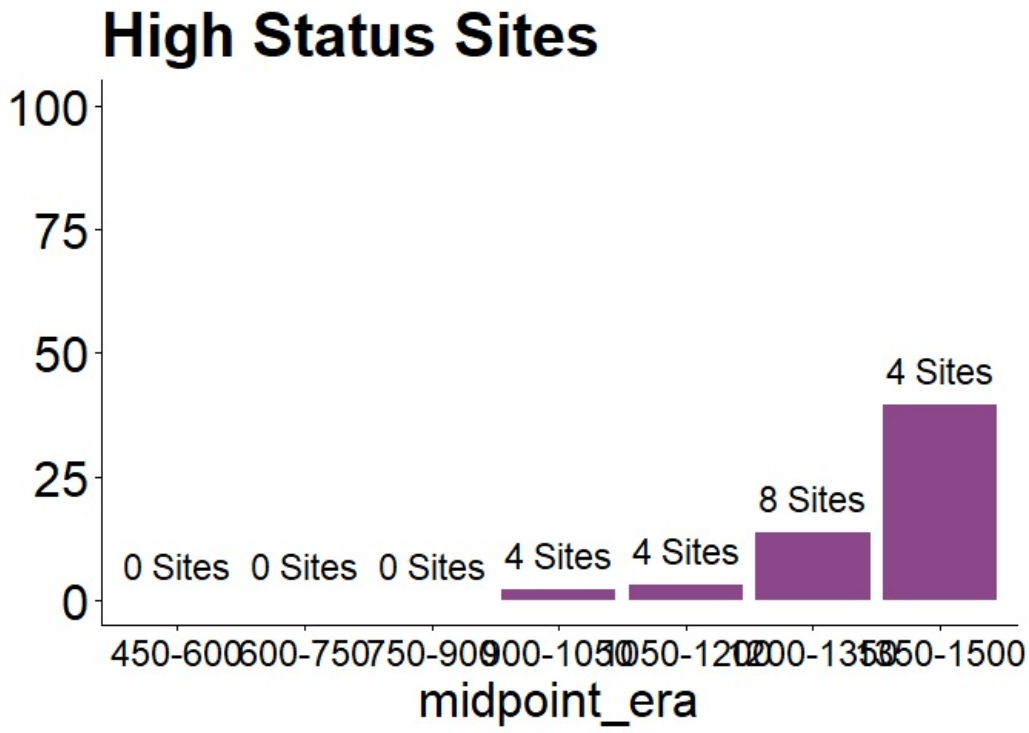


```
## Warning: Removed 1 rows containing missing values (`position_stack()`).
## Removed 1 rows containing missing values (`geom_text()`).
```




```
Hprop <- HS_prop +  theme(legend.position = "none") + theme(axis.title.x = element_text(size=24), axis.t
Hprop
```

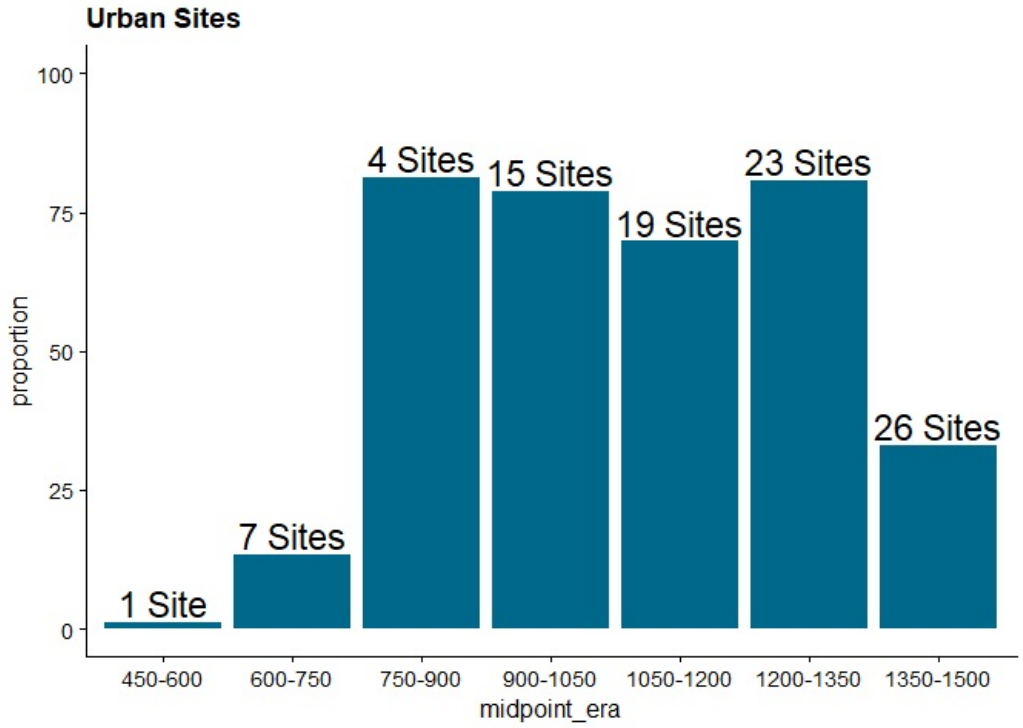
```
## Warning: Removed 1 rows containing missing values (`position_stack()`).
## Removed 1 rows containing missing values (`geom_text()`).
```




```
Urban_prop <- ggplot(Urban_Sites, aes(x=midpoint_era, y=proportion)) + geom_col(fill="deepskyblue4")+ sc
Urban_prop
```

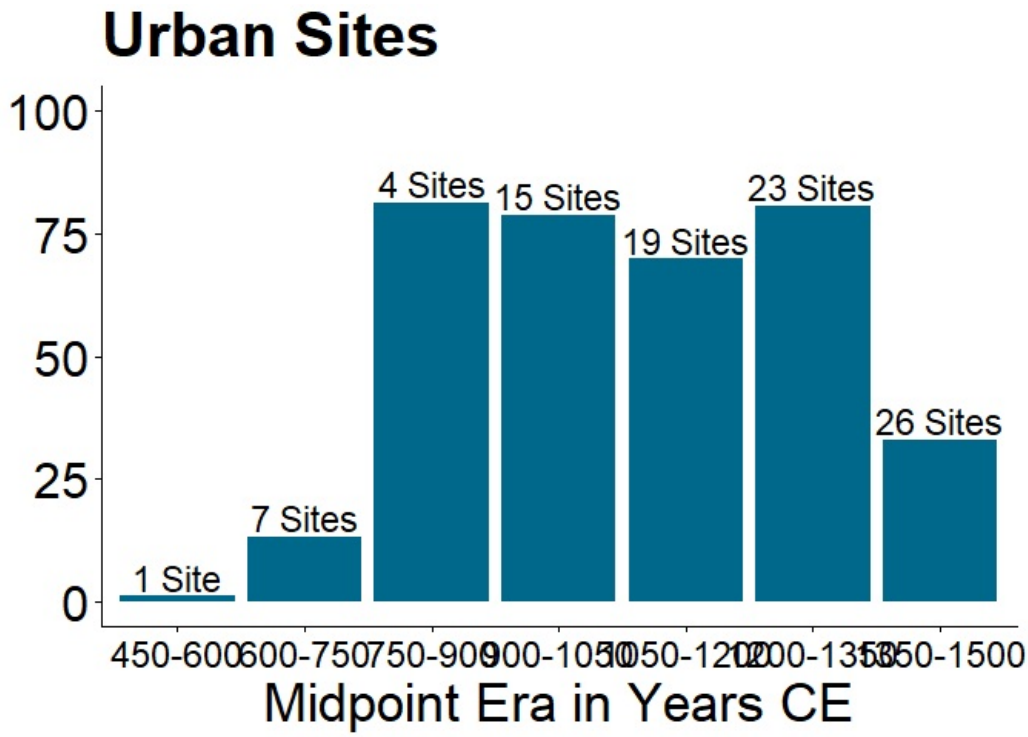


```
## Warning: Removed 1 rows containing missing values (`position_stack()`).
## Removed 1 rows containing missing values (`geom_text()`).
```




```
Uprop <- Urban_prop +  theme(legend.position = "none")+ theme(axis.title.y = element_blank())+ theme(leg
Uprop
```

```
## Warning: Removed 1 rows containing missing values (`position_stack()`).
## Removed 1 rows containing missing values (`geom_text()`).
```




```
yleft <- text_grob("Proportion of Total Salmonid NISP", rot= 90, size=24)

grid.arrange(Eprop, Hprop, Uprop, left= yleft)
```



```
## Warning: Removed 1 rows containing missing values (`position_stack()`).
## Removed 1 rows containing missing values (`geom_text()`).

## Warning: Removed 1 rows containing missing values (`position_stack()`).
```

```
## Warning: Removed 1 rows containing missing values (`geom_text()`).

## Warning: Removed 1 rows containing missing values (`position_stack()`).

## Warning: Removed 1 rows containing missing values (`geom_text()`).
```

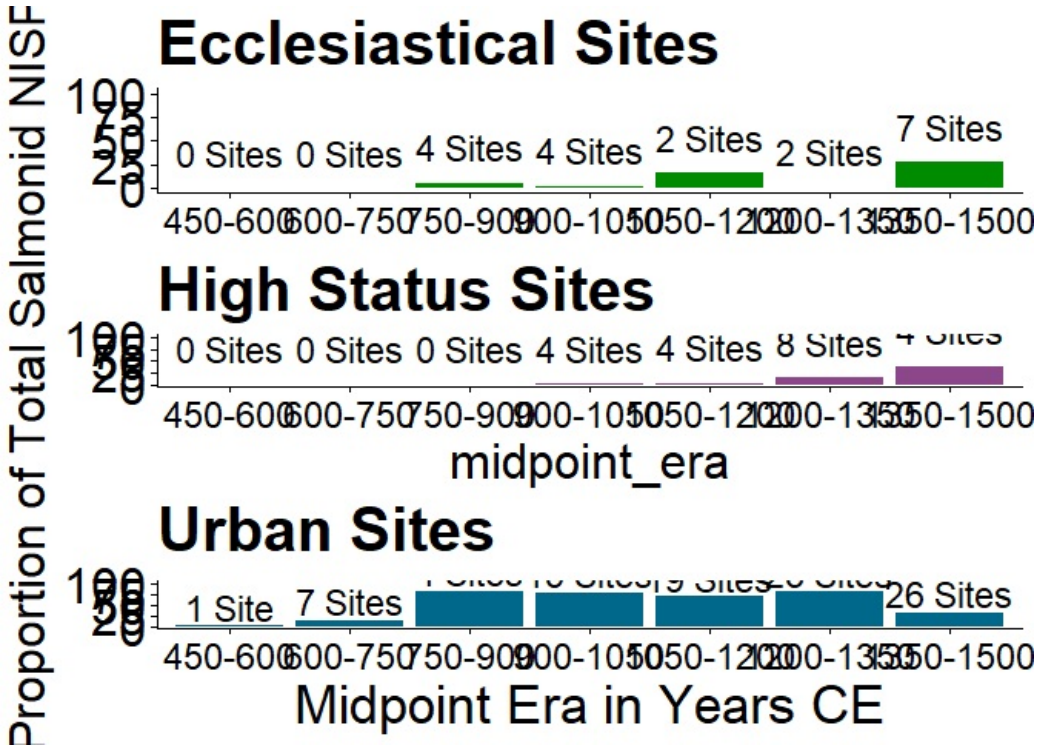


Figure 6.17

```
report_dates_NISP<- read.csv("Report_Dates_NISP.csv")

#Plot below is the plot showing usage of ID category by decade
ggplot(report_dates_NISP, aes(x=Decade, y=Value, fill=Species)) + geom_bar(stat='identity') + ylab("Cont
```

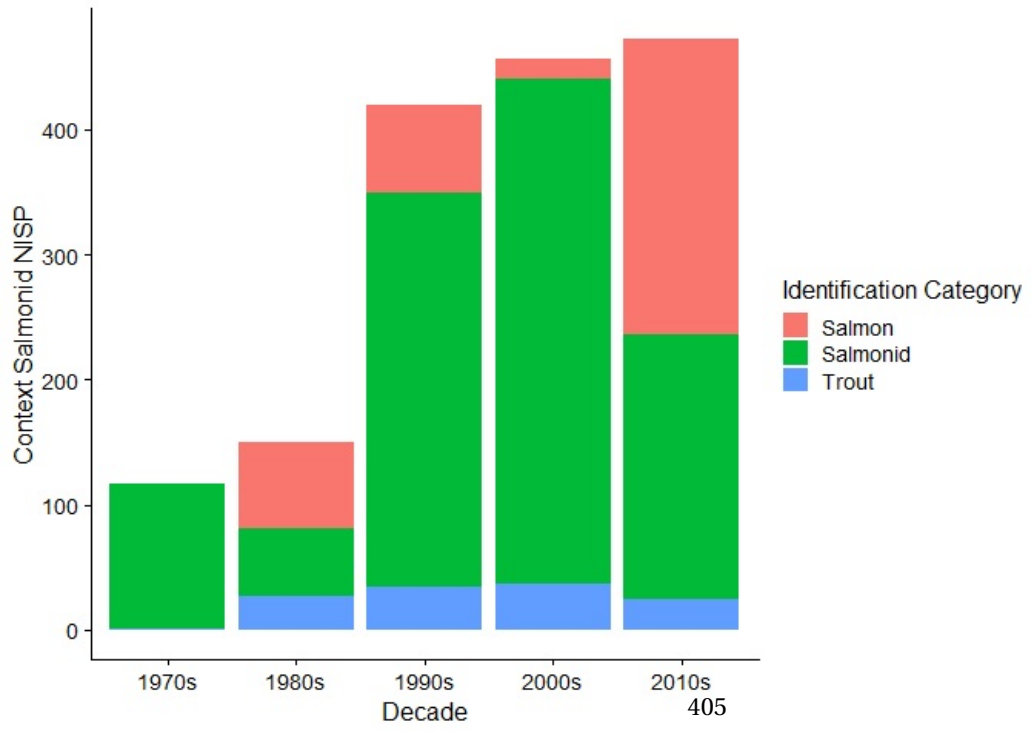


Figure 18

```
CM_Decades <- read.csv("Decade_Collection_Methods.csv")
```

```
ggplot(CM_Decades, aes(x=Decade, y=Value, fill=Method)) + geom_bar(position="dodge", stat="identity") +
```

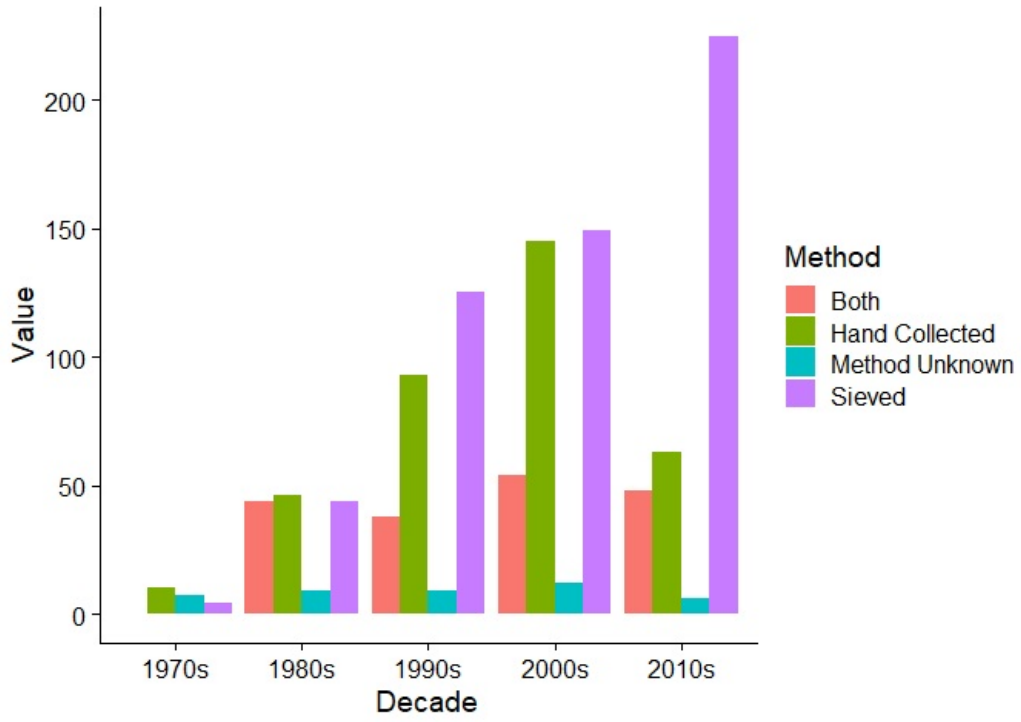
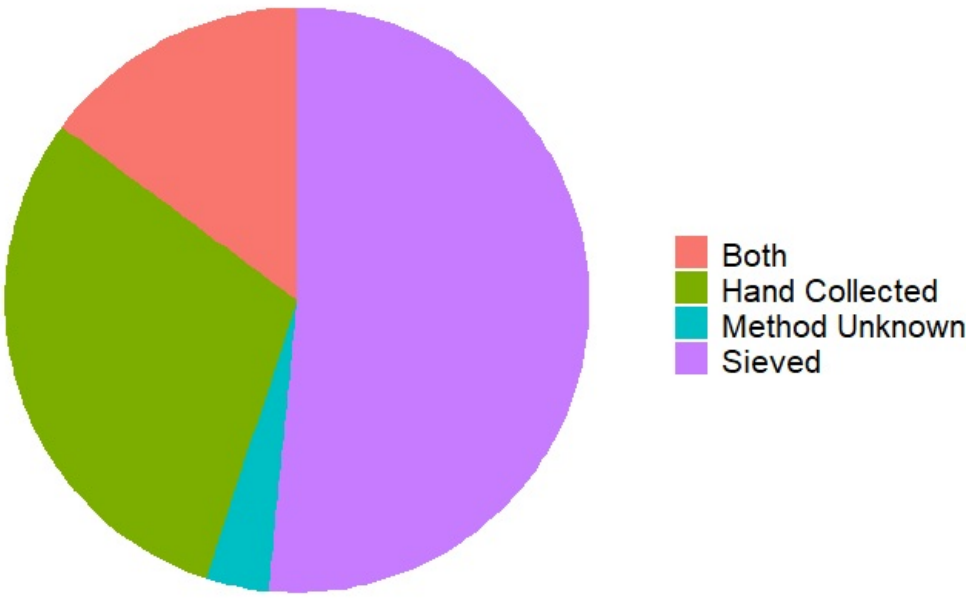


Figure 19

```
Values <- c(189, 382, 44, 655)
Type <- c("Both", "Hand Collected", "Method Unknown", "Sieved")
Prop <- c(14.9, 30.1, 3.4, 51.6)
CM_Proportions <- data.frame(Values, Type, Prop)

props <-  ggplot(CM_Proportions, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity")
props <- props + coord_polar(theta = 'y') + theme_void() + theme(legend.text=element_text(size=16)) + th
props
```



Chapter 7 - Biomolecular Identification of Salmo sp. Ecotypes

Code

Datasets

```
Ecotype_Master <- read.csv("Ecotype_Paper.csv")
Site_Locations <- read.csv("Site_Locations.csv")
Ecotype_Salmo <- subset(Ecotype_Master, sample_type != "Comparative")
Salmo_Only <- subset(Ecotype_Salmo, BioMol_Type == "Both")
Salmon <- subset(Salmo_Only, ZooMS_ID=="Salmo salar")
COP_Salmon <- subset(Salmon, site == "16-22 Coppergate")
```

Statistics

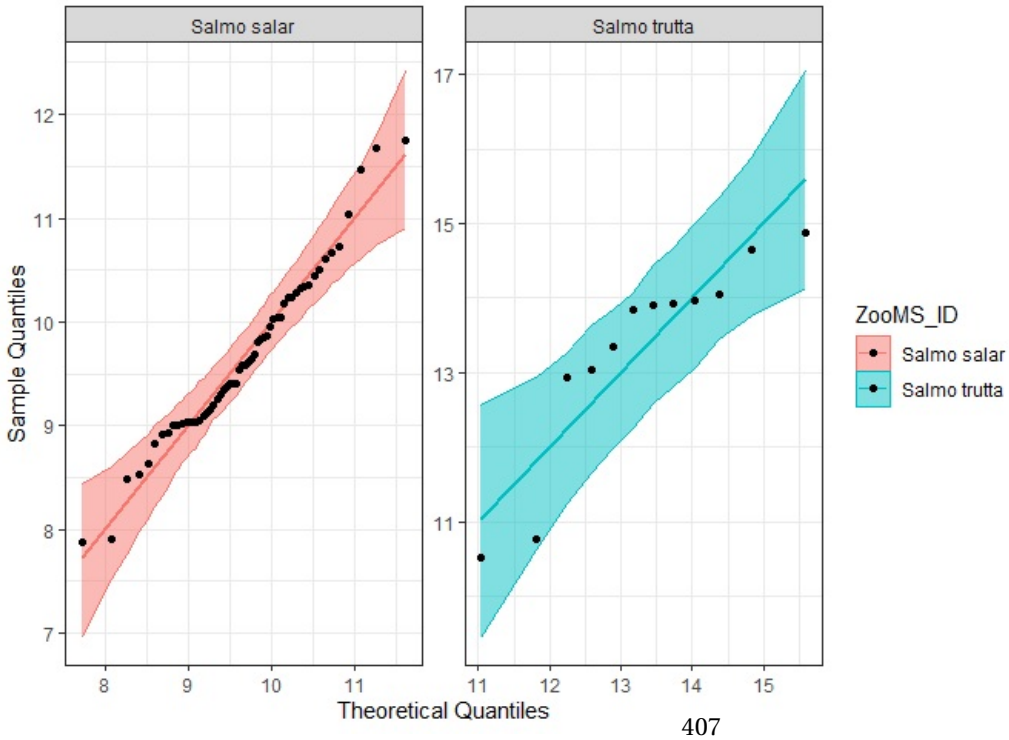
```
#Stats checks for normal distribution
Salmo_Only$ZooMS_ID<-as.factor(Salmo_Only$ZooMS_ID)
Salmo_Only$ecotype<-as.factor(Salmo_Only$ecotype)

Salmo_Only %>%
  group_by(ZooMS_ID) %>%
  summarise('W Stat' = shapiro.test(D15N)$statistic,
            p.value=shapiro.test(D15N)$p.value)
```

```
##      W Stat         p.value
## 1 0.8437312 0.0000005764989
```

```
#Not normally distributed, p value = 0.005256989501

ggplot(data = Salmo_Only, mapping = aes(sample = D15N, color = ZooMS_ID, fill = ZooMS_ID)) +
  stat_qq_band(alpha=0.5, conf=0.95, qtype=1, bandType = "boot") +
  stat_qq_line(identity=TRUE) +
  stat_qq_point(col="black") +
  facet_wrap(~ ZooMS_ID, scales = "free") +
  labs(x = "Theoretical Quantiles", y = "Sample Quantiles") + theme_bw()
```




```
#Mann-Whitney U Test
m1<- wilcox.test(D15N ~ ZooMS_ID, data=Salmo_Only, na.rm=TRUE, paired=FALSE, exact=FALSE, conf.int=TRUE)
m1
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  D15N by ZooMS_ID
## W = 11.5, p-value = 0.0000001861
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
##  -4.530044 -3.290021
## sample estimates:
## difference in location
##              -3.944998
```

```
m1$estimate
```

```
## difference in location
##              -3.944998
```

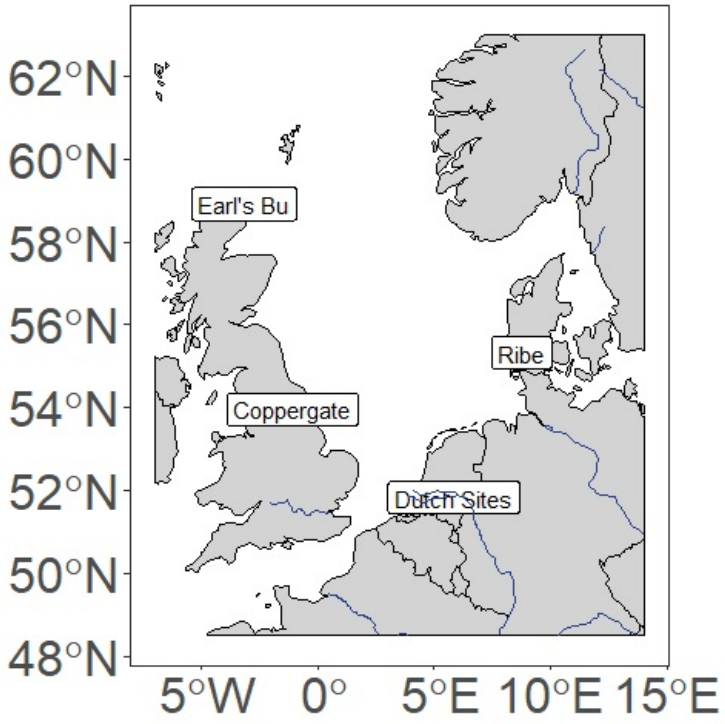
```
#The two groups of ZooMS identifications are not normally distributed, and are not dependent on each oth
#The mean and median values for these two groups are significantly statistically different from each oth
#with nearly 4.0 per mille difference between means

#Welch two-sample t-test to see if the results are the same lol
m1<-t.test(D15N ~ ZooMS_ID, data=Salmo_Only, var.equal=FALSE, na.rm=TRUE)
print(m1)
```

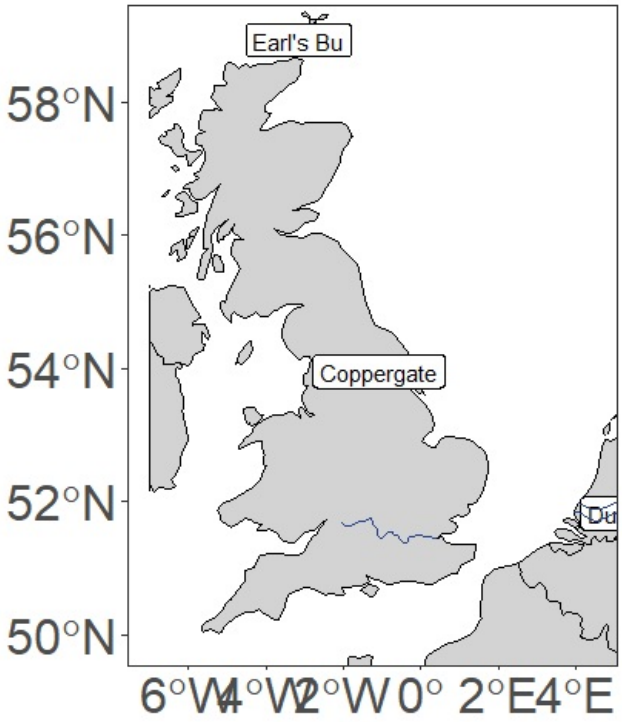
```
##
##  Welch Two Sample t-test
##
## data:  D15N by ZooMS_ID
## t = -8.8719, df = 12.769, p-value = 0.00000081
## alternative hypothesis: true difference in means between group Salmo salar and group Salmo trutta is
## 95 percent confidence interval:
##  -4.539329 -2.758885
## sample estimates:
##  mean in group Salmo salar mean in group Salmo trutta
##                   9.665893                  13.315000
```

Figure 7.4 (Annotations added in Inkscape)

```
River_map <- NS_Map + geom_sf(data = rivers_cropped, col = 'royalblue4')
River_map
```




```
Ecotype_Study_Map<- River_map + coord_sf(xlim= c(-7, 4.5), ylim= c(50,59))
Ecotype_Study_Map
```




```
Ecotype_Sites <- subset(Site_Locations, Site == "16-22 Coppergate" | Site == "Earl's Bu")

Ecotype_Study_Map + geom_point(data=Ecotype_Sites, aes(x= Lat, y= Long, color= Site), size=9, stroke=3,
```

```
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```

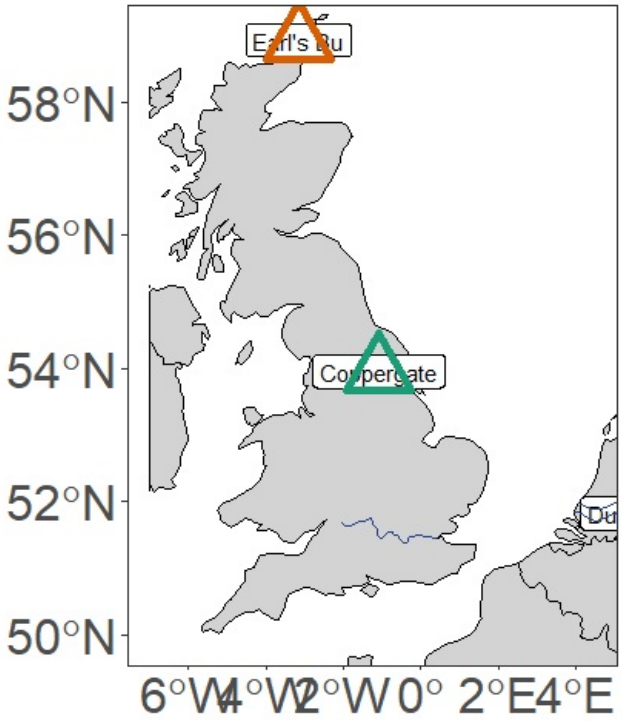


Figure 7.5

```
p <- ggplot(Salmo_Only, aes(x=D13C, y=D15N, color=site, shape=ZooMS_ID)) + geom_point(size = 8, stroke=3
  xlab(expression(paste(delta^{13}, "C(‰)"))) +
  ylab(expression(paste(delta^{15}, "N(‰)"))) + theme_cowplot(12)
all_salmo <- p+ scale_shape_manual(values= c("Salmo salar"=4, "Salmo trutta"=2)) +
  scale_color_manual(values= c("Earl's Bu" = "#435ED1", "16-22 Coppergate"= "#f89540")) +
  theme(text = element_text(size=30),
        axis.text = element_text(size=24),
        legend.text = element_text(margin = margin(t = 10, b = 10, unit = "pt")))+
  labs(color="Archaeological Site", shape="ZooMS Species ID")
all_salmo
```

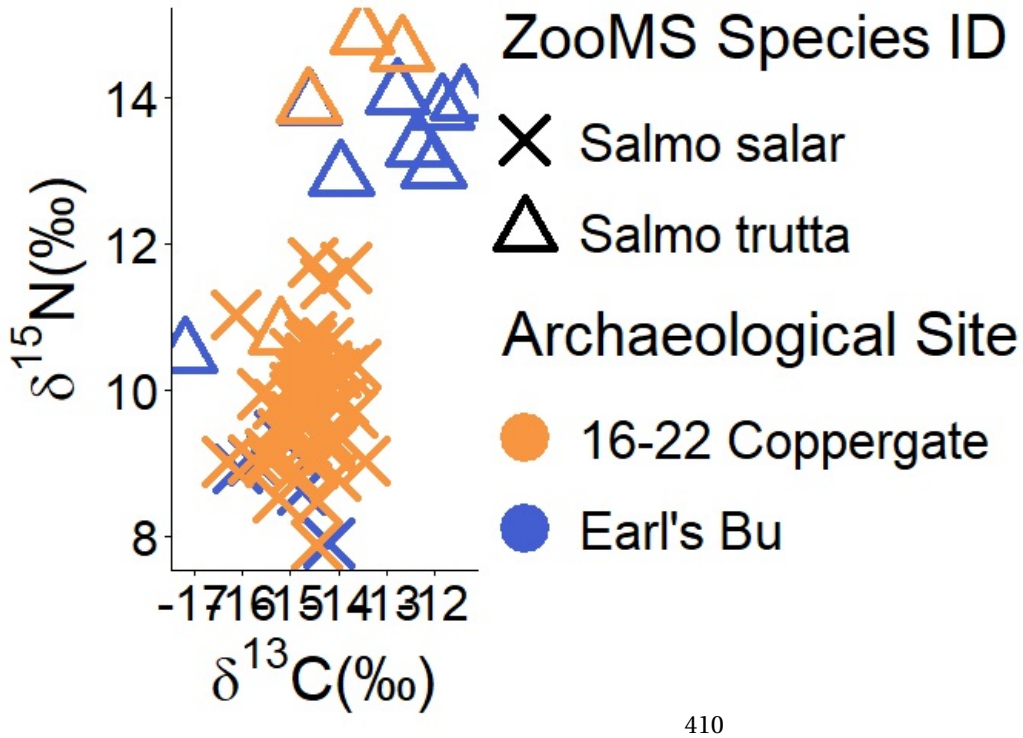


Figure 7.6

```
Ecotype_plot <- ggplot(Salmo_Only, aes(x=D13C, y=D15N, color=ecotype, shape=ecotype)) + geom_point(size
  xlab(expression(paste(delta^{13}, "C(‰)"))) +
  ylab(expression(paste(delta^{15}, "N(‰)"))) + theme_cowplot(12) +
```

```
  scale_shape_manual(values= c(4,2,3)) +
  scale_color_manual(values= c("#EF7687","#21918c","#7D5238")) +
  theme(text = element_text(size=30),
        axis.text = element_text(size=24),
        legend.text = element_text(margin = margin(t = 10, b = 10, unit = "pt")))+
  labs(color="Salmo sp. Ecotype", shape="Salmo sp. Ecotype")
Ecotype_plot
```

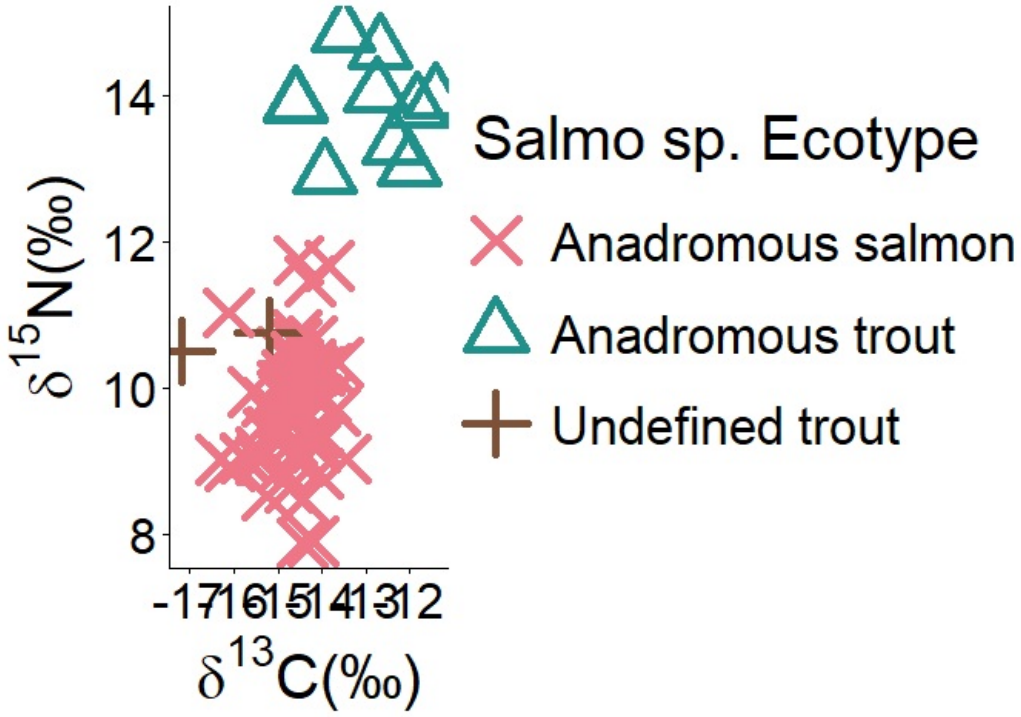


Figure 7.7

```
#Carbon and nitrogen box/violin plots of ecotypes
#removing outlier undefined trout
UD_removed <- subset(Salmo_Only, ecotype != "Undefined trout")
D15N_All <- ggplot(UD_removed, aes(x=ecotype, y=D15N, color=ecotype)) + geom_violin(linewidth=1) +
  geom_boxplot(width=0.1, linewidth=1.5,)+
  scale_color_manual(values= c("Anadromous trout" = "#21918c", "Anadromous salmon"= "#EF7687"))+
  geom_jitter()+
  theme_cowplot(12)+
  guides(color= FALSE)+
  theme(text=element_text(size=30),
        axis.text = element_text(size=24))
```

```
## Warning: The `<scale>` argument of `guides()` cannot be `FALSE`. Use "none" instead as
## of ggplot2 3.3.4.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
D15N_All +ylab(expression(paste(delta^{15},"N(‰)"))) + xlab("\nEcotype Identification")
```

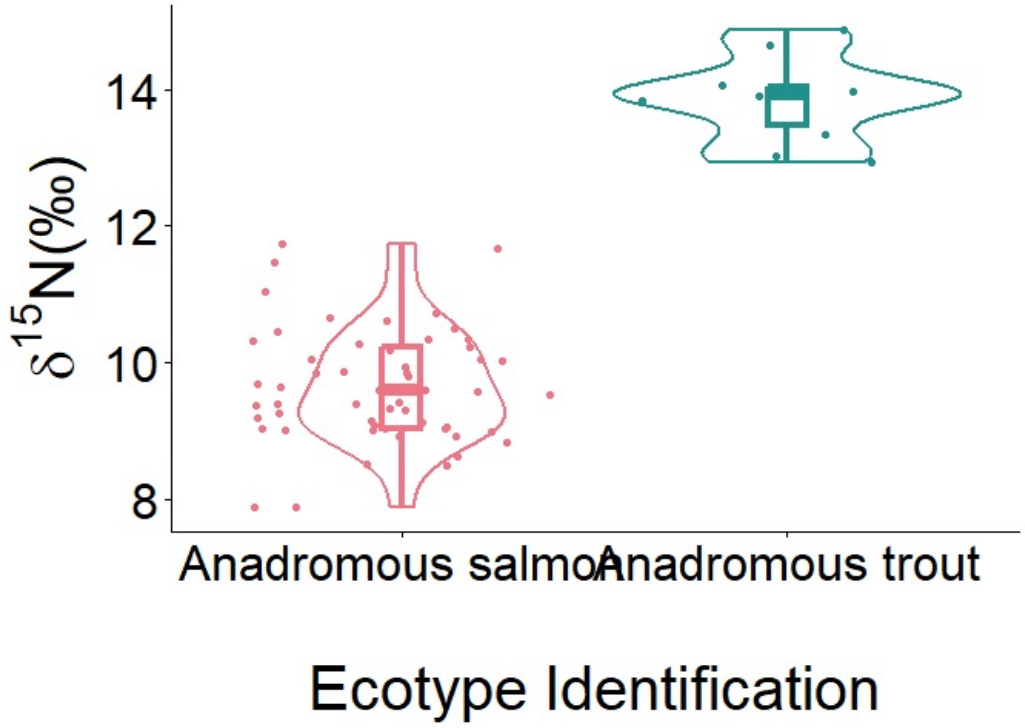


Figure 7.8

```
#Coppergate D15N and D13C box plots through time period

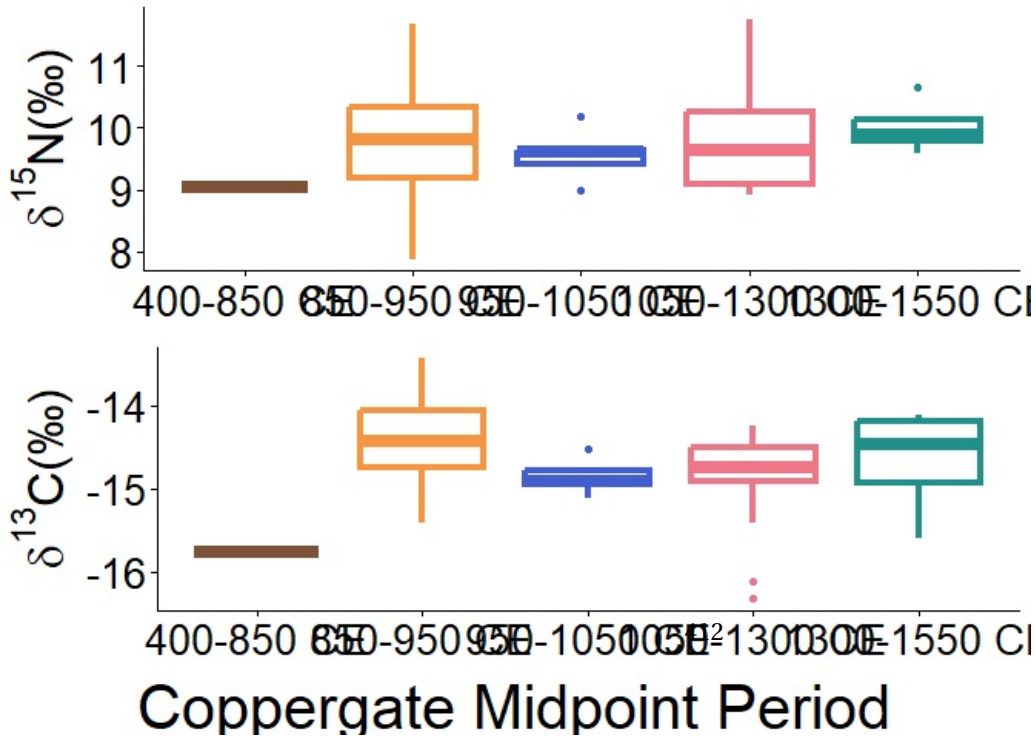
period_order<-(c("400-850 CE", "850-950 CE", "950-1050 CE", "1050-1300 CE", "1300-1550 CE"))

COP_Salmon_D15N <- ggplot(COP_Salmon, aes(x= factor(COP_Period,level=period_order), y=D15N, color= COP_P
COP_D15N <- COP_Salmon_D15N +scale_color_manual(values= c("400-850 CE" = "#7D5238", "850-950 CE"= "#f895

COP_Salmon_D13C <- ggplot(COP_Salmon, aes(x= factor(COP_Period,level=period_order), y=D13C, color= COP_P
COP_D13C <-COP_Salmon_D13C +scale_color_manual(values= c("400-850 CE" = "#7D5238", "850-950 CE"= "#f8954

cop_y_label <- text_grob("Coppergate Midpoint Period", size=30)

grid.arrange(COP_D15N, COP_D13C, bottom=cop_y_label)
```



Chapter 8 - Isotopic Characteristics of Salmo sp. Fish in the North

Sea Basin Area

Code

```
LMQ_Iso_Master <- read_csv("Intersite_Iso_Master.csv")
```

```
## Rows: 190 Columns: 44
## ── Column specification ────────────────────────────────────────────────────────
## Delimiter: ","
## chr (28): sample_ID, sample_type, Morphological_ID_Type, country, site, site...
## dbl (15): total_length, sample_weight, tube_weight, final_weight, collagen_m...
## lgl  (1): Notes
##
## ℹ Use `spec()` to retrieve the full column specification for this data.
## ℹ Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
Salmo_Master <- subset(LMQ_Iso_Master, sample_type=="Salmo")
Migratory_Iso <- subset(LMQ_Iso_Master, Iso_Groups=="Migratory")
Marine_Iso <- subset(LMQ_Iso_Master, Iso_Groups=="Marine")
Freshwater_Iso <-subset(LMQ_Iso_Master, Iso_Groups=="Freshwater")
Mean_SD<- read_csv("Intersite_Mean_SD.csv")
```

```
## Rows: 16 Columns: 6
## ── Column specification ────────────────────────────────────────────────────────
## Delimiter: ","
## chr (1): Taxa
## dbl (5): Count, D13C_Mean, D13C_SD, D15N_Mean, D15N_SD
##
## ℹ Use `spec()` to retrieve the full column specification for this data.
## ℹ Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
Site_Locations <- read.csv("Site_Locations.csv")
Salmon_Values <- subset(Salmo_Master, Iso_IDs == "Salmo salar")
Trout_Values <- subset(Salmo_Master, Iso_IDs == "Salmo trutta")
SeaTrout_Only <-subset(Salmo_Only, ecotype=="Anadromous trout")


#Removing sites not needed for this study
Site_Locations_Isotopes <- subset(Site_Locations, Site != "Heveskesklooster")
Site_Locations <-subset(Site_Locations_Isotopes, Site != "Johan van Oldenbarneveltlaan")
Site_Locations_Isotopes <- subset(Site_Locations, Site !="Huis Malburg")
```

Statistics

```
#Sea trout statistical testing -- trying to see if there is significant
#differences in sea trout populations based on country of origin
res.aov <- aov(D15N ~ country, data = SeaTrout_Only)
# Summary of the analysis
summary(res.aov)
```

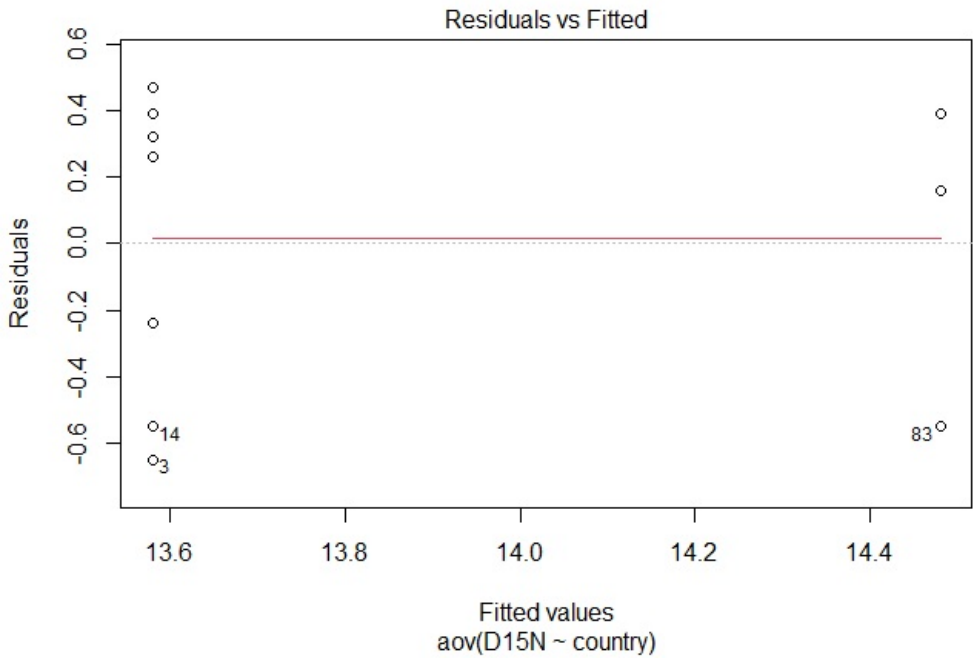
```
##             Df Sum Sq Mean Sq F value Pr(>F)
## country      1  1.701  1.7010   7.536 0.0252 *
## Residuals    8  1.806  0.2257
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
TukeyHSD(res.aov)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = D15N ~ country, data = SeaTrout_Only)
##
## $country
##                  diff       lwr        upr     p adj
## Scotland-England -0.9 -1.656032 -0.1439678 0.0252484
```

```
plot(res.aov,1)
```




```
library(car)
```

```
## Loading required package: carData

##
## Attaching package: 'car'

## The following object is masked from 'package:purrr':
##
##     some

## The following object is masked from 'package:maptools':
##
##     pointLabel

## The following object is masked from 'package:dplyr':
##
##     recode
```

```
leveneTest(D15N ~ country, data=SeaTrout_Only)
```



```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.

## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.0578 0.8161
```

```
##         8
```

```
#No statistically significant difference in variances between the groups
```

Figure 8.3 (Plot A, Figure combined in Inkscape)

```
#ZooMS pie charts

Values <- c(63, 27, 8, 2, 3, 1)
Type <- c("Salmo salar", "Salmo trutta", "Inconclusive Result", "Misidentified Cod", "Misidentified Pike
Prop <- c(60.6, 26.0, 7.7, 1.9, 2.9, .9)
ZooMS_Pie <- data.frame(Values, Type, Prop)

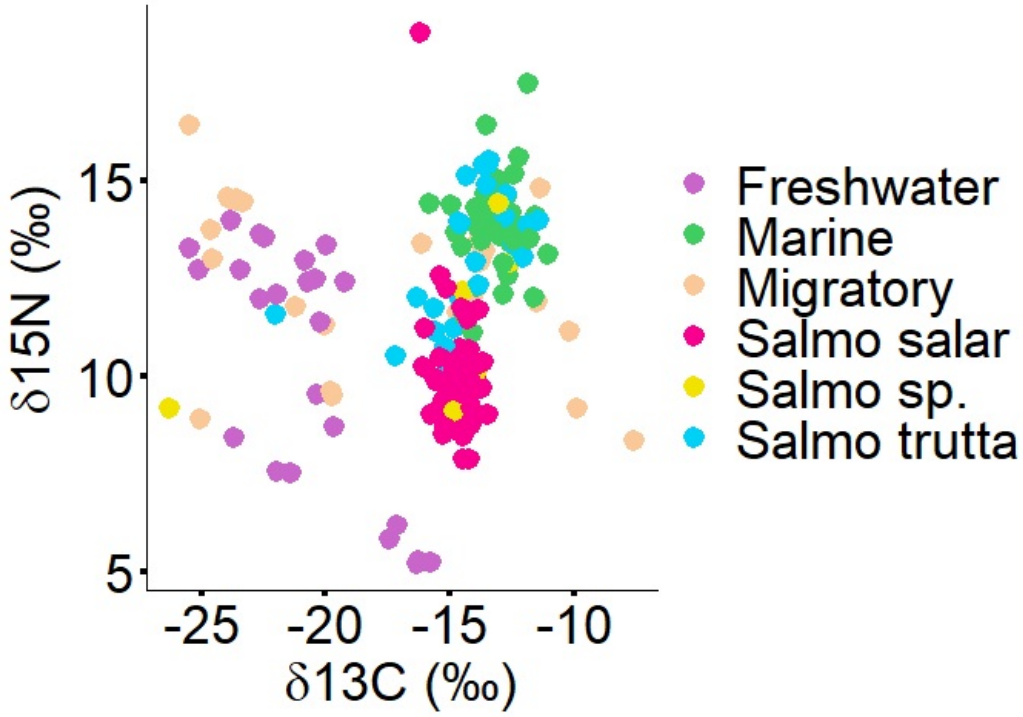
ZooMS_piechart <-  ggplot(ZooMS_Pie, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity") +
ZooMS_piechart <- ZooMS_piechart + coord_polar(theta = 'y')
ZooMS_piechart
```



Figure 8.4 (Combination of the following two plots)

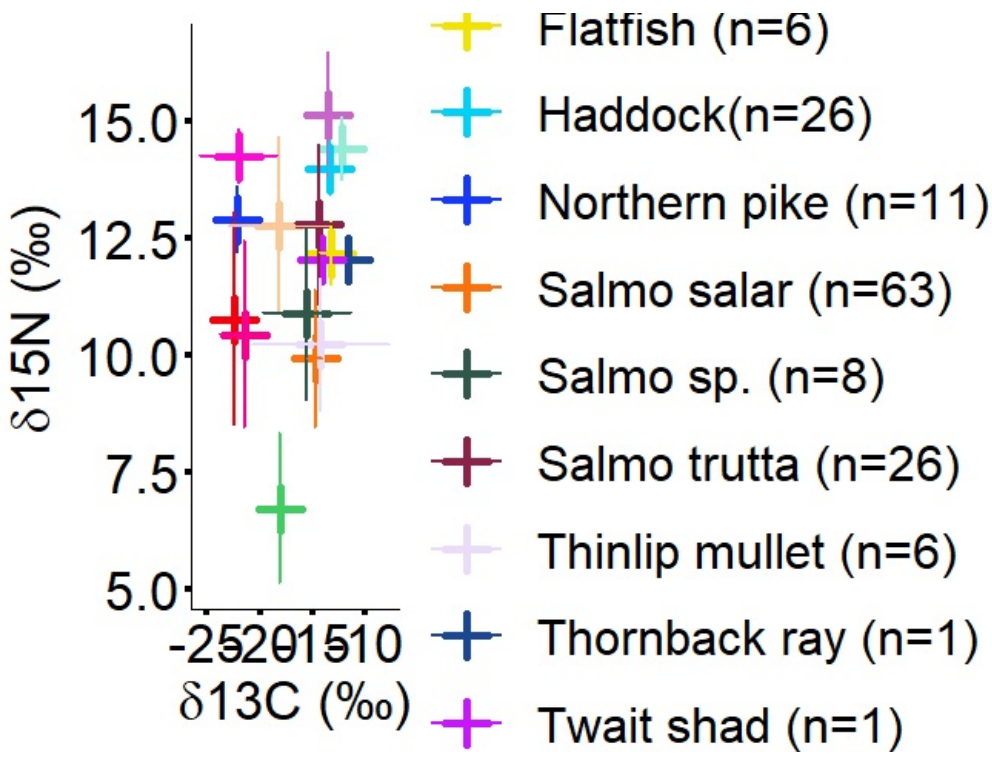
```
#Basic bi-plot of all smaples by category

p <- ggplot(LMQ_Iso_Master, aes(x=D13C, y=D15N, color=Iso_Groups)) + geom_point(size=3, stroke=2) + xlab
Iso_base_plot <- p +theme(legend.text=element_text(size=26),legend.title = element_blank(),text = elemen
Iso_base_plot
```




```
#Mean and error bars plot for all sample taxa
p <- ggplot(Mean_SD, aes(x=D13C_Mean, y=D15N_Mean, color=Taxa)) + geom_point(shape= 3, size=5, stroke=3)
Mean_Error_Plot <- p+theme(legend.text=element_text(size=24),legend.title = element_blank(),text = eleme

Mean_Error_Plot
```




```
addSmallLegend <- function(myPlot, pointSize = 1, textSize = 24, spaceLegend = 0.5) {
  myPlot +
    guides(shape = guide_legend(override.aes = list(size = pointSize)),
           color = guide_legend(override.aes = list(size = pointSize))) +
    theme(legend.text  = element_text(size = textSize),
          legend.key.size = unit(spaceLegend, "lines"))
}

Mean_Error<-addSmallLegend(Mean_Error_Plot)
Mean_Error
```

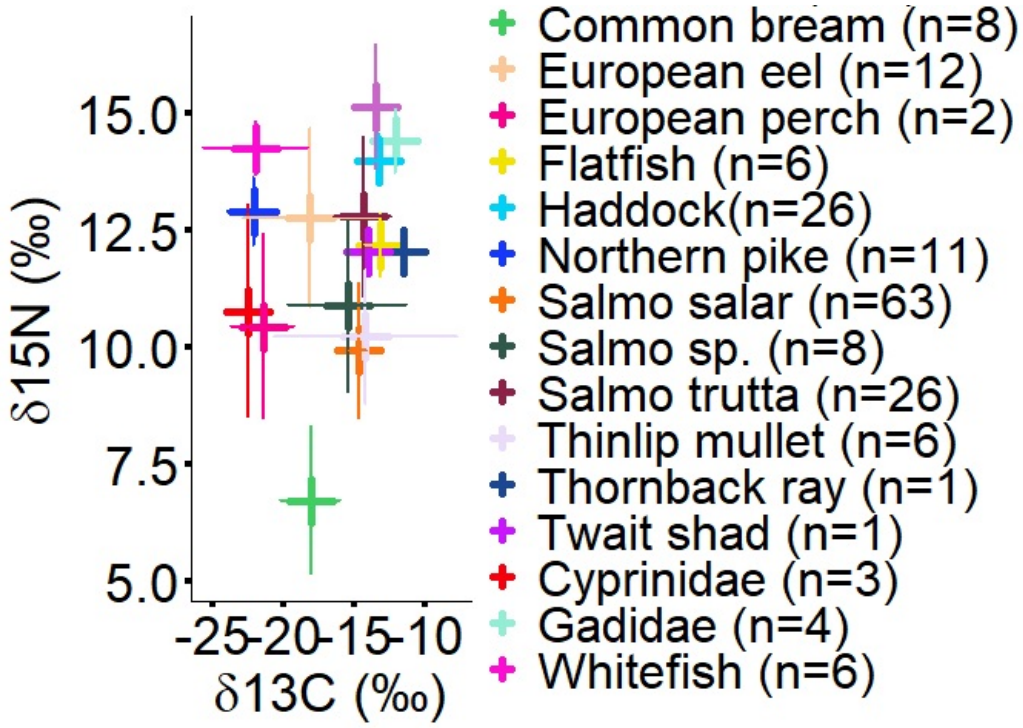
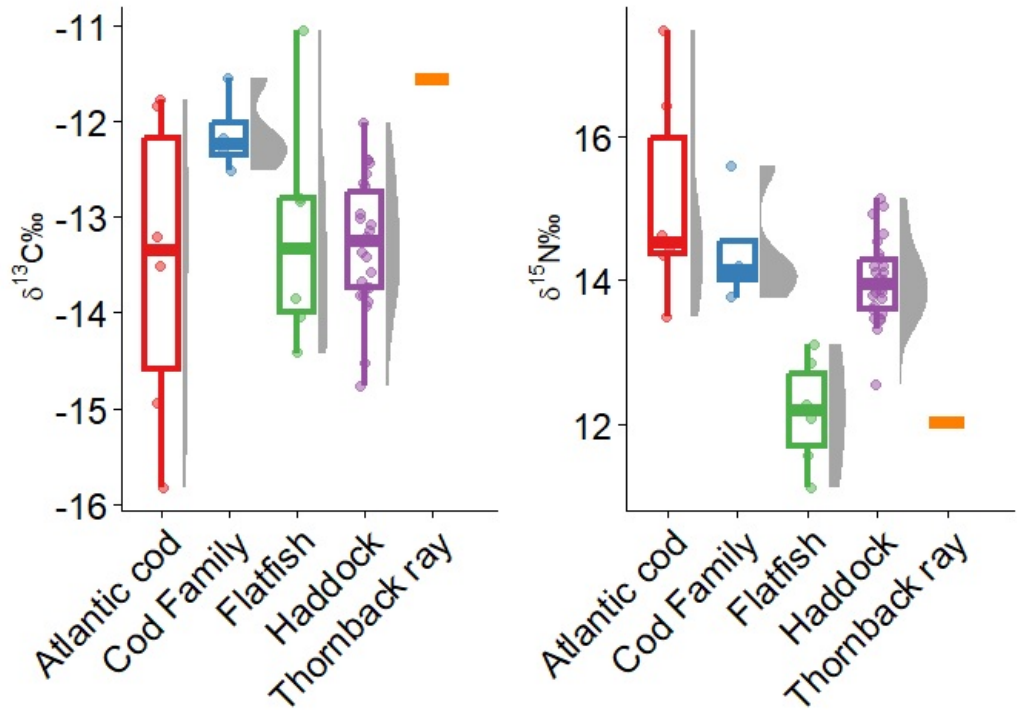


Figure 8.5 (Combined the following three plots in Inkscape for best visibility)

```
#First Marine, nitrogen then carbon - to be combined together
Marine_Iso_N<-ggplot(Marine_Iso, aes(x = common_name, y = D15N, color=common_name)) +
  ggdist::stat_halfeye(
    adjust = 1,
    width = .6,
    .width = 0,
    justification = -0.6,
    point_colour = NA) +
  geom_boxplot(
    width = .5,
    outlier.shape = NA,
    linewidth=1.5
  ) +
  geom_point(
    size = 2,
    alpha = .5,
    position = position_jitter(
      seed = 1, width = .1
    )
  ) + theme_cowplot() + scale_color_brewer(palette="Set1") + theme(legend.position = "none", axis.title.

Marine_Iso_C<-ggplot(Marine_Iso, aes(x = common_name, y = D13C, color=common_name)) +
  ggdist::stat_halfeye(
    adjust = 1,
    width = .6,
    .width = 0,
    justification = -0.6,
    point_colour = NA) +
  geom_boxplot(
    width = .5,
    outlier.shape = NA,
    linewidth=1.5
  ) +
  geom_point(
    size = 2,
    alpha = .5,
    position = position_jitter(
      seed = 1, width = .1
    )
  ) + theme_cowplot() + scale_color_brewer(palette="Set1") + theme(legend.position = "none", axis.title.

Marine_plots<-ggarrange(Marine_Iso_C,Marine_Iso_N, nrow=1)
Marine_plots
```




```
p <- ggplot(Marine_Iso, aes(x=D13C, y=D15N, color=common_name)) + geom_point(size=3, stroke=2) + xlab(ex
Marine_Iso_plot <- p +theme(legend.text=element_text(size=26),legend.title = element_blank(),text = elem
Marine_Iso_plot
```

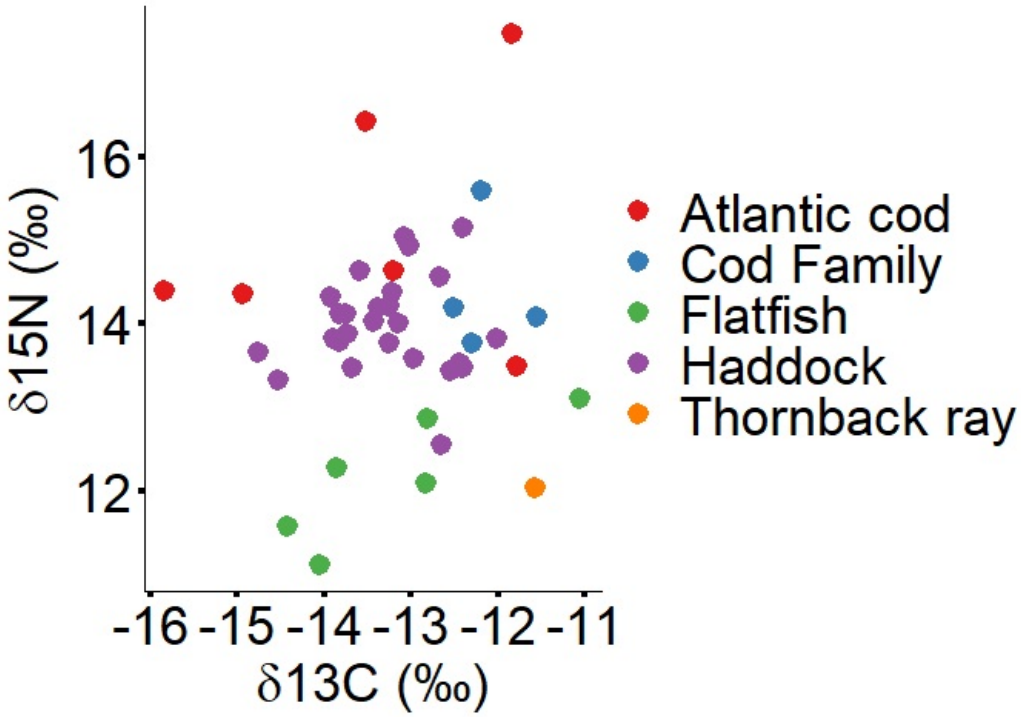
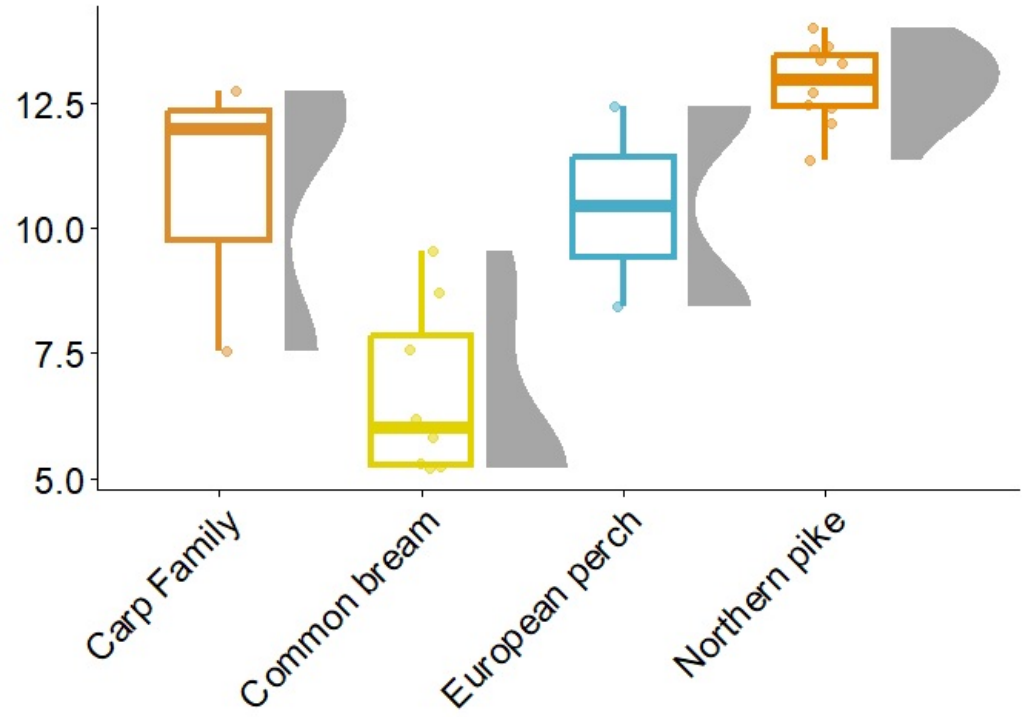


Figure 8.6 (Combined in Inkscape for legibility)

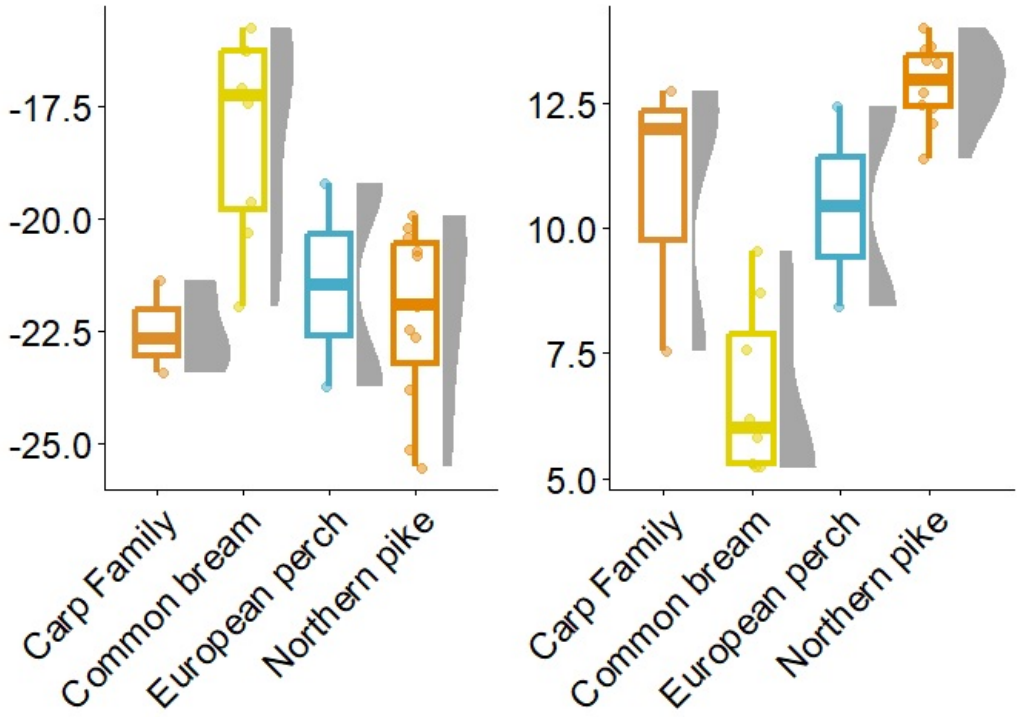
```
#Now Freshwater, same as above, but with a different color palette to avoid confusion
Freshwater_Iso_N<-ggplot(Freshwater_Iso, aes(x = common_name, y = D15N, color=common_name)) +
  ggdist::stat_halfeye(
    adjust = 1,
    width = .6,
    .width = 0,
    justification = -0.6,
    point_colour = NA) +
  geom_boxplot(
    width = .5,
```

```
    outlier.shape = NA,
    linewidth=1.5
  ) +
  geom_point(
    size = 2,
    alpha = .5,
    position = position_jitter(
      seed = 1, width = .1
    )
  )  + theme_cowplot() + scale_color_manual(values= wes_palette("FantasticFox1", n=4)) + theme(legend.po
Freshwater_Iso_N
```




```
Freshwater_Iso_C<-ggplot(Freshwater_Iso, aes(x = common_name, y = D13C, color=common_name)) +
  ggdist::stat_halfeye(
    adjust = 1,
    width = .6,
    .width = 0,
    justification = -0.6,
    point_colour = NA) +
  geom_boxplot(
    width = .5,
    outlier.shape = NA,
    linewidth=1.5
  ) +
  geom_point(
    size = 2,
    alpha = .5,
    position = position_jitter(
      seed = 1, width = .1
    )
  ) + theme_cowplot() + scale_color_manual(values= wes_palette("FantasticFox1", n=4)) + theme(legend.pos

Freshwater_plots<-ggarrange(Freshwater_Iso_C,Freshwater_Iso_N, nrow=1)
Freshwater_plots
```




```
p <- ggplot(Freshwater_Iso, aes(x=D13C, y=D15N, color=common_name)) + geom_point(size=3, stroke=2) + xlal
Freshwater_Iso_plot <- p +theme(legend.text=element_text(size=26),legend.title = element_blank(),text = 
Freshwater_Iso_plot
```

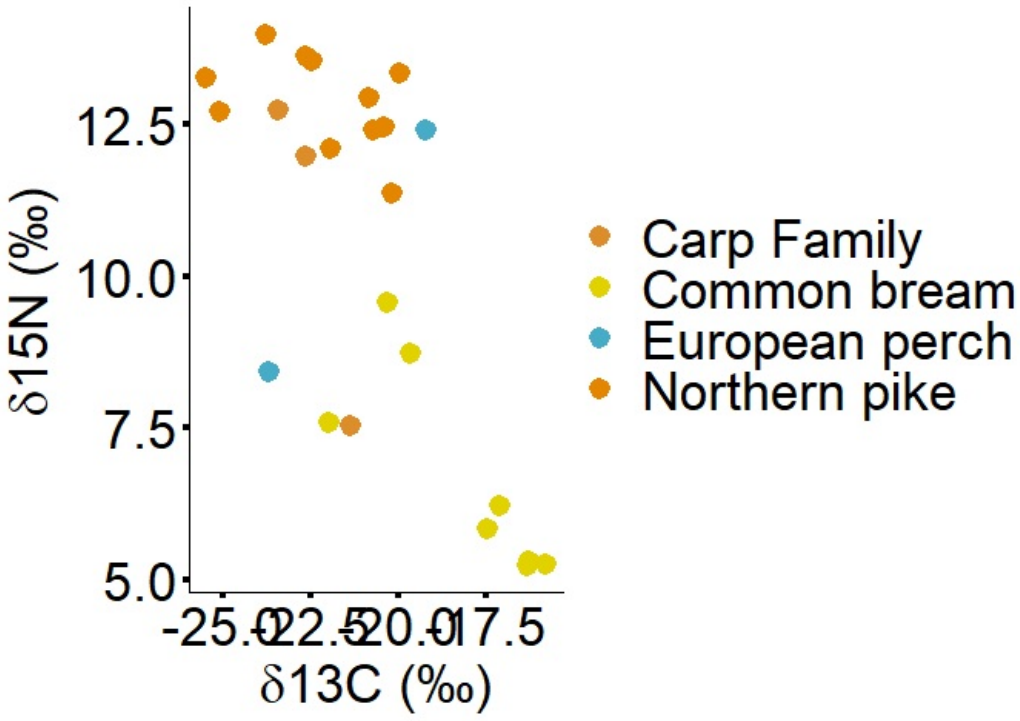


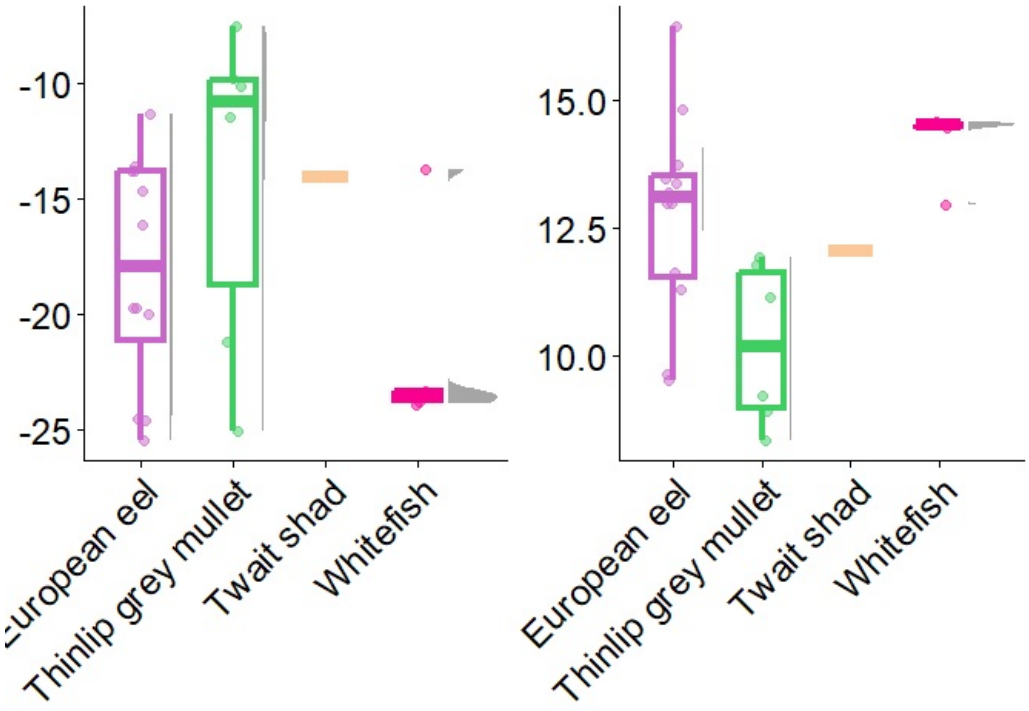
Figure 8.7 (Combined in Inkscape for legibility)

```
#Migratory plots
Migratory_Iso_N<-ggplot(Migratory_Iso, aes(x = common_name, y = D15N, color=common_name)) +
  ggdist::stat_halfeye(
    adjust = 1,
    width = 0.6,
    .width = 0,
    justification = -0.6,
    point_colour = NA) +
  geom_boxplot(
    width = .5,
    outlier.shape = NA,
    linewidth=1.5
```

```
  ) +
  geom_point(
    size = 2,
    alpha = .5,
    position = position_jitter(
      seed = 1, width = .1
    )
  ) + theme_cowplot() +scale_color_manual(values=Liz_PhD) + theme(legend.position = "none", axis.title.y

Migratory_Iso_C<-ggplot(Migratory_Iso, aes(x = common_name, y = D13C, color=common_name)) +
  ggdist::stat_halfeye(
    adjust = 1,
    width = 0.6,
    .width = 0,
    justification = -0.6,
    point_colour = NA) +
  geom_boxplot(
    width = .5,
    outlier.shape = NA,
    linewidth=1.5
  ) +
  geom_point(
    size = 2,
    alpha = .5,
    position = position_jitter(
      seed = 1, width = .1
    )
  )  + theme_cowplot() +scale_color_manual(values=Liz_PhD) + theme(legend.position = "none", axis.title.y

Migratory_plots<-ggarrange(Migratory_Iso_C,Migratory_Iso_N, nrow=1)
Migratory_plots
```




```
p <- ggplot(Migratory_Iso, aes(x=D13C, y=D15N, color=common_name)) + geom_point(size=3, stroke=2) + xlab
Migratory_Iso_plot <- p +theme(legend.text=element_text(size=26),legend.title = element_blank(),text = e
Migratory_Iso_plot
```

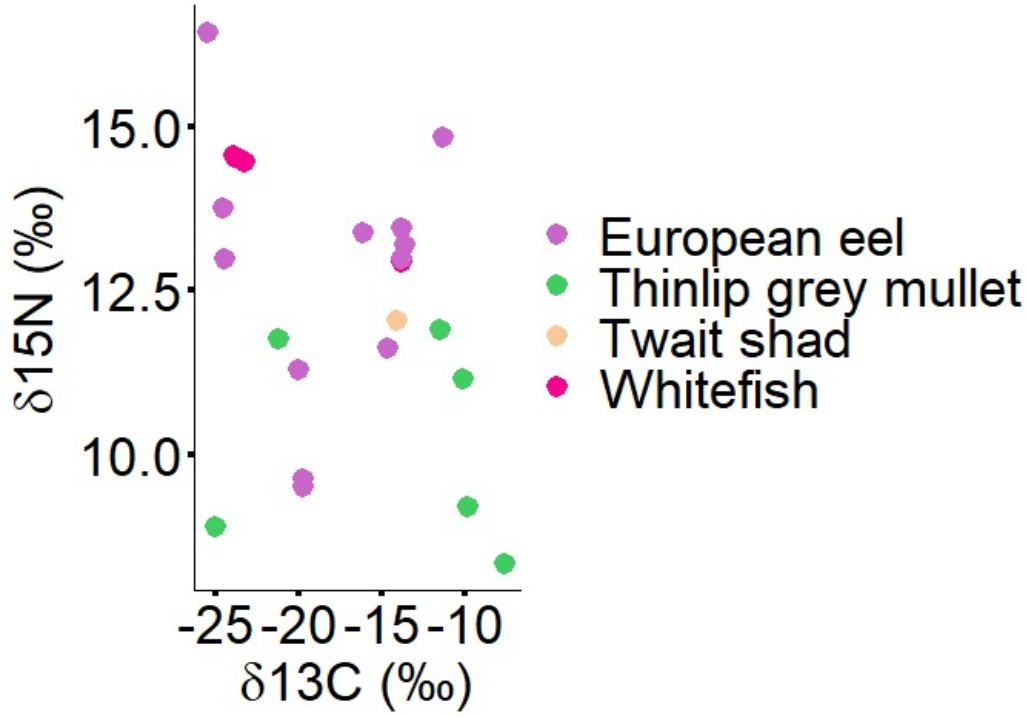
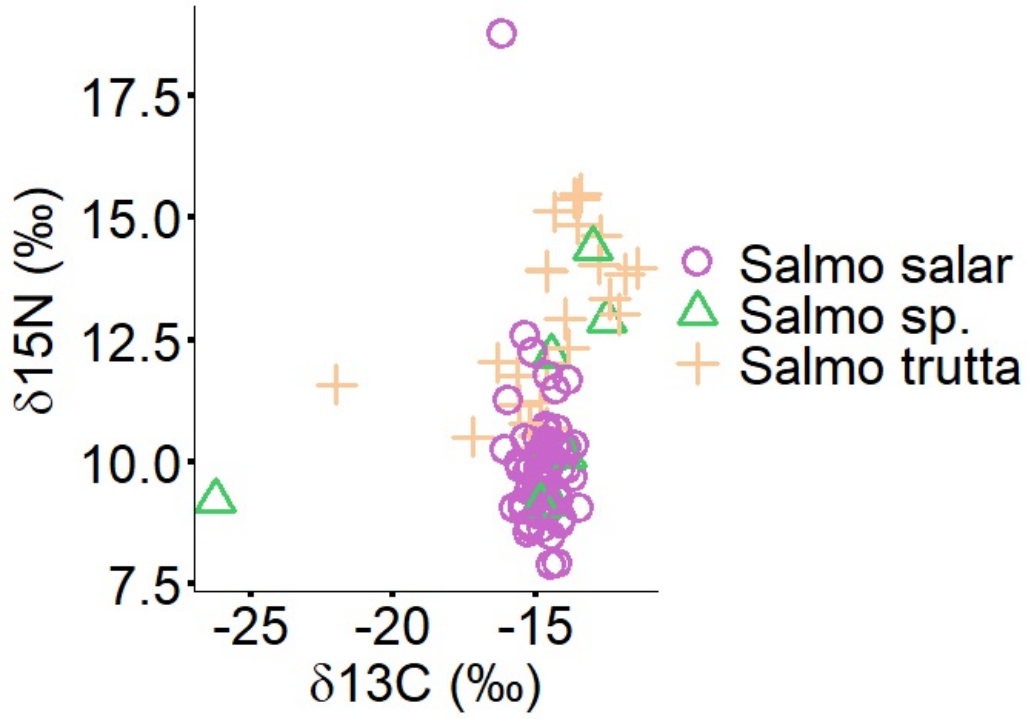


Figure 8.8

```
#Basic bi-plot of just the salmonid samples from all sites, including unspecified salmonids

p <- ggplot(Salmo_Master, aes(x=D13C, y=D15N, color=Iso_IDs, shape= Iso_IDs)) + geom_point(size=5, strok
Salmo_Base <- p+theme(legend.text=element_text(size=26),legend.title = element_blank(),text = element_te
Salmo_Base
```




```
#Adding ellipses
#set ellipse size
p.ell<- 0.95
ellipse_plot <- Salmo_Base  + stat_ellipse(aes(linetype=Iso_IDs), type="t", lwd=2)+ scale_linetype_manua
ellipse_plot
```



```
## Warning in MASS::cov.trob(data[, vars]): Probable convergence failure
```

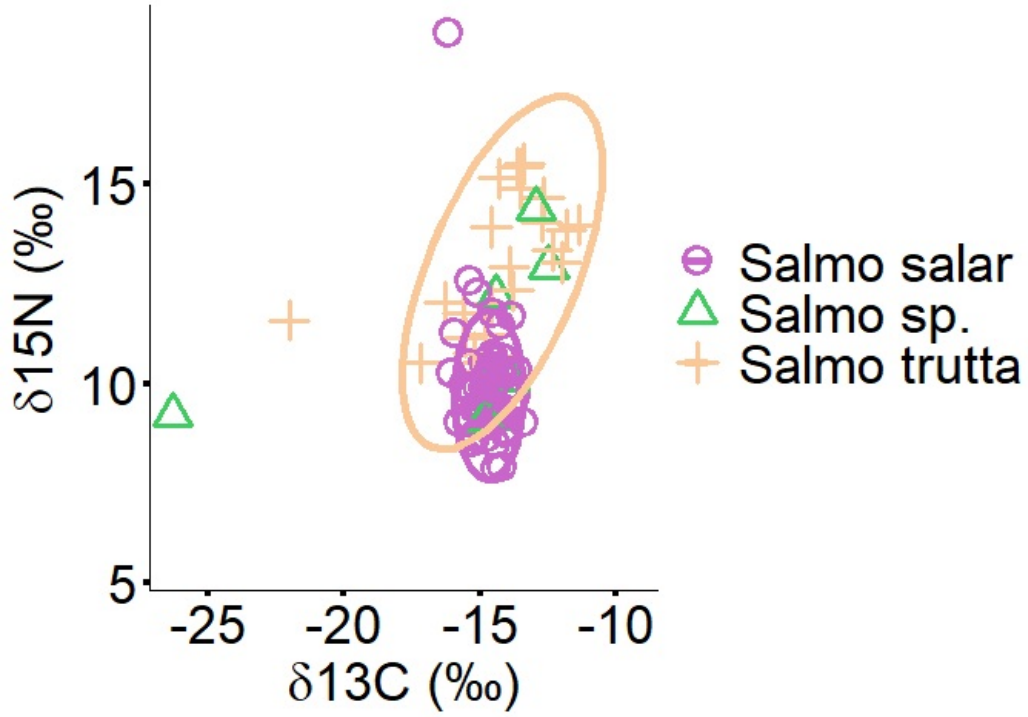
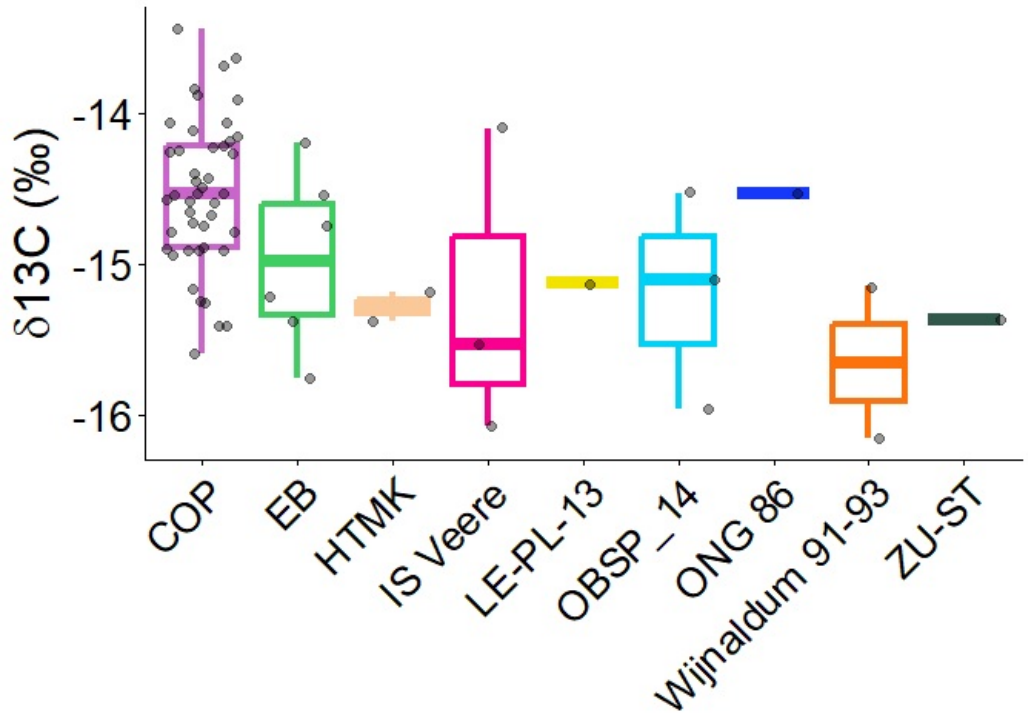


Figure 8.9 (Combined in Inkscape for legibility)

```
#Box plot of Salmo salar D13C values by site

D13C_Box_Salmon2 <- ggplot(Salmon_Values, aes(x=site_code, y=D13C, color= site_code)) + geom_boxplot(lwd
D13C_Box_Salmon2
```




```
#Box plot of Salmo salar D15N values by site
D15N_Box_Salmon2 <- ggplot(Salmon_Values, aes(x=site_code, y=D15N, color= site_code)) + geom_boxplot(lwd
D15N_Box_Salmon2
```

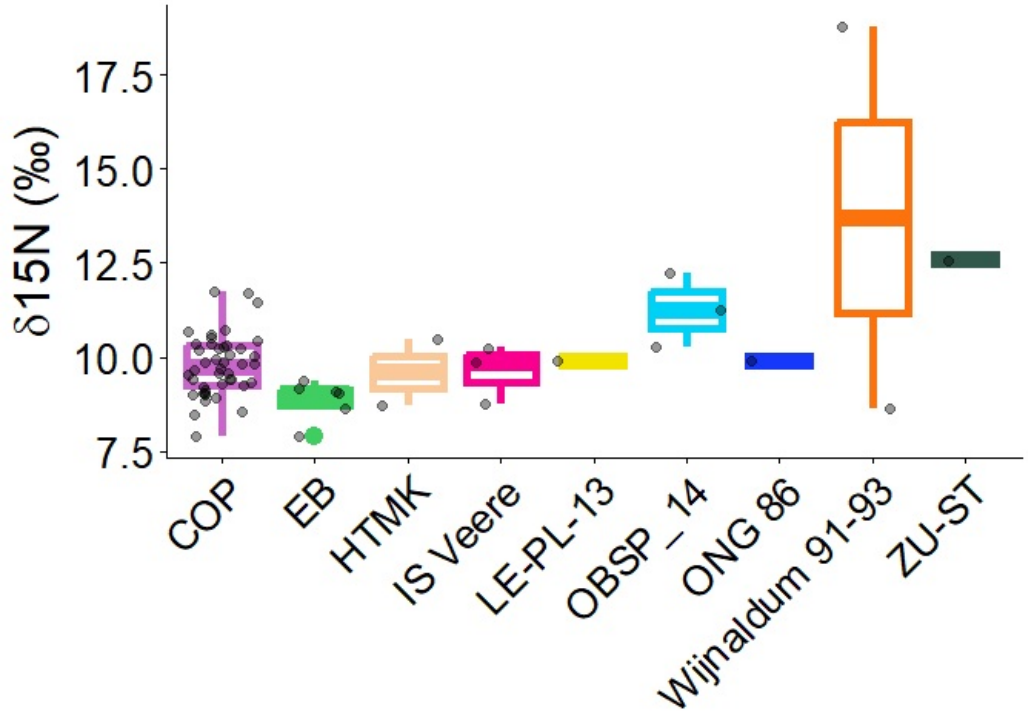


Figure 8.10

```
#TL correlations for all salmon
TL_D15N <- read.csv("TL_D15N.csv")
All_TL<- ggscatter(TL_D15N, x="TL", y="D15N",
          add= "reg.line", conf.int= TRUE,
          cor.coef = TRUE, cor.method= "pearson",
          color="gray", alpha=0.0, cor.coef.size = 8) +
  ylab(expression(italic(delta)^15*N*"(‰) of Salmon Samples")) +
  xlab ("Total Length (cm)") +
  theme_cowplot(12)+
  theme(text = element_text(size=20),
        axis.text = element_text(size=20),
        axis.ticks = element_line(linewidth = 1.5))+
  geom_point(data=TL_D15N, mapping=aes(x=TL, y=D15N, color=site), shape=16, size=5, stroke=2) + scale_co

check1 <- cor.test(TL_D15N$TL, TL_D15N$D15N,
                method = "pearson")
check1
```

```
##
##  Pearson's product-moment correlation
##
## data:  TL_D15N$TL and TL_D15N$D15N
## t = 3.0543, df = 46, p-value = 0.003744
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.1431937 0.6221670
## sample estimates:
##       cor
## 0.4106217
```

```
#TL correlations for just Coppergate
TL_D15N_Coppergate <- subset(TL_D15N, site=="16-22 Coppergate")
COP_TL<-ggscatter(TL_D15N_Coppergate, x="TL", y="D15N", add= "reg.line", conf.int= TRUE,
          cor.coef = TRUE, cor.method= "pearson", color="#CC66CC",
          size=5, shape=16, stroke=2, cor.coef.size = 8, add.params = list(color = "gray", fill = "gray"
  ylab(expression(italic(delta)^15*N*"(‰) of Salmon Samples")) +
  xlab ("Total Length (cm)") +
  theme_cowplot(12)+
  theme(text = element_text(size=20),
```

```
        axis.text = element_text(size=20),
        axis.ticks = element_line(linewidth = 1.5))

check2 <- cor.test(TL_D15N_Coppergate$TL, TL_D15N_Coppergate$D15N,
                   method = "pearson")
check2
```

```
##
##  Pearson's product-moment correlation
##
## data:  TL_D15N_Coppergate$TL and TL_D15N_Coppergate$D15N
## t = 3.3577, df = 33, p-value = 0.001993
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.2060189 0.7172519
## sample estimates:
##       cor
## 0.5046207
```

```
ggarrange(All_TL, COP_TL, nrow=2)
```

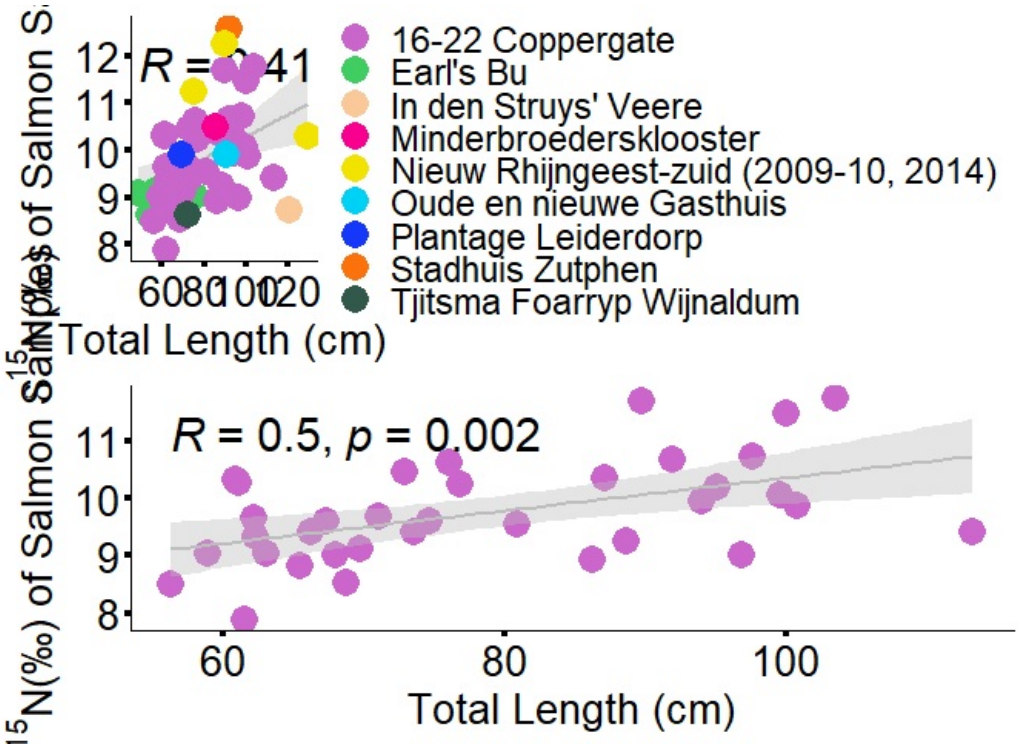
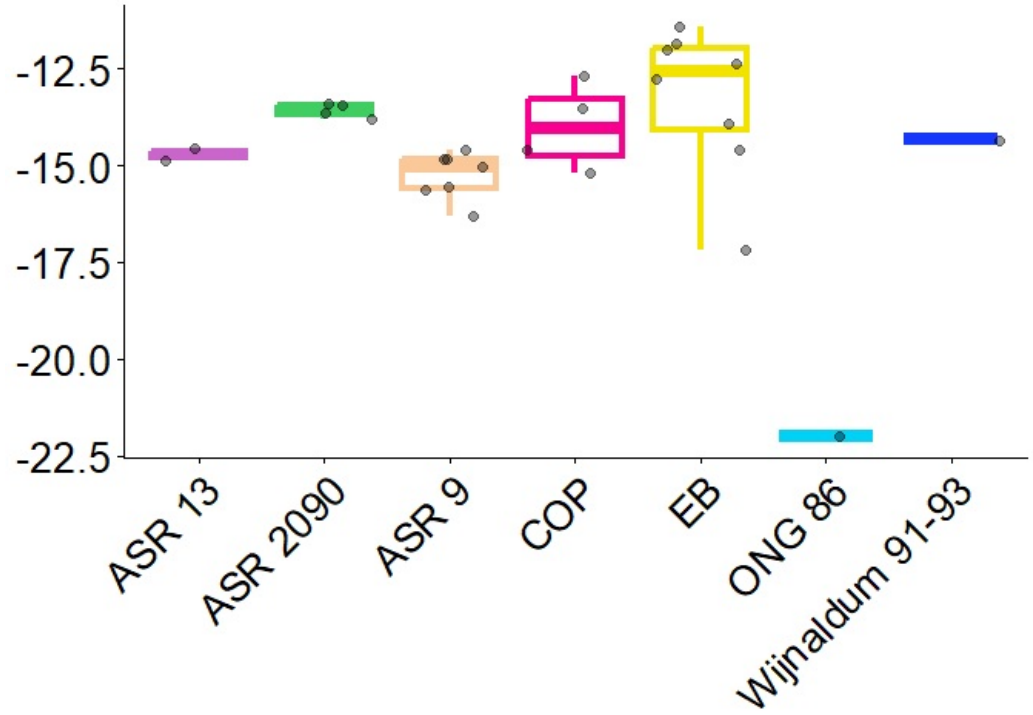


Figure 8.11

```
D13C_Box_Trout2 <- ggplot(Trout_Values, aes(x=site_code, y=D13C, color= site_code)) + geom_boxplot(lwd=1
D13C_Box_Trout2
```




```
D15N_Box_Trout2 <- ggplot(Trout_Values, aes(x=site_code, y=D15N, color= site_code)) + geom_boxplot(lwd=1
D15N_Box_Trout2
```

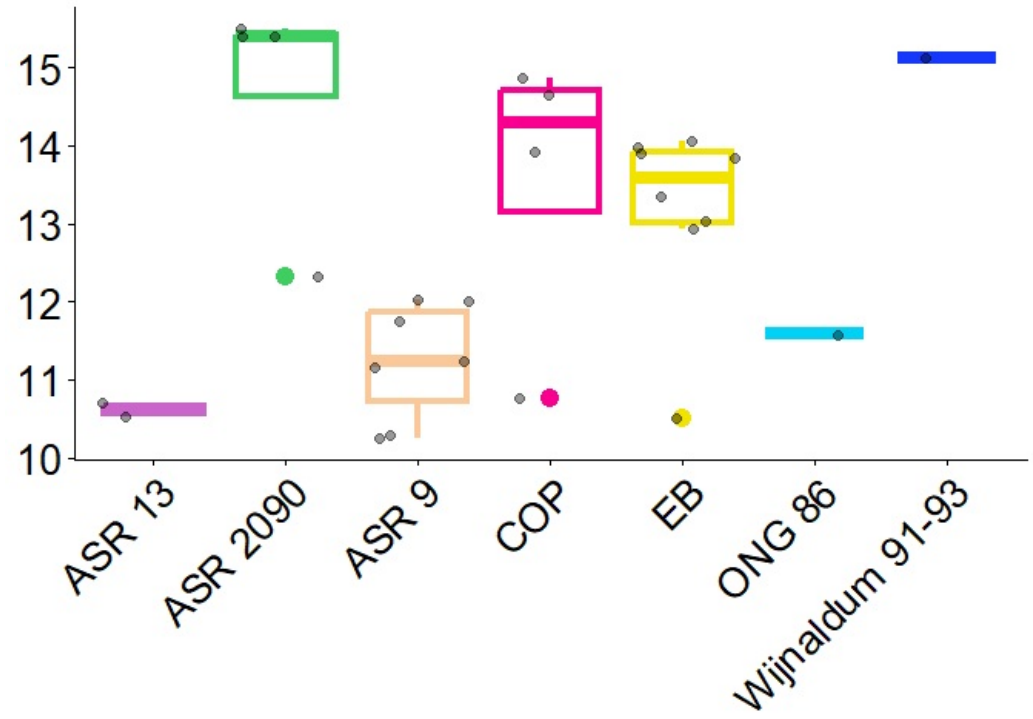
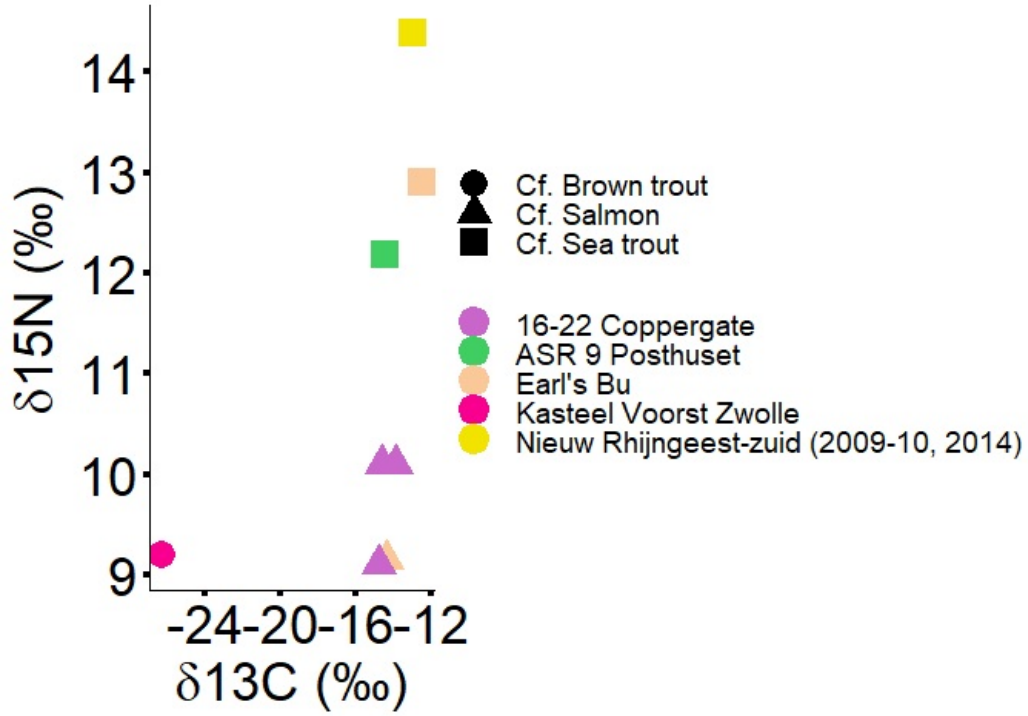


Figure 8.12

```
ZooMS_Salmo <- subset(Salmo_Master, Iso_IDs == "Salmo sp.")
p <- ggplot(ZooMS_Salmo, aes(x=D13C, y=D15N, shape= ecotype, color=site)) + geom_point(size=5, stroke=2)
Salmo_ZooMS_Plot<- p+theme(legend.text=element_text(size=14),legend.title = element_blank(),text = eleme
Salmo_ZooMS_Plot
```




```
addSmallLegend <- function(myPlot, pointSize = 1, textSize = 18, spaceLegend = 0.5) {
  myPlot +
    guides(shape = guide_legend(override.aes = list(size = pointSize)),
           color = guide_legend(override.aes = list(size = pointSize))) +
    theme(legend.text  = element_text(size = textSize),
          legend.key.size = unit(spaceLegend, "lines"))
}
Salmo_Only<-addSmallLegend(Salmo_ZooMS_Plot)
Salmo_Only
```

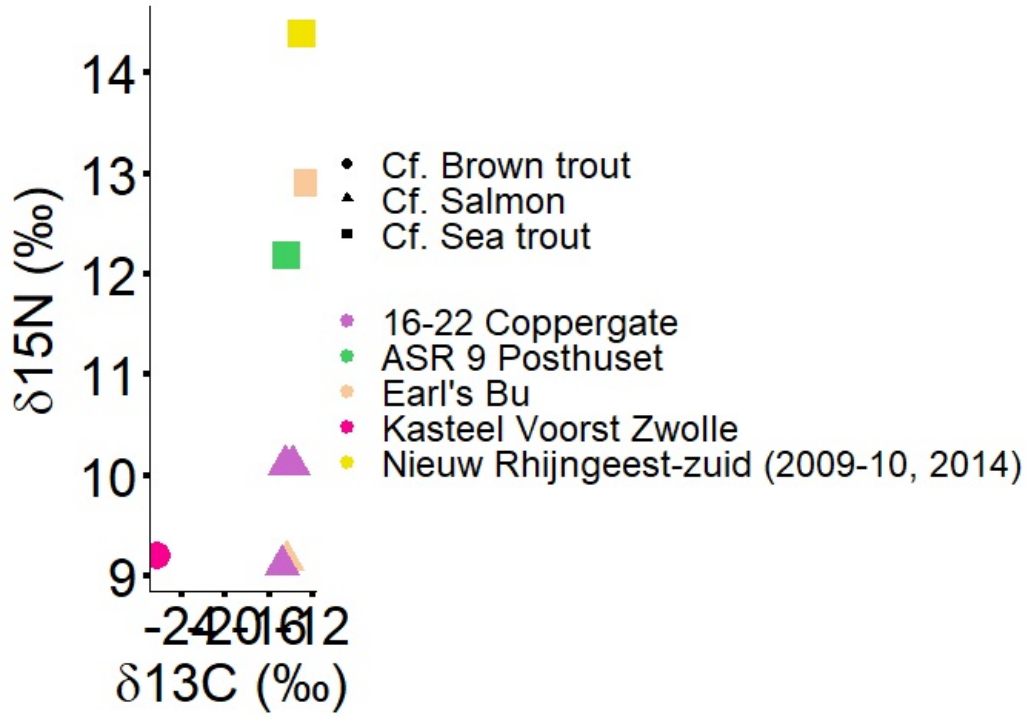


Figure 8.13 (Combined in Inkscape for legibility)

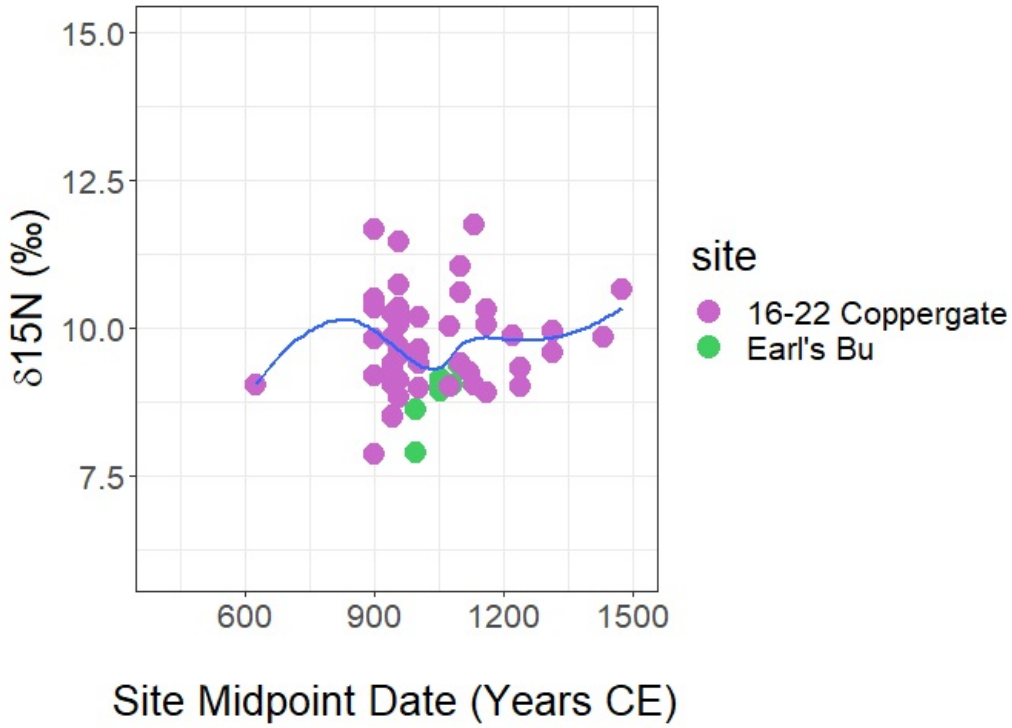

```
#Salmo salar D15N and D13C, sorted by time period from several subsets
#Nothing particularly interesting showing here, other than a SLIGHTLY wiggly line for nitrogen over time

S_timeseries_N <- ggplot(Salmon, aes(x=midpoint, y=D15N)) +
  geom_point (aes(col=site, size=2)) + geom_smooth(method="loess", se=F) +
  xlim(c(400,1500)) + ylim(c(6,15)) + theme_bw() +
```

```
  theme(text=element_text(size=20)) + ylab(expression(delta *"15N (‰)")) +
  xlab("\nSite Midpoint Date (Years CE)") + scale_color_manual(values=Liz_PhD)+
  guides(color = guide_legend(override.aes = list(size = 5)), size="none")

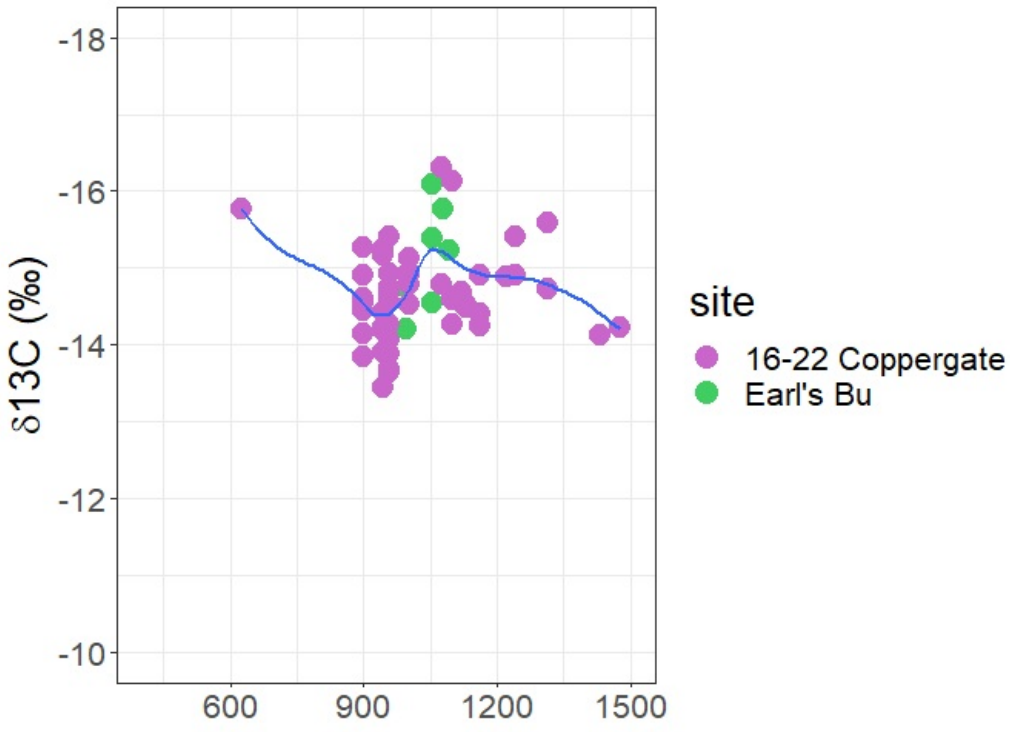
S_timeseries_N
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



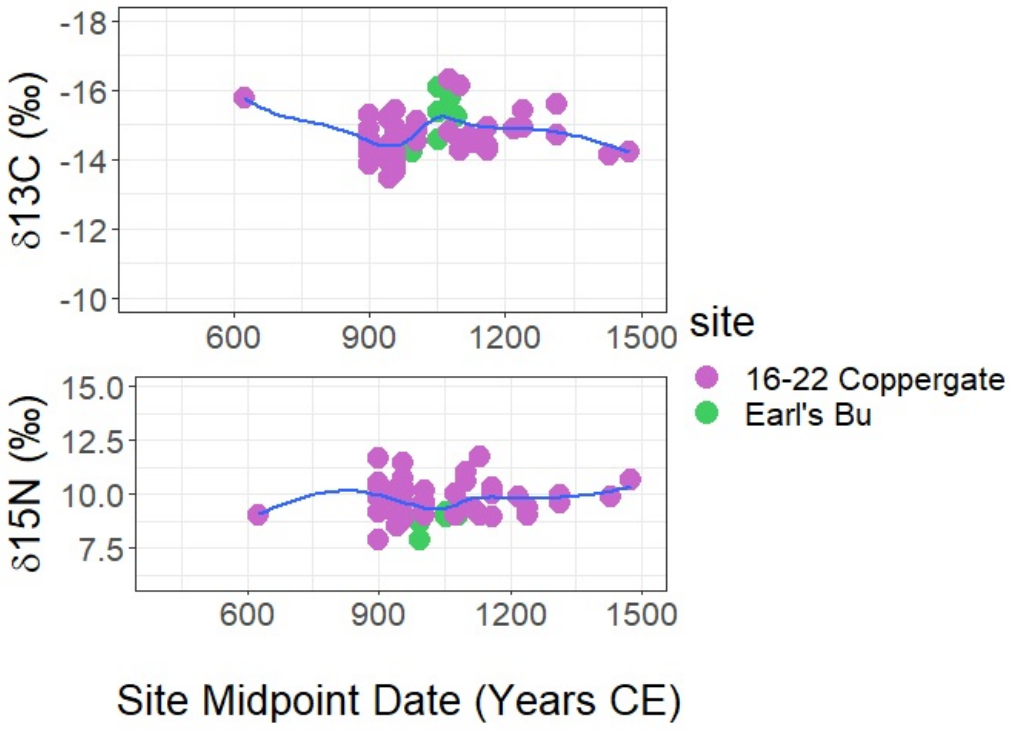

```
S_timeseries_C <- ggplot(Salmon, aes(x=midpoint, y=D13C)) + geom_point (aes(col=site, size=2)) +
  geom_smooth(method="loess", se=F) +xlim(c(400,1500)) +
  ylim(c(-10,-18)) + theme_bw() + theme(text=element_text(size=20), axis.title.x = element_blank()) +
  ylab(expression(delta *"13C (‰)")) + scale_color_manual(values=Liz_PhD) +
  guides(color = guide_legend(override.aes = list(size = 5)), size="none")
S_timeseries_C
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
ggarrange(S_timeseries_C, S_timeseries_N, nrow=2, common.legend = TRUE, legend = "right")
```

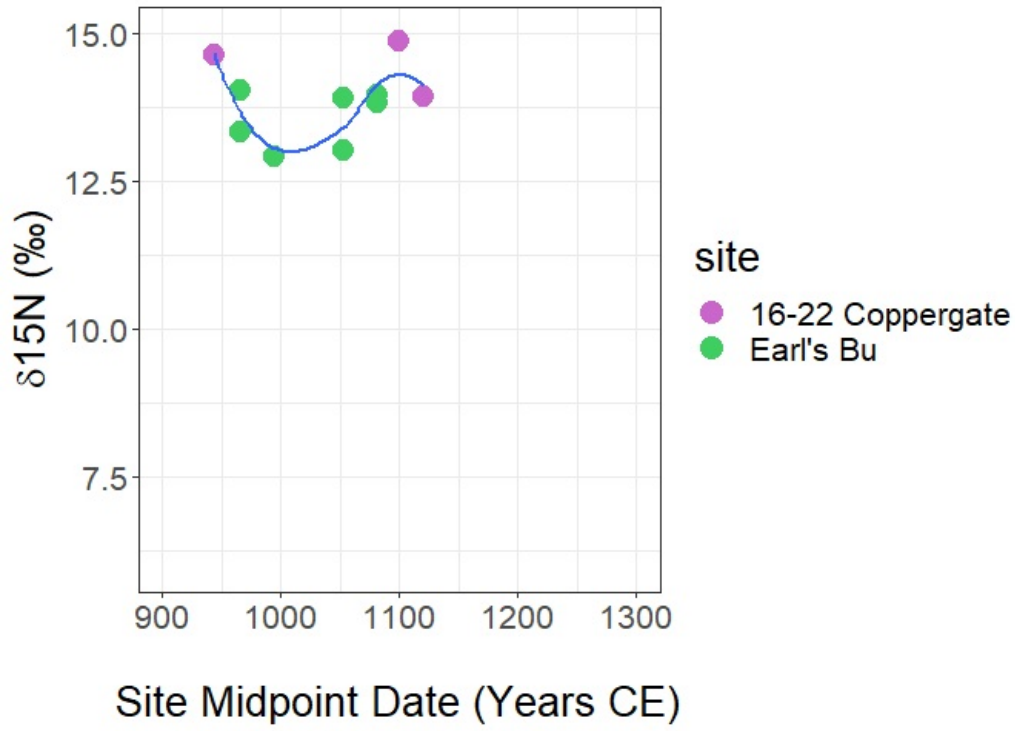
```
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```




```
#Same as above but for Sea Trout


ST_timeseries_N <- ggplot(SeaTrout_Only, aes(x=midpoint, y=D15N)) +
  geom_point (aes(col=site, size=2)) + geom_smooth(method="loess", se=F) +
  xlim(c(900,1300)) + ylim(c(6,15)) + theme_bw() +
  theme(text=element_text(size=20)) + ylab(expression(delta *"15N (‰)")) +
  xlab("\nSite Midpoint Date (Years CE)") + scale_color_manual(values=Liz_PhD) +
  guides(color = guide_legend(override.aes = list(size = 5)), size="none")
ST_timeseries_N
```

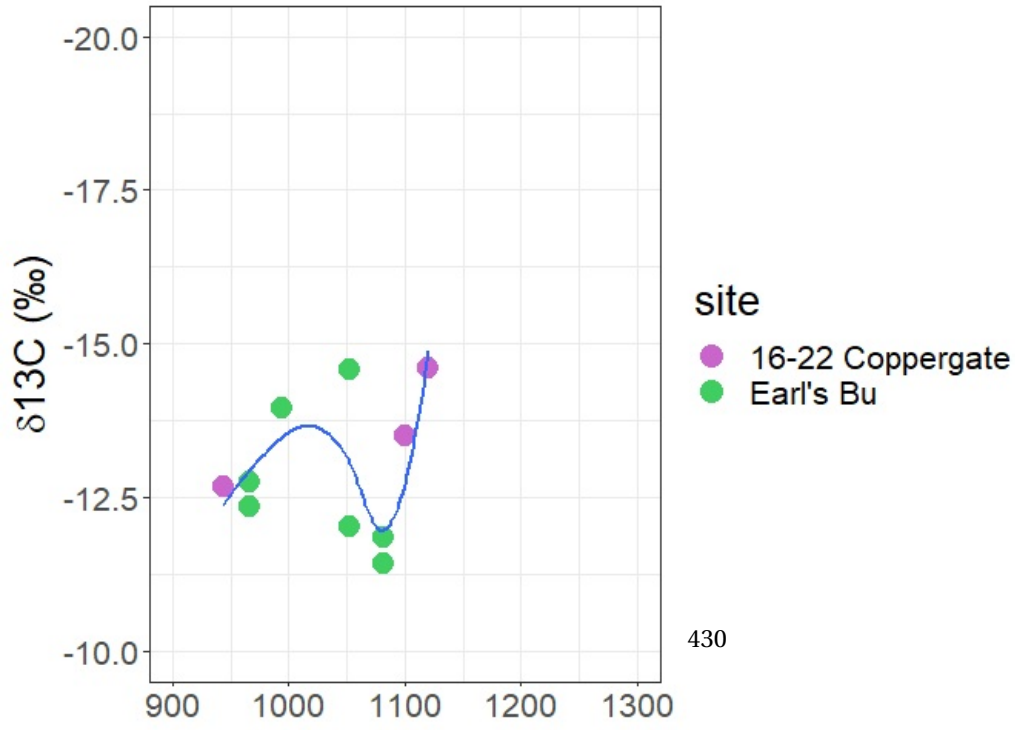
```
## `geom_smooth()` using formula = 'y ~ x'
```




```
ST_timeseries_C <- ggplot(SeaTrout_Only, aes(x=midpoint, y=D13C)) +
  geom_point (aes(col=site, size=2)) + geom_smooth(method="loess", se=F) +
  xlim(c(900,1300)) + ylim(c(-10,-20)) + theme_bw() +
  theme(text=element_text(size=20), axis.title.x = element_blank()) + ylab(expression(delta *"13C (‰)")) +
  scale_color_manual(values=Liz_PhD) +
  guides(color = guide_legend(override.aes = list(size = 5)), size="none")

ST_timeseries_C
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
ggarrange(ST_timeseries_C, ST_timeseries_N, nrow=2, common.legend = TRUE, legend="right")
```

```
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```

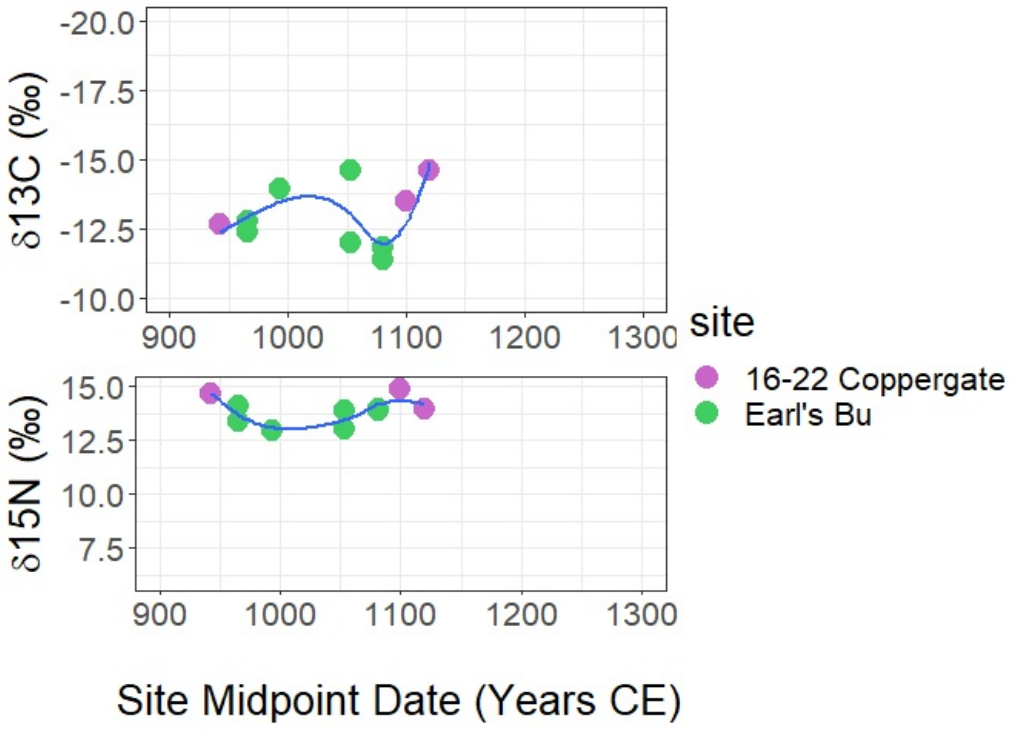


Figure 8.14 (Figures combined, with common legend, in Inkscape and further labelling done there as well)

```
multi_species_data <- read.csv("rKIN_comps.csv")

test.kin<- estKIN(data=multi_species_data, smallSamp = TRUE, x="Ave_C", y="Ave_N", group="Species",
                  levels=c(50, 75, 95), scaler=2)
# Extract the area of each polygon
kin.area<- getArea(test.kin)
kin.area
```

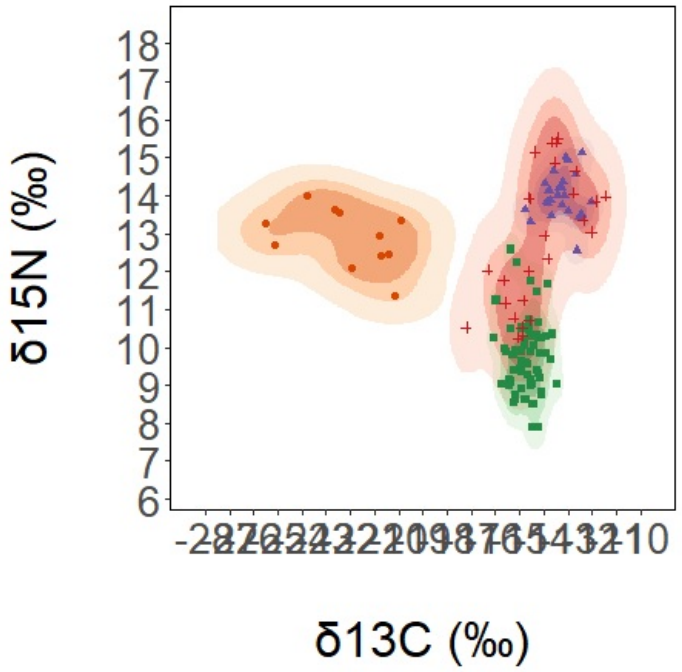
```
##    Method                    Group ConfInt ShapeArea
## 1  Kernel              Esox lucius      50  8.788320
## 2  Kernel              Esox lucius      75 16.304530
## 3  Kernel              Esox lucius      95 29.745966
## 4  Kernel Melanogrammus aeglefinus      50  1.832850
## 5  Kernel Melanogrammus aeglefinus      75  3.829628
## 6  Kernel Melanogrammus aeglefinus      95  7.748752
## 7  Kernel              Salmo salar      50  2.567767
## 8  Kernel              Salmo salar      75  5.429648
## 9  Kernel              Salmo salar      95 11.649348
## 10 Kernel             Salmo trutta      50 11.339031
## 11 Kernel             Salmo trutta      75 20.614780
## 12 Kernel             Salmo trutta      95 38.468264
```

```
# determine polygon overlap for all polygons
kin.olp<- calcOverlap(test.kin)
kin.olp
```

```
##                     OverlapID Esox lucius_50 Esox lucius_75 Esox lucius_95
## 1               Esox lucius_50          1.000          1.000              1
## 2               Esox lucius_75          0.539          1.000              1
## 3               Esox lucius_95          0.295          0.548              1
## 4  Melanogrammus aeglefinus_50          0.000          0.000              0
## 5  Melanogrammus aeglefinus_75          0.000          0.000              0
## 6  Melanogrammus aeglefinus_95          0.000          0.000              0
```

```
## 7               Salmo salar_50          0.000          0.000              0
## 8               Salmo salar_75          0.000          0.000              0
## 9               Salmo salar_95          0.000          0.000              0
## 10             Salmo trutta_50          0.000          0.000              0
## 11             Salmo trutta_75          0.000          0.000              0
## 12             Salmo trutta_95          0.000          0.000              0
##    Melanogrammus aeglefinus_50 Melanogrammus aeglefinus_75
## 1                        0.000                       0.000
## 2                        0.000                       0.000
## 3                        0.000                       0.000
## 4                        1.000                       1.000
## 5                        0.479                       1.000
## 6                        0.237                       0.494
## 7                        0.000                       0.000
## 8                        0.000                       0.000
## 9                        0.000                       0.000
## 10                       0.156                       0.307
## 11                       0.089                       0.186
## 12                       0.048                       0.100
##    Melanogrammus aeglefinus_95 Salmo salar_50 Salmo salar_75 Salmo salar_95
## 1                        0.000          0.000          0.000          0.000
## 2                        0.000          0.000          0.000          0.000
## 3                        0.000          0.000          0.000          0.000
## 4                        1.000          0.000          0.000          0.000
## 5                        1.000          0.000          0.000          0.000
## 6                        1.000          0.000          0.000          0.000
## 7                        0.000          1.000          1.000          1.000
## 8                        0.000          0.473          1.000          1.000
## 9                        0.000          0.220          0.466          1.000
## 10                       0.456          0.086          0.154          0.341
## 11                       0.360          0.084          0.135          0.302
## 12                       0.201          0.067          0.125          0.234
##    Salmo trutta_50 Salmo trutta_75 Salmo trutta_95
## 1            0.000           0.000           0.000
## 2            0.000           0.000           0.000
## 3            0.000           0.000           0.000
## 4            0.967           1.000           1.000
## 5            0.908           1.000           1.000
## 6            0.668           0.957           1.000
## 7            0.378           0.671           1.000
## 8            0.321           0.514           0.884
## 9            0.332           0.534           0.773
## 10           1.000           1.000           1.000
## 11           0.550           1.000           1.000
## 12           0.295           0.536           1.000
```

```
# plot the kernel estimates
KU<-plotKIN(test.kin,xlab="\nδ13C (‰)", ylab="δ15N (‰)\n") + theme(legend.position = "none", text=elemen
KU
```




```
test.elp<- estEllipse(data=multi_species_data, smallSamp = TRUE, x="Ave_C", y="Ave_N", group="Species",
```

```
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
```

```
# Extract the area of each polygon
elp.area<- getArea(test.elp)
elp.area
```

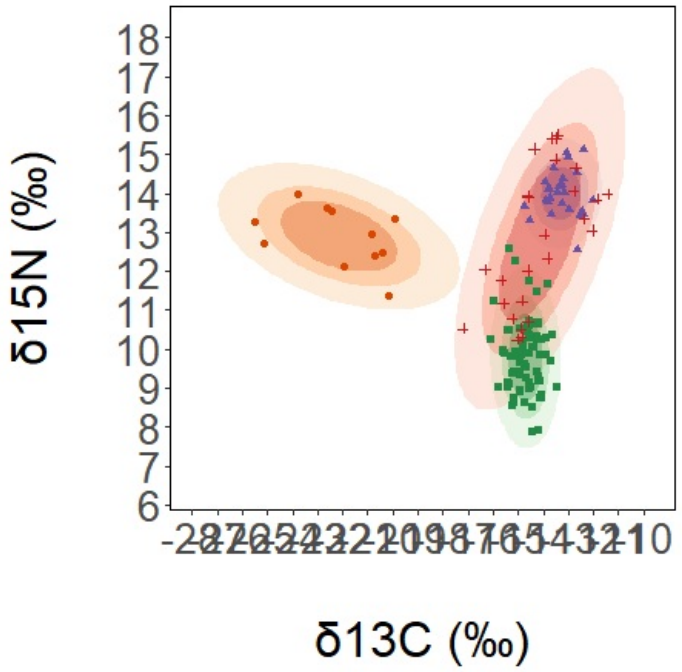
```
##     Method                    Group ConfInt ShapeArea
## 1  Ellipse              Esox lucius      50  5.935080
## 2  Ellipse              Esox lucius      75 11.870161
## 3  Ellipse              Esox lucius      95 25.650991
## 4  Ellipse Melanogrammus aeglefinus      50  1.677458
## 5  Ellipse Melanogrammus aeglefinus      75  3.354915
## 6  Ellipse Melanogrammus aeglefinus      95  7.249851
## 7  Ellipse              Salmo salar      50  2.390141
## 8  Ellipse              Salmo salar      75  4.780282
## 9  Ellipse              Salmo salar      95 10.330017
## 10 Ellipse             Salmo trutta      50  8.522715
## 11 Ellipse             Salmo trutta      75 17.045431
## 12 Ellipse             Salmo trutta      95 36.834563
```



```
#determine polygon overlap
elp.olp<- calcOverlap(test.elp)
elp.olp
```

```
##                     OverlapID Esox lucius_50 Esox lucius_75 Esox lucius_95
## 1               Esox lucius_50          1.000          1.000              1
## 2               Esox lucius_75          0.500          1.000              1
## 3               Esox lucius_95          0.231          0.463              1
## 4  Melanogrammus aeglefinus_50          0.000          0.000              0
## 5  Melanogrammus aeglefinus_75          0.000          0.000              0
## 6  Melanogrammus aeglefinus_95          0.000          0.000              0
## 7               Salmo salar_50          0.000          0.000              0
## 8               Salmo salar_75          0.000          0.000              0
## 9               Salmo salar_95          0.000          0.000              0
## 10             Salmo trutta_50          0.000          0.000              0
## 11             Salmo trutta_75          0.000          0.000              0
## 12             Salmo trutta_95          0.000          0.000              0
##    Melanogrammus aeglefinus_50 Melanogrammus aeglefinus_75
## 1                        0.000                       0.000
## 2                        0.000                       0.000
## 3                        0.000                       0.000
## 4                        1.000                       1.000
## 5                        0.500                       1.000
## 6                        0.231                       0.463
## 7                        0.000                       0.000
## 8                        0.000                       0.000
## 9                        0.000                       0.000
## 10                       0.197                       0.340
## 11                       0.098                       0.197
## 12                       0.046                       0.091
##    Melanogrammus aeglefinus_95 Salmo salar_50 Salmo salar_75 Salmo salar_95
## 1                        0.000          0.000          0.000          0.000
## 2                        0.000          0.000          0.000          0.000
## 3                        0.000          0.000          0.000          0.000
## 4                        1.000          0.000          0.000          0.000
## 5                        1.000          0.000          0.000          0.000
## 6                        1.000          0.000          0.000          0.000
## 7                        0.000          1.000          1.000          1.000
## 8                        0.000          0.500          1.000          1.000
## 9                        0.000          0.231          0.463          1.000
## 10                       0.483          0.005          0.060          0.222
## 11                       0.407          0.044          0.099          0.229
## 12                       0.197          0.057          0.100          0.190
##    Salmo trutta_50 Salmo trutta_75 Salmo trutta_95
## 1            0.000           0.000           0.000
## 2            0.000           0.000           0.000
## 3            0.000           0.000           0.000
## 4            1.000           1.000           1.000
## 5            0.863           1.000           1.000
## 6            0.568           0.957           1.000
## 7            0.017           0.314           0.879
## 8            0.106           0.355           0.772
## 9            0.183           0.378           0.677
## 10           1.000           1.000           1.000
## 11           0.500           1.000           1.000
## 12           0.231           0.463           1.000
```

```
#plot kernel estimates
ELP<-plotKIN(test.elp,xlab="\nδ13C (‰)", ylab="δ15N (‰)\n") + theme(legend.position = "none", text=eleme
ELP
```




```
test.mcp<- estMCP(data=multi_species_data, smallSamp = TRUE, x="Ave_C", y="Ave_N", group="Species", leve
```

```
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
```

```
# Extract the area of each polygon
mcp.area<- getArea(test.mcp)
mcp.area
```

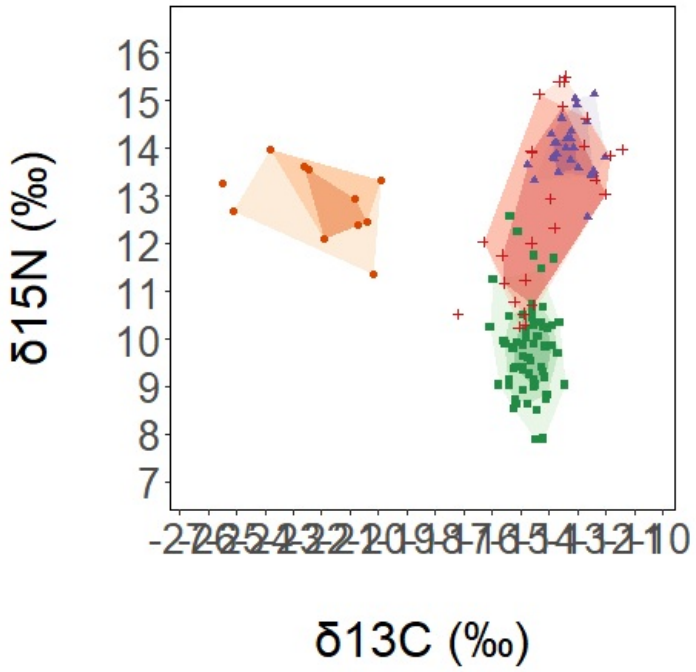
```
##    Method                    Group ConfInt ShapeArea
## 1     MCP              Esox lucius      50   1.57460
## 2     MCP              Esox lucius      75   3.60340
## 3     MCP              Esox lucius      95   7.93780
## 4     MCP Melanogrammus aeglefinus      50   0.53840
## 5     MCP Melanogrammus aeglefinus      75   1.59990
## 6     MCP Melanogrammus aeglefinus      95   2.83720
## 7     MCP              Salmo salar      50   1.43150
## 8     MCP              Salmo salar      75   3.00320
## 9     MCP              Salmo salar      95   6.74710
## 10    MCP             Salmo trutta      50   7.93285
## 11    MCP             Salmo trutta      75  11.39900
## 12    MCP             Salmo trutta      95  12.51365
```



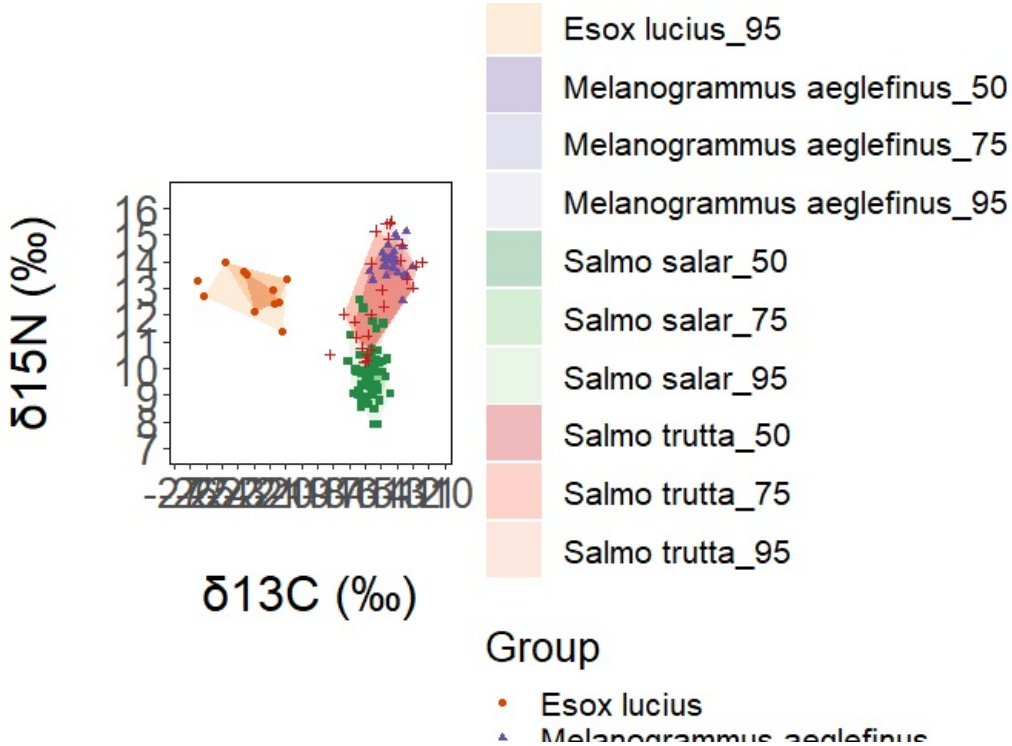
```
# determine polygon overlap for all polygons
mcp.olp<- calcOverlap(test.mcp)
mcp.olp
```

```
##                     OverlapID Esox lucius_50 Esox lucius_75 Esox lucius_95
## 1               Esox lucius_50          1.000          1.000              1
## 2               Esox lucius_75          0.437          1.000              1
## 3               Esox lucius_95          0.198          0.454              1
## 4  Melanogrammus aeglefinus_50          0.000          0.000              0
## 5  Melanogrammus aeglefinus_75          0.000          0.000              0
## 6  Melanogrammus aeglefinus_95          0.000          0.000              0
## 7               Salmo salar_50          0.000          0.000              0
## 8               Salmo salar_75          0.000          0.000              0
## 9               Salmo salar_95          0.000          0.000              0
## 10             Salmo trutta_50          0.000          0.000              0
## 11             Salmo trutta_75          0.000          0.000              0
## 12             Salmo trutta_95          0.000          0.000              0
##    Melanogrammus aeglefinus_50 Melanogrammus aeglefinus_75
## 1                        0.000                       0.000
## 2                        0.000                       0.000
## 3                        0.000                       0.000
## 4                        1.000                       1.000
## 5                        0.337                       1.000
## 6                        0.190                       0.564
## 7                        0.000                       0.000
## 8                        0.000                       0.000
## 9                        0.000                       0.000
## 10                       0.068                       0.154
## 11                       0.047                       0.137
## 12                       0.043                       0.128
##    Melanogrammus aeglefinus_95 Salmo salar_50 Salmo salar_75 Salmo salar_95
## 1                        0.000          0.000          0.000          0.000
## 2                        0.000          0.000          0.000          0.000
## 3                        0.000          0.000          0.000          0.000
## 4                        1.000          0.000          0.000          0.000
## 5                        1.000          0.000          0.000          0.000
## 6                        1.000          0.000          0.000          0.000
## 7                        0.000          1.000          1.000          1.000
## 8                        0.000          0.477          1.000          1.000
## 9                        0.000          0.212          0.445          1.000
## 10                       0.212          0.000          0.000          0.083
## 11                       0.208          0.000          0.002          0.074
## 12                       0.202          0.004          0.015          0.095
##    Salmo trutta_50 Salmo trutta_75 Salmo trutta_95
## 1            0.000           0.000           0.000
## 2            0.000           0.000           0.000
## 3            0.000           0.000           0.000
## 4            1.000           1.000           1.000
## 5            0.763           0.974           1.000
## 6            0.592           0.834           0.890
## 7            0.000           0.000           0.032
## 8            0.000           0.009           0.062
## 9            0.098           0.125           0.176
## 10           1.000           1.000           1.000
## 11           0.696           1.000           1.000
## 12           0.634           0.911           1.000
```

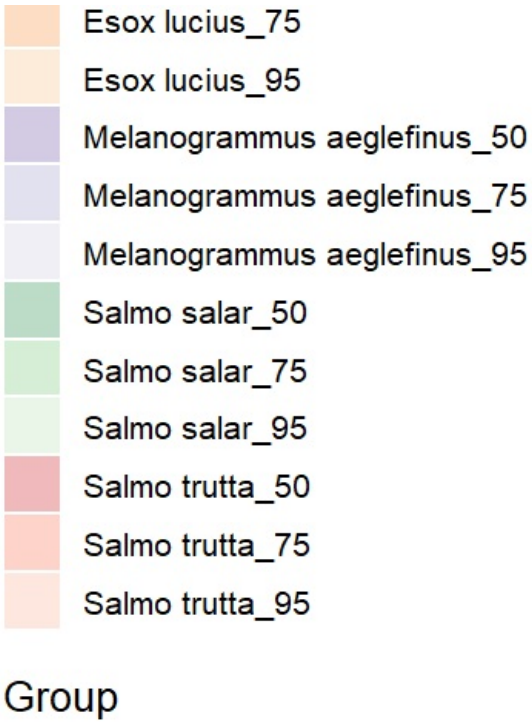
```
# plot the mcp estimates
MCP<-plotKIN(test.mcp,xlab="\nδ13C (‰)", ylab="δ15N (‰)\n") + theme(legend.position="none",text=element_
MCP
```




```
#Re-create last plot with legend, to export legend separately
MCP<-plotKIN(test.mcp,xlab="\nδ13C (‰)", ylab="δ15N (‰)\n") + theme(text=element_text(size=20), axis.tex
MCP
```




```
legend <- get_legend(MCP)
as_ggplot(legend)
```




```
#Organizing data from rKIN analysis to export, then export and save data as CSV, to be used to construct
df<- rbind(getArea(test.kin), getArea(test.mcp), getArea(test.elp))
#use the reshape2 package to pivot the data
df<- dcast(data = df, Group+ConfInt~Method, value.var="ShapeArea")
df
```

```
##                     Group ConfInt   Ellipse    Kernel      MCP
## 1              Esox lucius      50  5.935080  8.788320  1.57460
## 2              Esox lucius      75 11.870161 16.304530  3.60340
## 3              Esox lucius      95 25.650991 29.745966  7.93780
## 4  Melanogrammus aeglefinus      50  1.677458  1.832850  0.53840
## 5  Melanogrammus aeglefinus      75  3.354915  3.829628  1.59990
## 6  Melanogrammus aeglefinus      95  7.249851  7.748752  2.83720
## 7              Salmo salar      50  2.390141  2.567767  1.43150
## 8              Salmo salar      75  4.780282  5.429648  3.00320
## 9              Salmo salar      95 10.330017 11.649348  6.74710
## 10             Salmo trutta      50  8.522715 11.339031  7.93285
## 11             Salmo trutta      75 17.045431 20.614780 11.39900
## 12             Salmo trutta      95 36.834563 38.468264 12.51365
```

```
df2 <-rbind(calcOverlap(test.kin), calcOverlap(test.elp), calcOverlap(test.mcp))
write.csv(df2, "C:\\Users\\Liz Quinlan\\Documents\\Thesis_Data_Files\\Overlaps.csv", row.names=TRUE)
write.csv(df, "C:\\Users\\Liz Quinlan\\Documents\\Thesis_Data_Files\\NicheWidths.csv", row.names=TRUE)
```

Figure 8.15

```
#Regional Salmo sp. investigations using rKIN

salmo <- read.csv("rKIN_LMQ_Salmo.csv")
salmo_data <- subset(salmo, Group != "NA")

test.kin<- estKIN(data=salmo_data, smallSamp=TRUE, x="Ave_C", y="Ave_N", group="Group",
                  levels=c(50, 75, 95), scaler=2)
# Extract the area of each polygon
kin.area<- getArea(test.kin)
kin.area
```



```
##    Method                    Group ConfInt ShapeArea
## 1  Kernel          Wadden Sea Trout      50  7.924293
```

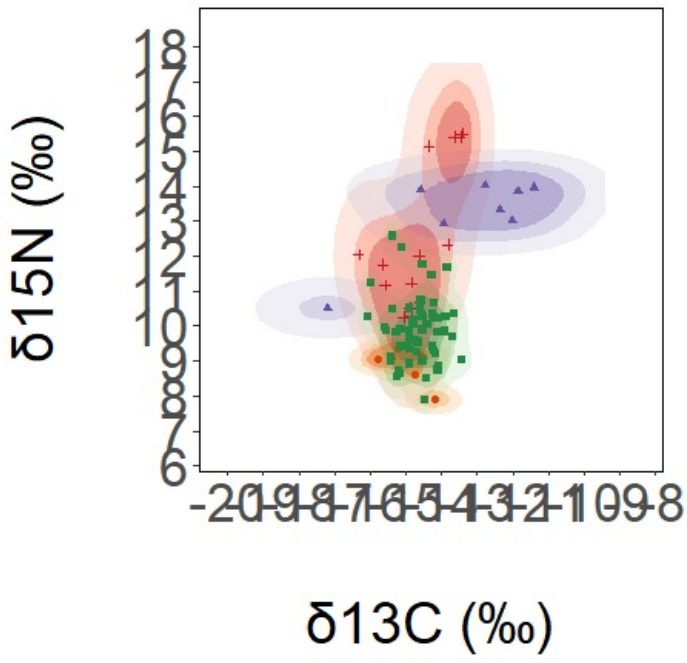
```
## 2  Kernel          Wadden Sea Trout      75 15.327102
## 3  Kernel          Wadden Sea Trout      95 28.417639
## 4  Kernel Northern North Sea Salmon      50  1.146159
## 5  Kernel Northern North Sea Salmon      75  2.278328
## 6  Kernel Northern North Sea Salmon      95  4.542435
## 7  Kernel  Northern North Sea Trout      50  5.434273
## 8  Kernel  Northern North Sea Trout      75 11.300555
## 9  Kernel  Northern North Sea Trout      95 23.968415
## 10 Kernel Southern North Sea Salmon      50  2.480918
## 11 Kernel Southern North Sea Salmon      75  5.158280
## 12 Kernel Southern North Sea Salmon      95 11.296400
```

```
# determine polygon overlap for all polygons
kin.olp<- calcOverlap(test.kin)
kin.olp
```

```
##                      OverlapID Wadden Sea Trout_50 Wadden Sea Trout_75
## 1           Wadden Sea Trout_50               1.000               1.000
## 2           Wadden Sea Trout_75               0.517               1.000
## 3           Wadden Sea Trout_95               0.279               0.539
## 4  Northern North Sea Salmon_50               0.321               0.771
## 5  Northern North Sea Salmon_75               0.220               0.511
## 6  Northern North Sea Salmon_95               0.162               0.330
## 7   Northern North Sea Trout_50               0.008               0.247
## 8   Northern North Sea Trout_75               0.042               0.268
## 9   Northern North Sea Trout_95               0.092               0.256
## 10 Southern North Sea Salmon_50               0.661               0.898
## 11 Southern North Sea Salmon_75               0.483               0.689
## 12 Southern North Sea Salmon_95               0.434               0.617
##    Wadden Sea Trout_95 Northern North Sea Salmon_50
## 1                1.000                        0.046
## 2                1.000                        0.058
## 3                1.000                        0.040
## 4                1.000                        1.000
## 5                0.864                        0.503
## 6                0.743                        0.252
## 7                0.425                        0.000
## 8                0.472                        0.000
## 9                0.465                        0.000
## 10               1.000                        0.259
## 11               0.970                        0.186
## 12               0.880                        0.097
##    Northern North Sea Salmon_75 Northern North Sea Salmon_95
## 1                         0.063                        0.093
## 2                         0.076                        0.098
## 3                         0.069                        0.119
## 4                         1.000                        1.000
## 5                         1.000                        1.000
## 6                         0.502                        1.000
## 7                         0.000                        0.000
## 8                         0.000                        0.000
## 9                         0.000                        0.000
## 10                        0.372                        0.494
## 11                        0.304                        0.483
## 12                        0.178                        0.314
##    Northern North Sea Trout_50 Northern North Sea Trout_75
## 1                        0.006                       0.059
## 2                        0.088                       0.197
## 3                        0.081                       0.188
## 4                        0.000                       0.000
## 5                        0.000                       0.000
## 6                        0.000                       0.000
## 7                        1.000                       1.000
## 8                        0.481                       1.000
## 9                        0.227                       0.471
## 10                       0.000                       0.000
## 11                       0.000                       0.000
## 12                       0.000                       0.000
```

```
##    Northern North Sea Trout_95 Southern North Sea Salmon_50
## 1                        0.279                         0.207
## 2                        0.400                         0.145
## 3                        0.392                         0.087
## 4                        0.000                         0.560
## 5                        0.000                         0.405
## 6                        0.000                         0.270
## 7                        1.000                         0.000
## 8                        1.000                         0.000
## 9                        1.000                         0.000
## 10                       0.000                         1.000
## 11                       0.049                         0.481
## 12                       0.180                         0.220
##    Southern North Sea Salmon_75 Southern North Sea Salmon_95
## 1                         0.314                         0.619
## 2                         0.232                         0.454
## 3                         0.176                         0.350
## 4                         0.838                         0.953
## 5                         0.688                         0.883
## 6                         0.548                         0.780
## 7                         0.000                         0.000
## 8                         0.000                         0.000
## 9                         0.011                         0.085
## 10                        1.000                         1.000
## 11                        1.000                         1.000
## 12                        0.457                         1.000
```

```
# plot the kernel estimates
KU<-plotKIN(test.kin,xlab="\nδ13C (‰)", ylab="δ15N (‰)\n") + theme(legend.position="none",text=element_t
KU
```




```
test.elp<- estEllipse(data=salmo_data, smallSamp = TRUE, x="Ave_C", y="Ave_N", group="Group", levels=c(5
```



```
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
## [1] "data.frame"
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## [1] "data.frame"
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```

```
# Extract the area of each polygon
elp.area<- getArea(test.elp)
elp.area
```

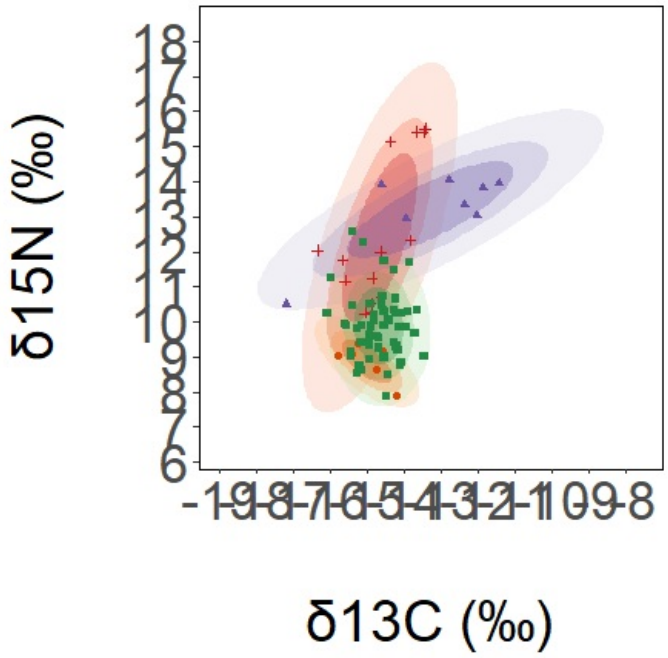
```
##     Method                    Group ConfInt  ShapeArea
## 1  Ellipse          Wadden Sea Trout      50  5.6646659
## 2  Ellipse          Wadden Sea Trout      75 11.3293318
## 3  Ellipse          Wadden Sea Trout      95 24.4822786
## 4  Ellipse Northern North Sea Salmon      50  0.9944867
## 5  Ellipse Northern North Sea Salmon      75  1.9889733
## 6  Ellipse Northern North Sea Salmon      95  4.2980999
## 7  Ellipse  Northern North Sea Trout      50  5.8927911
## 8  Ellipse  Northern North Sea Trout      75 11.7855823
## 9  Ellipse  Northern North Sea Trout      95 25.4682195
## 10 Ellipse Southern North Sea Salmon      50  2.3366059
## 11 Ellipse Southern North Sea Salmon      75  4.6732118
## 12 Ellipse Southern North Sea Salmon      95 10.0986427
```

```
#determine polygon overlap
elp.olp<- calcOverlap(test.elp)
elp.olp
```

```
##                      OverlapID Wadden Sea Trout_50 Wadden Sea Trout_75
## 1           Wadden Sea Trout_50               1.000               1.000
## 2           Wadden Sea Trout_75               0.500               1.000
## 3           Wadden Sea Trout_95               0.231               0.463
## 4  Northern North Sea Salmon_50               0.000               0.195
## 5  Northern North Sea Salmon_75               0.000               0.263
## 6  Northern North Sea Salmon_95               0.001               0.236
## 7   Northern North Sea Trout_50               0.355               0.458
## 8   Northern North Sea Trout_75               0.290               0.413
## 9   Northern North Sea Trout_95               0.195               0.294
## 10 Southern North Sea Salmon_50               0.183               0.493
## 11 Southern North Sea Salmon_75               0.237               0.480
## 12 Southern North Sea Salmon_95               0.230               0.455
##    Wadden Sea Trout_95 Northern North Sea Salmon_50
## 1                1.000                         0.000
## 2                1.000                         0.017
## 3                1.000                         0.031
## 4                0.767                         1.000
## 5                0.691                         0.500
## 6                0.628                         0.231
## 7                0.620                         0.000
## 8                0.580                         0.000
## 9                0.439                         0.000
## 10               0.916                         0.101
## 11               0.805                         0.179
## 12               0.701                         0.098
##    Northern North Sea Salmon_75 Northern North Sea Salmon_95
## 1                         0.000                         0.001
## 2                         0.046                         0.089
## 3                         0.056                         0.110
## 4                         1.000                         1.000
## 5                         1.000                         1.000
## 6                         0.463                         1.000
## 7                         0.000                         0.000
## 8                         0.000                         0.000
## 9                         0.000                         0.000
## 10                        0.186                         0.343
```

```
## 11                       0.254                       0.375
## 12                       0.197                       0.369
##    Northern North Sea Trout_50 Northern North Sea Trout_75
## 1                        0.369                       0.604
## 2                        0.238                       0.429
## 3                        0.149                       0.279
## 4                        0.000                       0.000
## 5                        0.000                       0.000
## 6                        0.000                       0.000
## 7                        1.000                       1.000
## 8                        0.500                       1.000
## 9                        0.231                       0.463
## 10                       0.000                       0.000
## 11                       0.000                       0.001
## 12                       0.028                       0.102
##    Northern North Sea Trout_95 Southern North Sea Salmon_50
## 1                        0.876                       0.075
## 2                        0.661                       0.102
## 3                        0.457                       0.087
## 4                        0.000                       0.238
## 5                        0.000                       0.218
## 6                        0.000                       0.187
## 7                        1.000                       0.000
## 8                        1.000                       0.000
## 9                        1.000                       0.003
## 10                       0.031                       1.000
## 11                       0.136                       0.500
## 12                       0.239                       0.231
##    Southern North Sea Salmon_75 Southern North Sea Salmon_95
## 1                        0.195                       0.410
## 2                        0.198                       0.405
## 3                        0.154                       0.289
## 4                        0.840                       1.000
## 5                        0.596                       1.000
## 6                        0.408                       0.867
## 7                        0.000                       0.048
## 8                        0.000                       0.088
## 9                        0.025                       0.095
## 10                       1.000                       1.000
## 11                       1.000                       1.000
## 12                       0.463                       1.000
```

```
#plot kernel estimates
ELP<-plotKIN(test.elp,xlab="\nδ13C (‰)", ylab="δ15N (‰)\n") + theme(legend.position="none",text=element_
ELP
```




```
test.mcp<- estMCP(data=salmo_data, smallSamp = TRUE, x="Ave_C", y="Ave_N", group="Group", levels=c(50, 7
```

```
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```

```
# Extract the area of each polygon
mcp.area<- getArea(test.mcp)
mcp.area
```

```
##    Method                     Group ConfInt ShapeArea
## 1     MCP          Wadden Sea Trout      50   2.17380
## 2     MCP          Wadden Sea Trout      75   2.64935
## 3     MCP          Wadden Sea Trout      95   7.57095
## 4     MCP Northern North Sea Salmon      50   0.20980
## 5     MCP Northern North Sea Salmon      75   0.32535
## 6     MCP Northern North Sea Salmon      95   0.48195
## 7     MCP  Northern North Sea Trout      50   1.01620
## 8     MCP  Northern North Sea Trout      75   2.33890
## 9     MCP  Northern North Sea Trout      95   2.61140
## 10    MCP Southern North Sea Salmon      50   1.34865
## 11    MCP Southern North Sea Salmon      75   2.90765
## 12    MCP Southern North Sea Salmon      95   6.49475
```

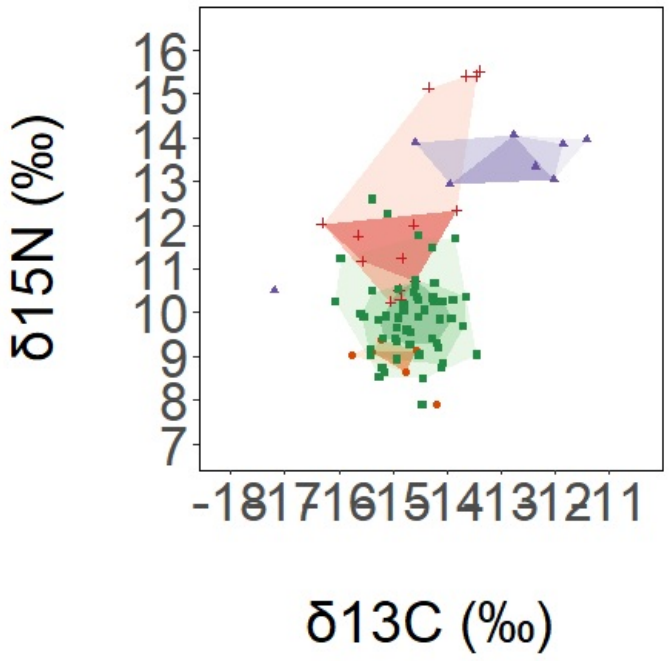


```
# determine polygon overlap for all polygons
mcp.olp<- calcOverlap(test.mcp)
mcp.olp
```

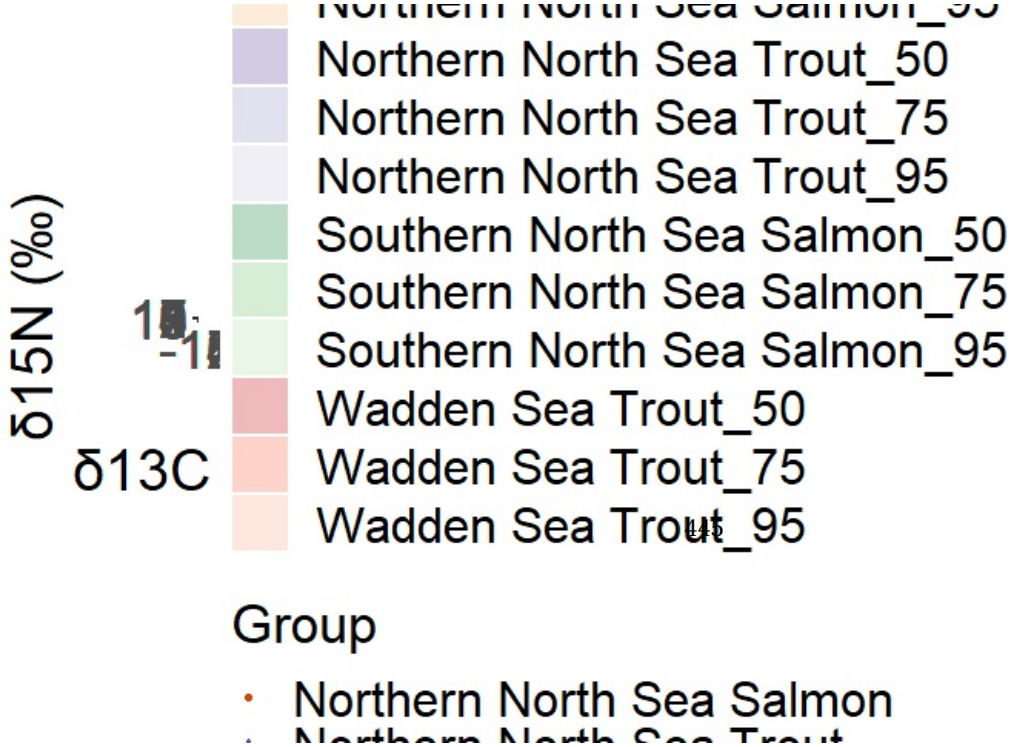
```
##                      OverlapID Wadden Sea Trout_50 Wadden Sea Trout_75
## 1           Wadden Sea Trout_50               1.000               1.000
## 2           Wadden Sea Trout_75               0.821               1.000
## 3           Wadden Sea Trout_95               0.287               0.350
## 4  Northern North Sea Salmon_50               0.000               0.000
## 5  Northern North Sea Salmon_75               0.000               0.000
## 6  Northern North Sea Salmon_95               0.000               0.000
## 7   Northern North Sea Trout_50               0.000               0.000
## 8   Northern North Sea Trout_75               0.000               0.000
## 9   Northern North Sea Trout_95               0.000               0.000
## 10 Southern North Sea Salmon_50               0.000               0.049
## 11 Southern North Sea Salmon_75               0.000               0.052
## 12 Southern North Sea Salmon_95               0.137               0.204
##    Wadden Sea Trout_95 Northern North Sea Salmon_50
## 1                1.000                       0.000
## 2                1.000                       0.000
## 3                1.000                       0.000
## 4                0.000                       1.000
## 5                0.000                       0.645
## 6                0.000                       0.435
## 7                0.020                       0.000
## 8                0.256                       0.000
## 9                0.229                       0.000
## 10               0.049                       0.000
## 11               0.052                       0.046
## 12               0.204                       0.032
##    Northern North Sea Salmon_75 Northern North Sea Salmon_95
## 1                         0.000                        0.000
## 2                         0.000                        0.000
## 3                         0.000                        0.000
## 4                         1.000                        1.000
## 5                         1.000                        1.000
## 6                         0.675                        1.000
## 7                         0.000                        0.000
## 8                         0.000                        0.000
## 9                         0.000                        0.000
## 10                        0.000                        0.000
## 11                        0.086                        0.097
## 12                        0.050                        0.069
##    Northern North Sea Trout_50 Northern North Sea Trout_75
## 1                        0.000                       0.000
## 2                        0.000                       0.000
## 3                        0.003                       0.079
## 4                        0.000                       0.000
## 5                        0.000                       0.000
## 6                        0.000                       0.000
## 7                        1.000                       1.000
## 8                        0.434                       1.000
## 9                        0.389                       0.896
## 10                       0.000                       0.000
## 11                       0.000                       0.000
## 12                       0.000                       0.000
##    Northern North Sea Trout_95 Southern North Sea Salmon_50
## 1                        0.000                        0.000
## 2                        0.000                        0.025
## 3                        0.079                        0.009
## 4                        0.000                        0.000
## 5                        0.000                        0.000
## 6                        0.000                        0.000
## 7                        1.000                        0.000
## 8                        1.000                        0.000
## 9                        1.000                        0.000
## 10                       0.000                        1.000
## 11                       0.000                        0.464
## 12                       0.000                        0.208
##    Southern North Sea Salmon_75 Southern North Sea Salmon_95
## 1                         0.000                        0.408
## 2                         0.058                        0.501
## 3                         0.020                        0.175
## 4                         0.634                        1.000
```

```
## 5                       0.764                       1.000
## 6                       0.588                       0.925
## 7                       0.000                       0.000
## 8                       0.000                       0.000
## 9                       0.000                       0.000
## 10                      1.000                       1.000
## 11                      1.000                       1.000
## 12                      0.448                       1.000
```

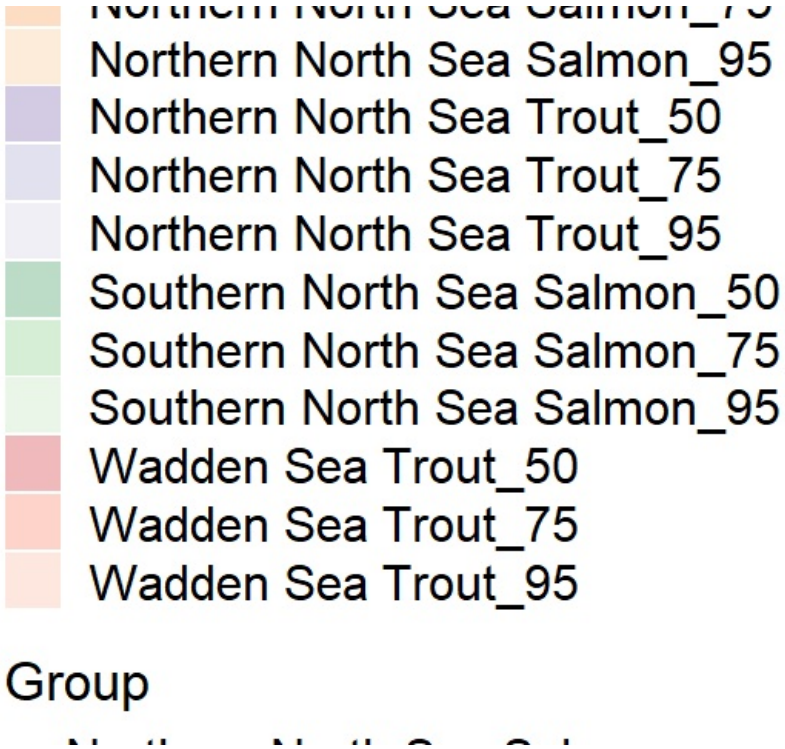
```
# plot the mcp estimates
MCP<-plotKIN(test.mcp,xlab="\nδ13C (‰)", ylab="δ15N (‰)\n") + theme(legend.position="none",text=element_
MCP
```




```
#temporarily remove legend.position="none" from previous line, then get the legend to export separately
MCP<-plotKIN(test.mcp,xlab="\nδ13C (‰)", ylab="δ15N (‰)\n") + theme(text=element_text(size=26), axis.tex
MCP
```



```
legend <- get_legend(MCP)
as_ggplot(legend)
```




```
#Organizing data from rKIN analysis to export
#then export and save data as CSV, to be used to construct data tables presenting calculated overlaps an
df3<- rbind(getArea(test.kin), getArea(test.elp), getArea(test.mcp))
#use the reshape2 package to pivot the data
df3<- dcast(data = df3, Group+ConfInt~Method, value.var="ShapeArea")
df3
```

```
##                        Group ConfInt    Ellipse    Kernel     MCP
## 1  Northern North Sea Salmon      50  0.9944867  1.146159 0.20980
## 2  Northern North Sea Salmon      75  1.9889733  2.278328 0.32535
## 3  Northern North Sea Salmon      95  4.2980999  4.542435 0.48195
## 4   Northern North Sea Trout      50  5.8927911  5.434273 1.01620
## 5   Northern North Sea Trout      75 11.7855823 11.300555 2.33890
## 6   Northern North Sea Trout      95 25.4682195 23.968415 2.61140
## 7  Southern North Sea Salmon      50  2.3366059  2.480918 1.34865
## 8  Southern North Sea Salmon      75  4.6732118  5.158280 2.90765
## 9  Southern North Sea Salmon      95 10.0986427 11.296400 6.49475
## 10          Wadden Sea Trout      50  5.6646659  7.924293 2.17380
## 11          Wadden Sea Trout      75 11.3293318 15.327102 2.64935
## 12          Wadden Sea Trout      95 24.4822786 28.417639 7.57095
```

```
df4 <-rbind(calcOverlap(test.kin), calcOverlap(test.elp), calcOverlap(test.mcp))
write.csv(df4, "C:\\Users\\Liz Quinlan\\Documents\\Thesis_Data_Files\\Overlaps2.csv", row.names=TRUE)
write.csv(df3, "C:\\Users\\Liz Quinlan\\Documents\\Thesis_Data_Files\\NicheWidths2.csv", row.names=TRUE)
```

Figure 8.16 (Legends required to be exported separately in order to put the final figure together nicely in Inkscape– I tried really hard to figure out a way to do this programatically, but currently I'm unable to.)


```
Comparative_Salmo_Iso<- read_csv("Baselines.csv")
```

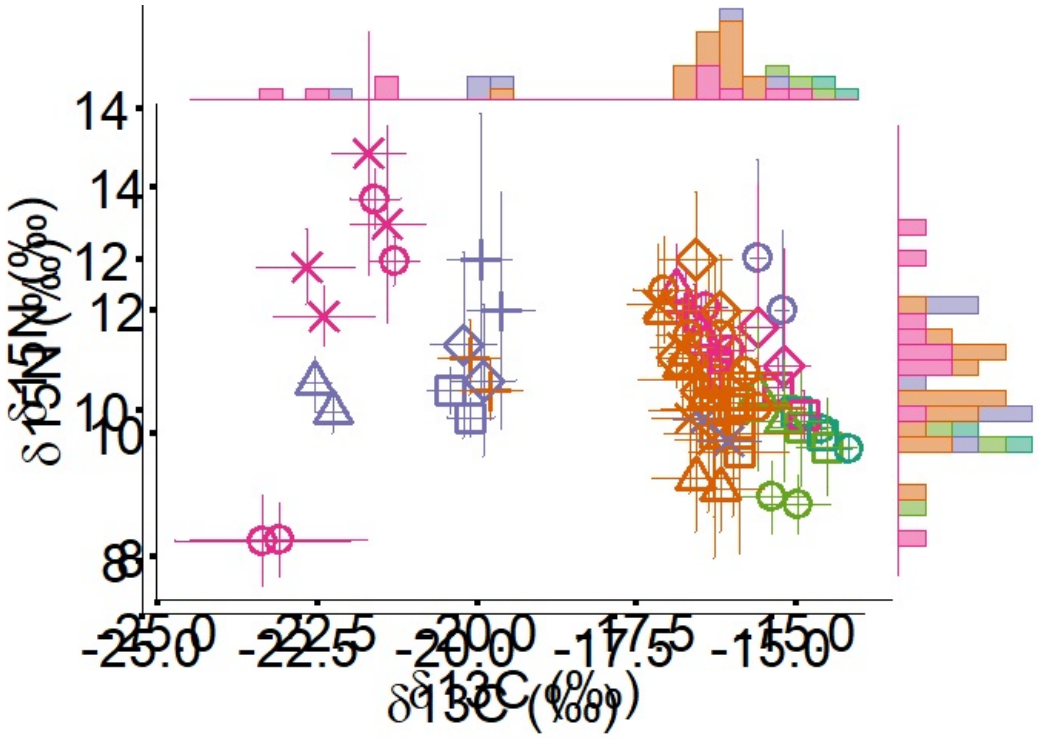
```
## Rows: 43 Columns: 23
## ── Column specification ────────────────────────────────────────────────────────
```

```
## Delimiter: ","
## chr (12): Catch_Location_Site, Species, Ecotype, Group, Time_Period, Region_...
## dbl (10): Mean_Mass, Sample_size, Min_D13C, Max_D13C, Mean_D13C, D13C_SD, Mi...
## lgl  (1): Notes
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
Comp_Salmon <- subset(Comparative_Salmo_Iso, Species== "Salmo salar")

Mean_Error_Comp_Salmon <- ggplot(Comp_Salmon,
                                 aes(x=Mean_D13C,
                                     y=Mean_D15N,
                                     color=Group,
                                     shape=Catch_Location_Site)) +
  geom_point(size=5, stroke=2) +
  xlab(expression(delta *"13C (‰)")) +
  ylab (expression(delta *"15N (‰)")) +
  theme_cowplot(12) +
  geom_errorbar(aes(ymin=Mean_D15N - D15N_SD, ymax= Mean_D15N + D15N_SD)) +
  geom_errorbarh(aes(xmin= Mean_D13C - D13C_SD, xmax= Mean_D13C + D13C_SD)) +
  scale_color_brewer(palette="Dark2") +
  theme(text = element_text(size=26),
        axis.text = element_text(size=26),
        axis.ticks = element_line(linewidth = 1.5),
        plot.margin = margin(0,3,0,0, unit="cm"),
        legend.position = "none") +
  scale_shape_manual(values =
                       c("16-22 Coppergate"=0,
                         "Earl's Bu" =1,
                         "Netherlands"=2,
                         "Knowth - Ireland"=0,
                         "Trou de Frontal - Belgium"=1,
                         "Northeast UK Coast"=0,
                         "River Bush"=1,
                         "River Dee"=2,
                         "River Erne"=3,
                         "River Frome"=4,
                         "River Sella"=5,
                         "Joseph Picard"=0,
                         "Mailhot-Curran - Anadromous"=1,
                         "Mailhot-Curran - Potomodromous"=2,
                         "Steven Patrick"=3,
                         "Summerstown"=4,
                         "Yatsihsta"=5,
                         "Big Salmon River"=0,
                         "Conne River"=1,
                         "Gaspereau River"=2,
                         "Gulf of St. Lawrence"=3,
                         "Koksoak River"=4,
                         "Upper Salmon River"=5))
Mean_Error_Comp_Salmon

ggMarginal(Mean_Error_Comp_Salmon,type="histogram", groupColour = TRUE, groupFill = TRUE)
```

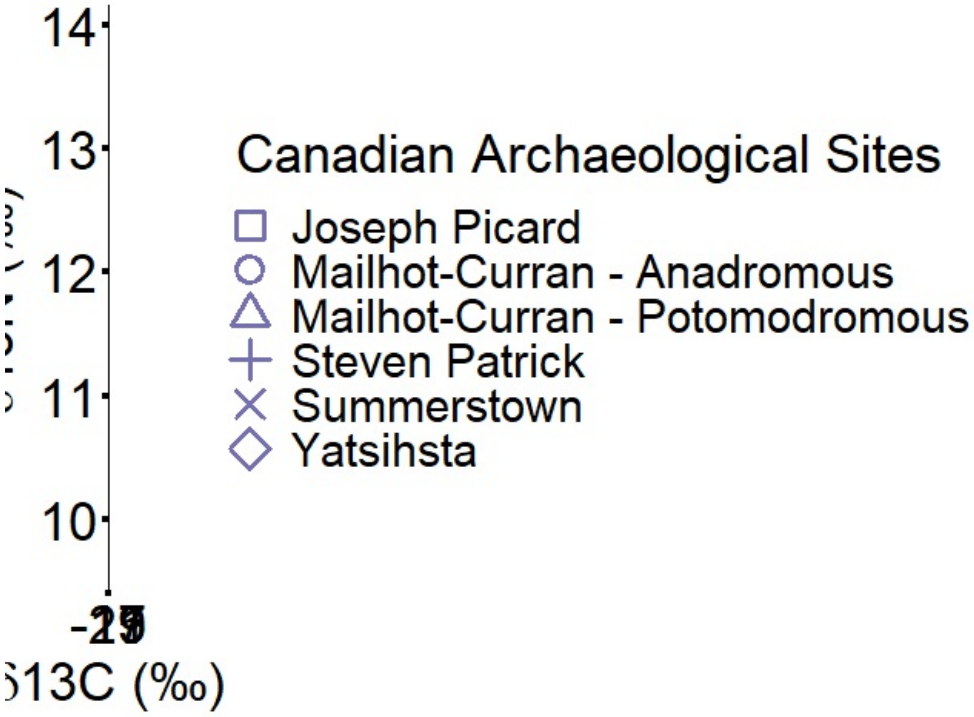



```
#Subsetting out each group and plotting in order to get the legends
# I am aware this is the silliest possible way to do this, but I just need to get it done

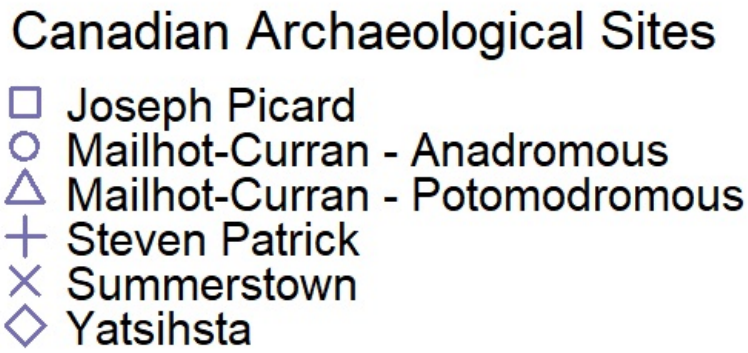
Comp_Mod_Europe <- subset(Comp_Salmon, Group== "Europe - Modern")
Comp_Mod_Canada <- subset(Comp_Salmon, Group== "North America - Modern")
Comp_Arch_Europe <- subset(Comp_Salmon, Group== "Europe - Archaeological")
Comp_Arch_Canada <- subset(Comp_Salmon, Group== "North America - Archaeological")
Comp_NSB <- subset(Comp_Salmon, Group=="North Sea Basin")

AC_Comp_Salmon <- ggplot(Comp_Arch_Canada,
                                aes(x=Mean_D13C,
                                    y=Mean_D15N,
                                    color=Group,
                                    shape=Catch_Location_Site)) +
  geom_point(size=5, stroke=2) +
  xlab(expression(delta *"13C (‰)")) +
  ylab (expression(delta *"15N (‰)")) +
  theme_cowplot(12) +
  geom_errorbar(aes(ymin=Mean_D15N - D15N_SD, ymax= Mean_D15N + D15N_SD)) +
  geom_errorbarh(aes(xmin= Mean_D13C - D13C_SD, xmax= Mean_D13C + D13C_SD)) +
  scale_color_manual(guide="none", values = c("#7570b3", "#7570b3","#7570b3","#7570b3","#7570b3","#7570b
  theme(text = element_text(size=26),
        axis.text = element_text(size=26),
        axis.ticks = element_line(linewidth = 1.5),
        legend.box.margin = margin(50,50,50,50),
        legend.margin=margin(0,0,0,0))+
  scale_shape_manual(guide=guide_legend(override.aes = list(color="#7570b3")), name= "Canadian Archaeolo
                     c("16-22 Coppergate"=0,
                       "Earl's Bu" =1,
                       "Netherlands"=2,
                       "Knowth - Ireland"=0,
                       "Trou de Frontal - Belgium"=1,
                       "Northeast UK Coast"=0,
                       "River Bush"=1,
                       "River Dee"=2,
                       "River Erne"=3,
                       "River Frome"=4,
                       "River Sella"=5,
                       "Joseph Picard"=0,
                       "Mailhot-Curran - Anadromous"=1,
                       "Mailhot-Curran - Potomodromous"=2,
                       "Steven Patrick"=3,
                       "Summerstown"=4,
                       "Yatsihsta"=5,
                       "Big Salmon River"=0,
```

```
                          "Conne River"=1,
                          "Gaspereau River"=2,
                          "Gulf of St. Lawrence"=3,
                          "Koksoak River"=4,
                          "Upper Salmon River"=5))
AC_Comp_Salmon
```




```
legend <- get_legend(AC_Comp_Salmon)
as_ggplot(legend)
```




```
AE_Comp_Salmon<- ggplot(Comp_Arch_Europe,
                        aes(x=Mean_D13C,
                            y=Mean_D15N,
                            color=Group,
                            shape=Catch_Location_Site)) +
  geom_point(size=5, stroke=2) +
  xlab(expression(delta *"13C (‰)")) +
```

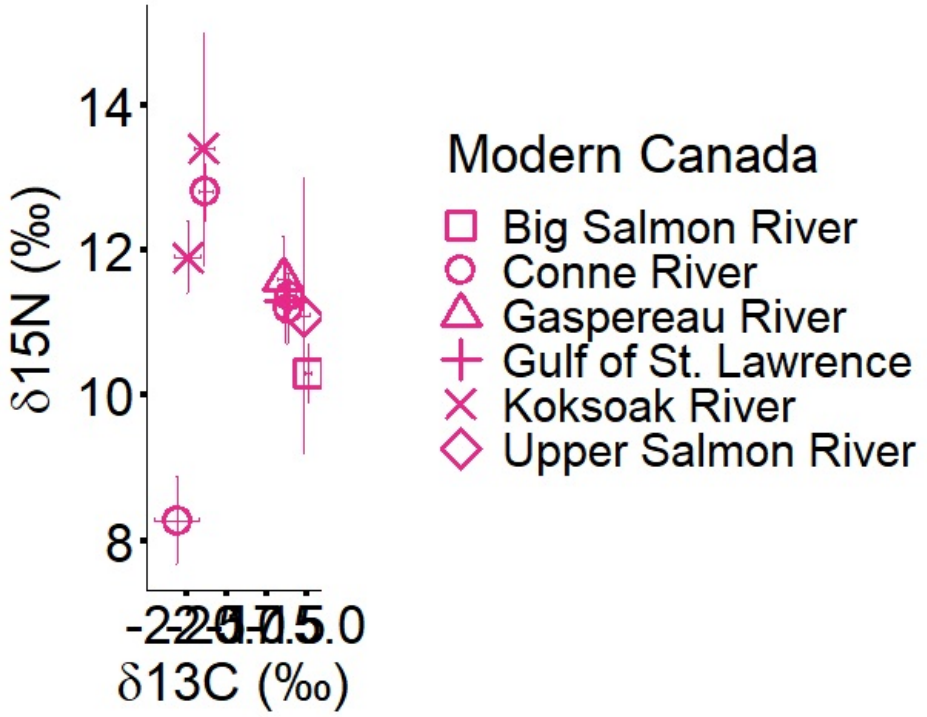
```
  ylab (expression(delta *"15N (‰)")) +
  theme_cowplot(12) +
  geom_errorbar(aes(ymin=Mean_D15N - D15N_SD, ymax= Mean_D15N + D15N_SD)) +
  geom_errorbarh(aes(xmin= Mean_D13C - D13C_SD, xmax= Mean_D13C + D13C_SD)) +
  scale_color_manual(guide="none", values = c("#1b9e77","#1b9e77","#1b9e77","#1b9e77","#1b9e77","#1b9e77
  theme(text = element_text(size=26),
        axis.text = element_text(size=26),
        axis.ticks = element_line(linewidth = 1.5),
        legend.box.margin = margin(50,50,50,50),
        legend.margin=margin(0,0,0,0)) +
  scale_shape_manual(guide=guide_legend(override.aes = list(color="#1b9e77")), name= "European Archaeolo
                     c("16-22 Coppergate"=0,
                       "Earl's Bu" =1,
                       "Netherlands"=2,
                       "Knowth - Ireland"=0,
                       "Trou de Frontal - Belgium"=1,
                       "Northeast UK Coast"=0,
                       "River Bush"=1,
                       "River Dee"=2,
                       "River Erne"=3,
                       "River Frome"=4,
                       "River Sella"=5,
                       "Joseph Picard"=0,
                       "Mailhot-Curran - Anadromous"=1,
                       "Mailhot-Curran - Potomodromous"=2,
                       "Steven Patrick"=3,
                       "Summerstown"=4,
                       "Yatsihsta"=5,
                       "Big Salmon River"=0,
                       "Conne River"=1,
                       "Gaspereau River"=2,
                       "Gulf of St. Lawrence"=3,
                       "Koksoak River"=4,
                       "Upper Salmon River"=5))
AE_Comp_Salmon
```




```
legend <- get_legend(AE_Comp_Salmon)
as_ggplot(legend)
```




```
MC_Comp_Salmon<- ggplot(Comp_Mod_Canada,
                        aes(x=Mean_D13C,
                            y=Mean_D15N,
                            color=Group,
                            shape=Catch_Location_Site)) +
  geom_point(size=5, stroke=2) +
  xlab(expression(delta *"13C (‰)")) +
  ylab (expression(delta *"15N (‰)")) +
  theme_cowplot(12) +
  geom_errorbar(aes(ymin=Mean_D15N - D15N_SD, ymax= Mean_D15N + D15N_SD)) +
  geom_errorbarh(aes(xmin= Mean_D13C - D13C_SD, xmax= Mean_D13C + D13C_SD)) +
  scale_color_manual(guide="none", values = c("#e7298a","#e7298a","#e7298a","#e7298a","#e7298a","#e7298a
  theme(text = element_text(size=26),
        axis.text = element_text(size=26),
        axis.ticks = element_line(linewidth = 1.5),
        legend.box.margin = margin(50,50,50,50),
        legend.margin=margin(0,0,0,0)) +
  scale_shape_manual(guide=guide_legend(override.aes = list(color="#e7298a")), name= "Modern Canada", va
                     c("16-22 Coppergate"=0,
                       "Earl's Bu" =1,
                       "Netherlands"=2,
                       "Knowth - Ireland"=0,
                       "Trou de Frontal - Belgium"=1,
                       "Northeast UK Coast"=0,
                       "River Bush"=1,
                       "River Dee"=2,
                       "River Erne"=3,
                       "River Frome"=4,
                       "River Sella"=5,
                       "Joseph Picard - Canada"=0,
                       "Mailhot-Curran - Anadromous"=1,
                       "Mailhot-Curran - Potomodromous"=2,
                       "Steven Patrick - Canada"=3,
                       "Summerstown - Canada"=4,
                       "Yatsihsta - Canada"=5,
                       "Big Salmon River"=0,
                       "Conne River"=1,
                       "Gaspereau River"=2,
                       "Gulf of St. Lawrence"=3,
                       "Koksoak River"=4,
                       "Upper Salmon River"=5))
MC_Comp_Salmon
```

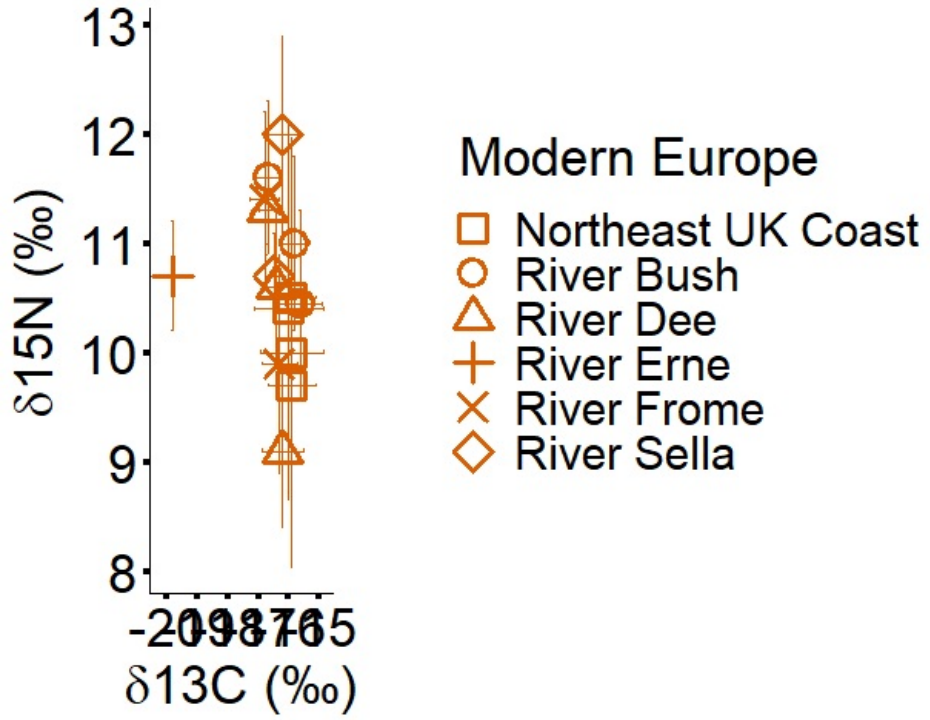



```
legend <- get_legend(MC_Comp_Salmon)
as_ggplot(legend)
```




```
ME_Comp_Salmon<- ggplot(Comp_Mod_Europe,
                        aes(x=Mean_D13C,
                            y=Mean_D15N,
                            color=Group,
                            shape=Catch_Location_Site)) +
  geom_point(size=5, stroke=2) +
  xlab(expression(delta *"13C (‰)")) +
  ylab (expression(delta *"15N (‰)")) +
  theme_cowplot(12) +
  geom_errorbar(aes(ymin=Mean_D15N - D15N_SD, ymax= Mean_D15N + D15N_SD)) +
  geom_errorbarh(aes(xmin= Mean_D13C - D13C_SD, xmax= Mean_D13C + D13C_SD)) +
  scale_color_manual(guide="none", values = c("#d95f02")) +
  theme(text = element_text(size=26),
        axis.text = element_text(size=26),
        axis.ticks = element_line(linewidth = 1.5),
```

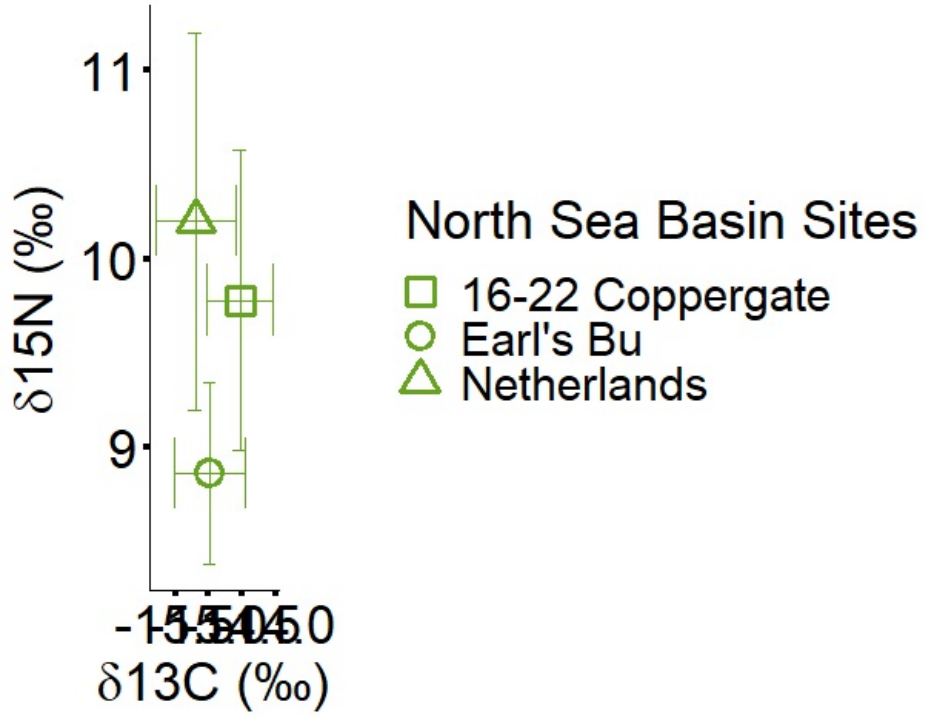
```
        legend.box.margin = margin(50,50,50,50),
        legend.margin=margin(0,0,0,0)) +
  scale_shape_manual(guide=guide_legend(override.aes = list(color="#d95f02")), name= "Modern Europe", va
                       c("16-22 Coppergate"=0,
                         "Earl's Bu" =1,
                         "Netherlands"=2,
                         "Knowth - Ireland"=0,
                         "Trou de Frontal - Belgium"=1,
                         "Northeast UK Coast"=0,
                         "River Bush"=1,
                         "River Dee"=2,
                         "River Erne"=3,
                         "River Frome"=4,
                         "River Sella"=5,
                         "Joseph Picard - Canada"=0,
                         "Mailhot-Curran - Anadromous"=1,
                         "Mailhot-Curran - Potomodromous"=2,
                         "Steven Patrick - Canada"=3,
                         "Summerstown - Canada"=4,
                         "Yatsihsta - Canada"=5,
                         "Big Salmon River"=0,
                         "Conne River"=1,
                         "Gaspereau River"=2,
                         "Gulf of St. Lawrence"=3,
                         "Koksoak River"=4,
                         "Upper Salmon River"=5))
ME_Comp_Salmon
```




```
legend <- get_legend(ME_Comp_Salmon)
as_ggplot(legend)
```




```
NSB_Comp_Salmon<- ggplot(Comp_NSB,
                         aes(x=Mean_D13C,
                             y=Mean_D15N,
                             color=Group,
                             shape=Catch_Location_Site)) +
  geom_point(size=5, stroke=2) +
  xlab(expression(delta *"13C (‰)")) +
  ylab (expression(delta *"15N (‰)")) +
  theme_cowplot(12) +
  geom_errorbar(aes(ymin=Mean_D15N - D15N_SD, ymax= Mean_D15N + D15N_SD)) +
  geom_errorbarh(aes(xmin= Mean_D13C - D13C_SD, xmax= Mean_D13C + D13C_SD)) +
  scale_color_manual(guide="none", values = c("#66a61e", "#66a61e")) +
  theme(text = element_text(size=26),
        axis.text = element_text(size=26),
        axis.ticks = element_line(linewidth = 1.5),
        legend.box.margin = margin(50,50,50,50),
        legend.margin=margin(0,0,0,0)) +
  scale_shape_manual(guide=guide_legend(override.aes = list(color="#66a61e")), name= "North Sea Basin Si
                       c("16-22 Coppergate"=0,
                         "Earl's Bu" =1,
                         "Netherlands"=2,
                         "Knowth - Ireland"=0,
                         "Trou de Frontal - Belgium"=1,
                         "Northeast UK Coast"=0,
                         "River Bush"=1,
                         "River Dee"=2,
                         "River Erne"=3,
                         "River Frome"=4,
                         "River Sella"=5,
                         "Joseph Picard - Canada"=0,
                         "Mailhot-Curran - Anadromous"=1,
                         "Mailhot-Curran - Potomodromous"=2,
                         "Steven Patrick - Canada"=3,
                         "Summerstown - Canada"=4,
                         "Yatsihsta - Canada"=5,
                         "Big Salmon River"=0,
                         "Conne River"=1,
                         "Gaspereau River"=2,
                         "Gulf of St. Lawrence"=3,
                         "Koksoak River"=4,
                         "Upper Salmon River"=5))
NSB_Comp_Salmon
```




```
legend <- get_legend(NSB_Comp_Salmon)
as_ggplot(legend)
```

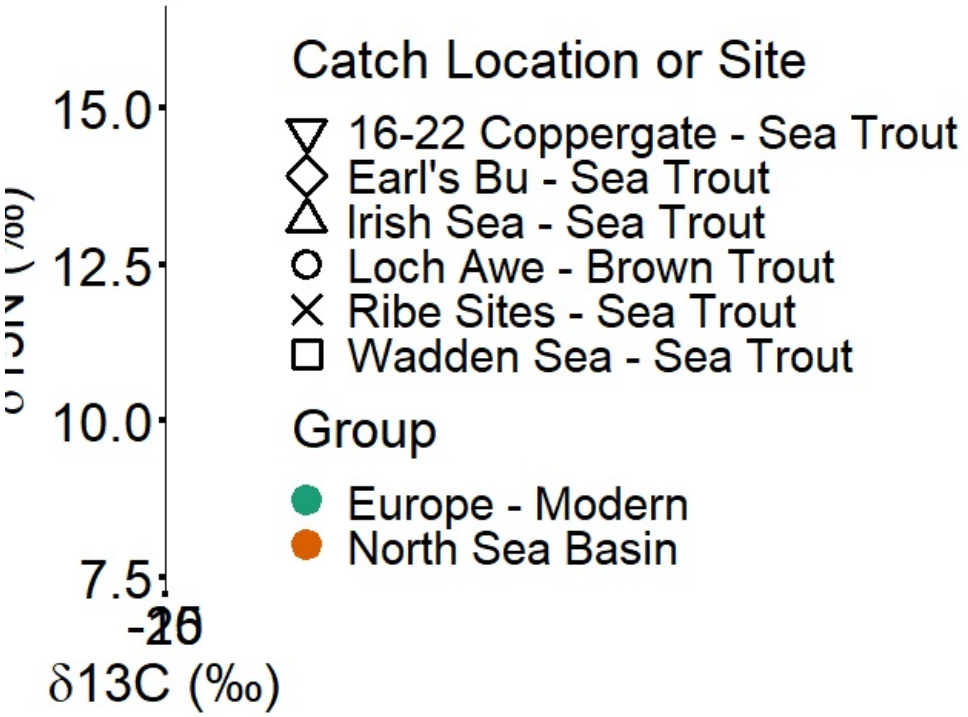


Figure 8.17 (Same as previous)

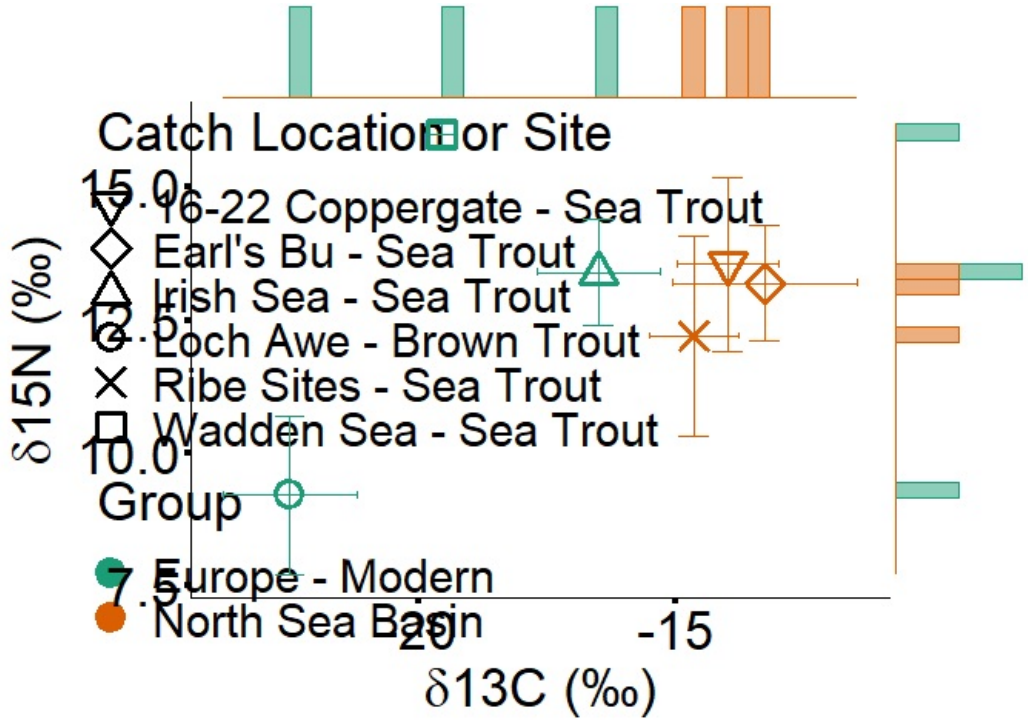
```
Comp_Trout <- subset(Comparative_Salmo_Iso, Species== "Salmo trutta")

Mean_Error_Comp_Trout <- ggplot(Comp_Trout,
                                aes(x=Mean_D13C,
                                    y=Mean_D15N,
                                    color=Group,
                                    shape=Catch_Location_Site)) +
  geom_point(size=5, stroke=2) +
  xlab(expression(delta *"13C (‰)")) +
  ylab (expression(delta *"15N (‰)")) +
  theme_cowplot(12) +
  geom_errorbar(aes(ymin=Mean_D15N - D15N_SD, ymax= Mean_D15N + D15N_SD)) +
  geom_errorbarh(aes(xmin= Mean_D13C - D13C_SD, xmax= Mean_D13C + D13C_SD)) +
```

```
  scale_color_brewer(palette="Dark2") +
  theme(text = element_text(size=26),
        axis.text = element_text(size=26),
        axis.ticks = element_line(linewidth = 1.5),
        legend.box.margin = margin(50,50,50,50)) +
  scale_shape_manual(values =
                     c("Wadden Sea - Sea Trout"=0,
                       "Loch Awe - Brown Trout"=1,
                       "Irish Sea - Sea Trout"=2,
                       "16-22 Coppergate - Sea Trout"=6,
                       "Ribe Sites - Sea Trout"=4,
                       "Earl's Bu - Sea Trout"=5
                       ))+
  labs(shape="Catch Location or Site")
Mean_Error_Comp_Trout
```




```
legend <- get_legend(Mean_Error_Comp_Trout)
as_ggplot(legend)
MECT_No_Legend<-Mean_Error_Comp_Trout+theme(legend.position = "none")
ggMarginal(MECT_No_Legend,type="histogram", groupColour = TRUE, groupFill = TRUE)
```



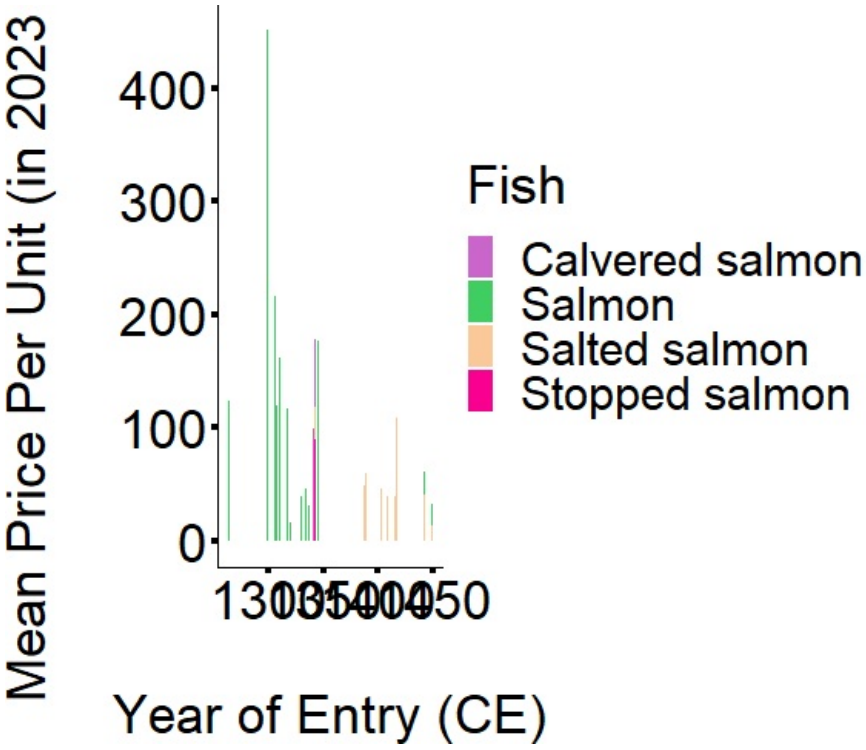
Chapter 9 - Medieval Perceptions of Salmo sp. Fishes

Code

Figure 9.1 - Records of Salmon from 1264-1444 CE

```
Whole_Fish_Means <- read.csv("Whole_Fish_Means.csv")
Salmon_Means_Only <- subset(Whole_Fish_Means, Fish == "Calvered salmon" | Fish == "Salmon" | Fish == "Sa

ggplot(Salmon_Means_Only, aes(fill=Fish, y=Mean_Price_Per_Unit, x=Year)) +
  geom_bar(position="stack", stat="identity") + scale_fill_manual(values=Liz_PhD) +
  theme_cowplot(12) +
  labs(x="\nYear of Entry (CE)", y="Mean Price Per Unit (in 2023 GPB)\n")+
  theme(text = element_text(size=26),
      axis.text = element_text(size=26),
      axis.ticks = element_line(linewidth = 1.5),
      plot.margin = margin(0,3,0,0, unit="cm"))
```



Chapter 10 - Discussion and Conclusion

Code

Figure 10.1 - Made using Canva Figure 10.2 - Edited to add labels in Inkscape

```
#scatter plot looking at TL estimates by ZooMS species ID
ZooMS_TL <- read.csv("ZooMS_TL.csv")

ggplot(ZooMS_TL, aes(x=total_length, y=ZooMS_ID, fill=ZooMS_ID)) +
  stat_halfeye(adjust = 0.25, justification=-0.2, .width=0, point_color=NA)+
  geom_boxplot(width=0.12, outlier.color=NA, alpha=0.5)+
  stat_dots(side="left", justification=1.1, binwidth=0.25, dotsize=4)+
  scale_fill_brewer(palette="Set2")+
  theme_cowplot()+
  labs(x="\nTotal Estimated Length (CM)", y="ZooMS Identification\n")+
  theme(legend.position = "none", text = element_text(size=24),
        axis.text = element_text(size=20), axis.title.y = element_blank(),
        axis.text.y = element_blank(), axis.ticks.y = element_blank())
```

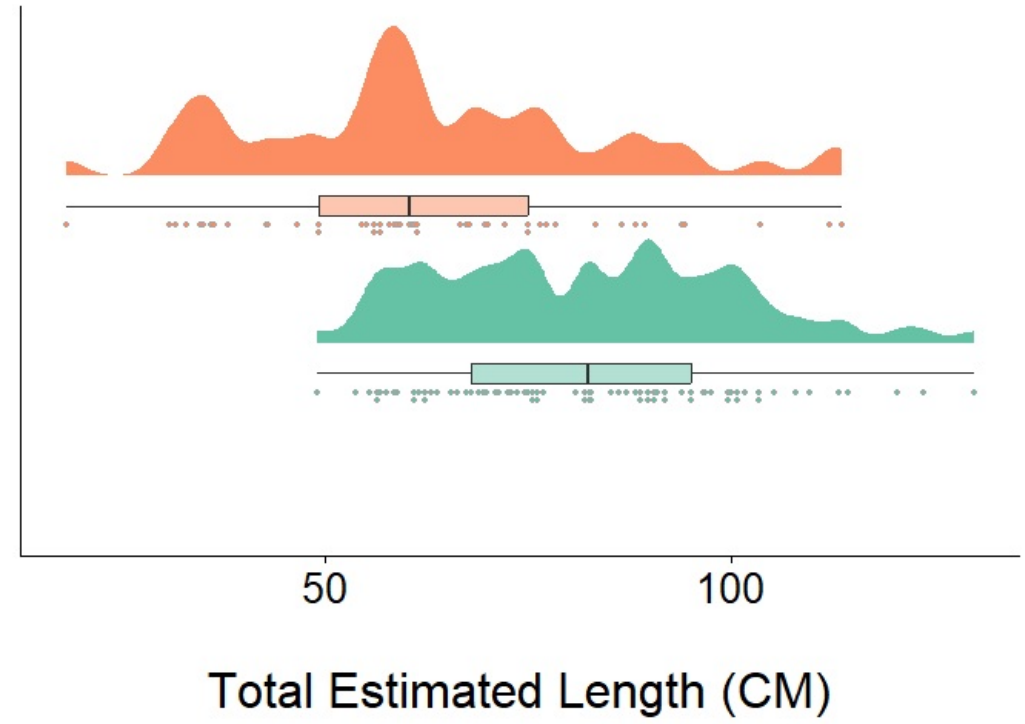
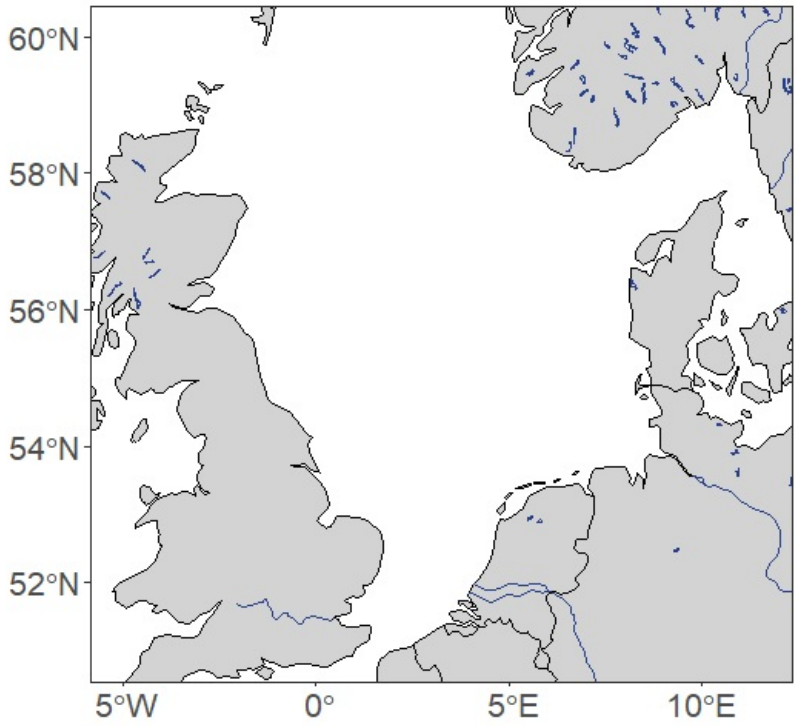


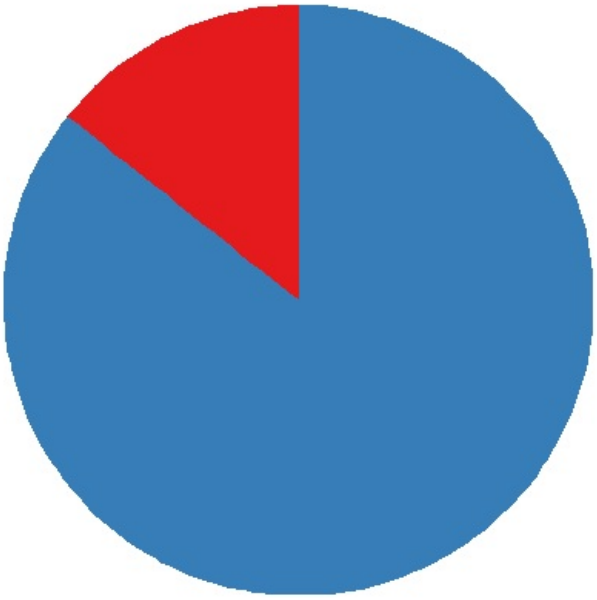
Figure 10.3 - All elements combined in Inkscape

```
NS_Map<- StudyArea_2 + coord_sf(xlim= c(-5, 11.5), ylim= c(51,60)) + theme(axis.text = element_text(size=
NS_Map
```



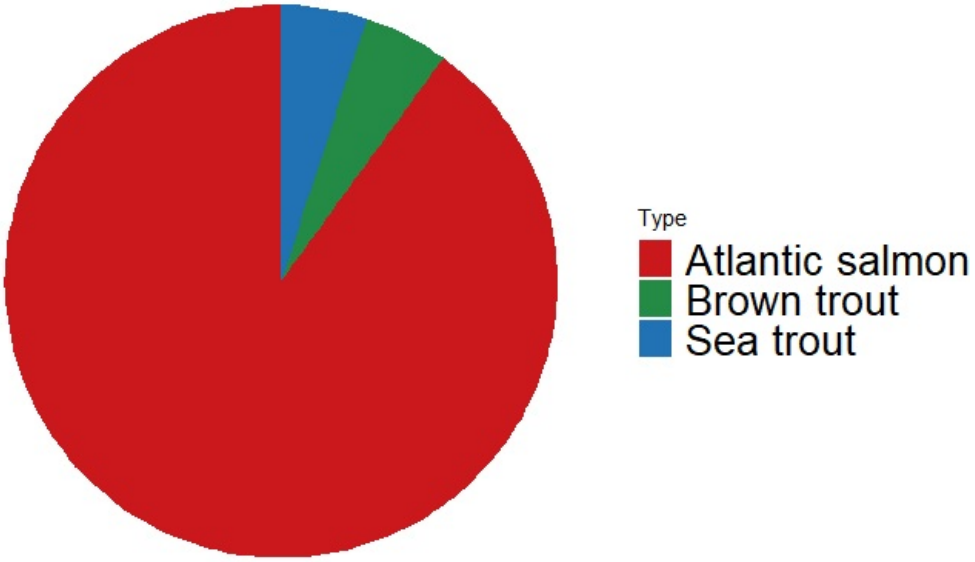

```
#Proportion pie charts for Salmo ecotypes, each country
Values <- c(3, 18)
Type <- c("Atlantic salmon", "Sea trout")
Prop <- c(14.3, 85.7)
DK_Proportions <- data.frame(Values, Type, Prop)

DK_ecotypes <-  ggplot(DK_Proportions, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity"
DK_ecotypes <- DK_ecotypes + coord_polar(theta = 'y') + theme_void() + scale_fill_brewer(palette= "Set1"
DK_ecotypes
```



```
Values <- c(18, 1, 1)
Type <- c("Atlantic salmon", "Brown trout","Sea trout")
Prop <- c(90.0, 5.0, 5.0)
NL_Proportions <- data.frame(Values, Type, Prop)

NL_ecotypes <-  ggplot(NL_Proportions, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity"
NL_ecotypes <- NL_ecotypes + coord_polar(theta = 'y') + theme_void() + scale_fill_manual(values=c("#cb18
NL_ecotypes
```




```
legend <- get_legend(NL_ecotypes)
as_ggplot(legend)
```

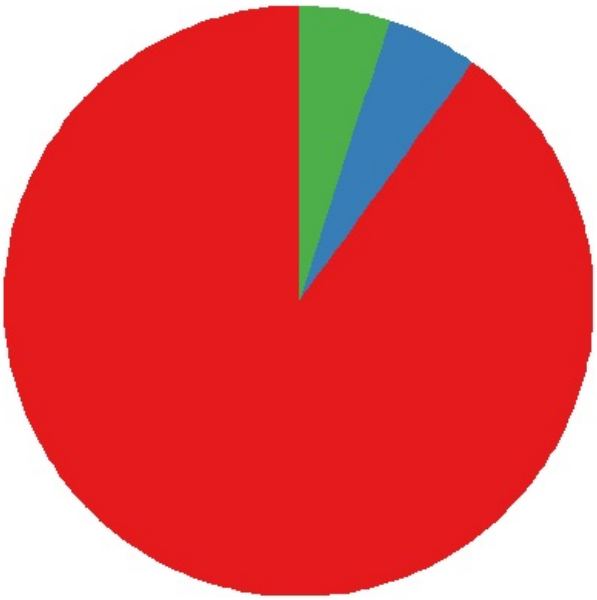



```
#remove legend

NL_ecotypes <- NL_ecotypes + coord_polar(theta = 'y') + theme_void() + scale_fill_brewer(palette= "Set1"
```

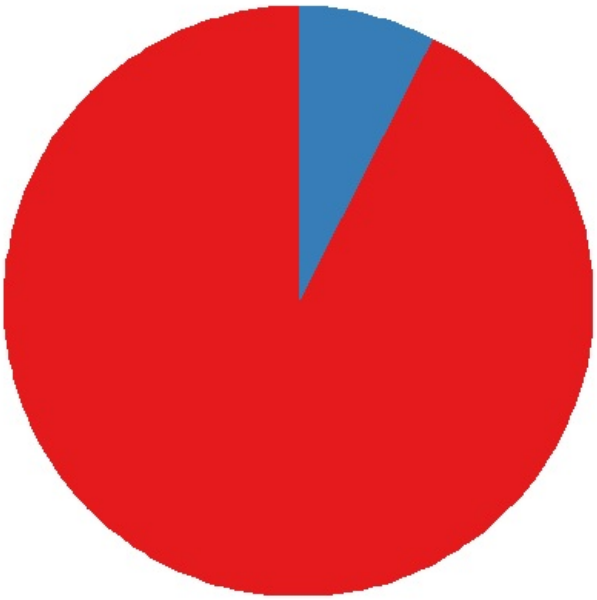
```
## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```

```
NL_ecotypes
```



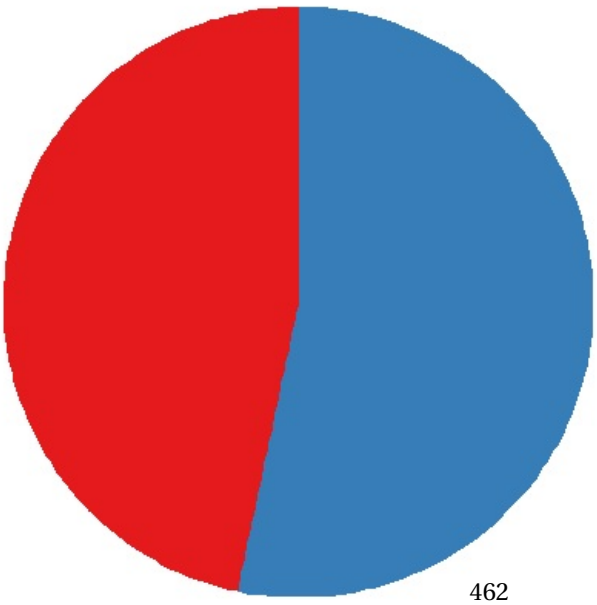

```
Values <- c(49, 4)
Type <- c("Atlantic salmon", "Sea trout")
Prop <- c(92.5, 7.5)
COP_Proportions <- data.frame(Values, Type, Prop)
```

```
COP_ecotypes <-  ggplot(COP_Proportions, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity
COP_ecotypes <- COP_ecotypes + coord_polar(theta = 'y') + theme_void() + scale_fill_brewer(palette= "Set
COP_ecotypes
```



```
Values <- c(7, 8)
Type <- c("Atlantic salmon", "Sea trout")
Prop <- c(53.3, 46.7)
EB_Proportions <- data.frame(Values, Type, Prop)

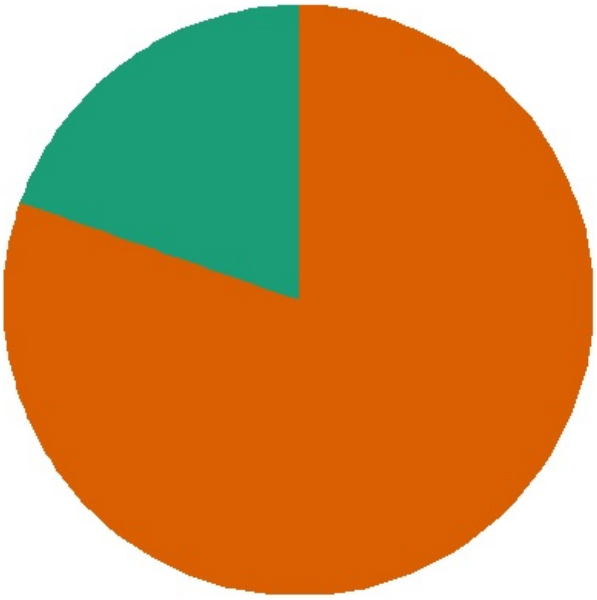
EB_ecotypes <-  ggplot(EB_Proportions, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity"
EB_ecotypes <- EB_ecotypes + coord_polar(theta = 'y') + theme_void() + scale_fill_brewer(palette= "Set1"
EB_ecotypes
```




```
#Same thing but with ZooMS IDs instead of ecotypes-- going to to make two side-by-side comparison plots
```

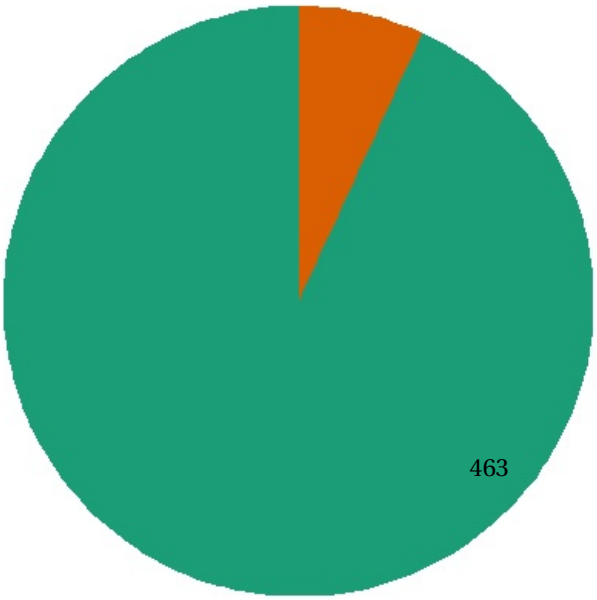
```
Values <- c(10, 41)
Type <- c("Salmo salar", "Salmo trutta")
Prop <- c(19.6, 80.4)
DK_Proportions <- data.frame(Values, Type, Prop)

DK_ecotypes <-  ggplot(DK_Proportions, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity"
DK_ecotypes <- DK_ecotypes + coord_polar(theta = 'y') + theme_void() + scale_fill_brewer(palette= "Dark2
DK_ecotypes
```



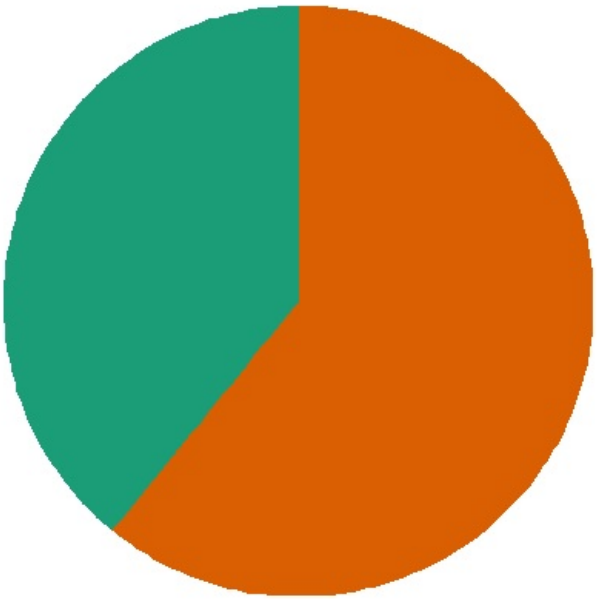
```
Values <- c(54, 4)
Type <- c("Salmo salar", "Salmo trutta")
Prop <- c(93.1, 6.9)
COP_Proportions <- data.frame(Values, Type, Prop)

COP_ecotypes <-  ggplot(COP_Proportions, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity
COP_ecotypes <- COP_ecotypes + coord_polar(theta = 'y') + theme_void() + scale_fill_brewer(palette= "Dar
COP_ecotypes
```



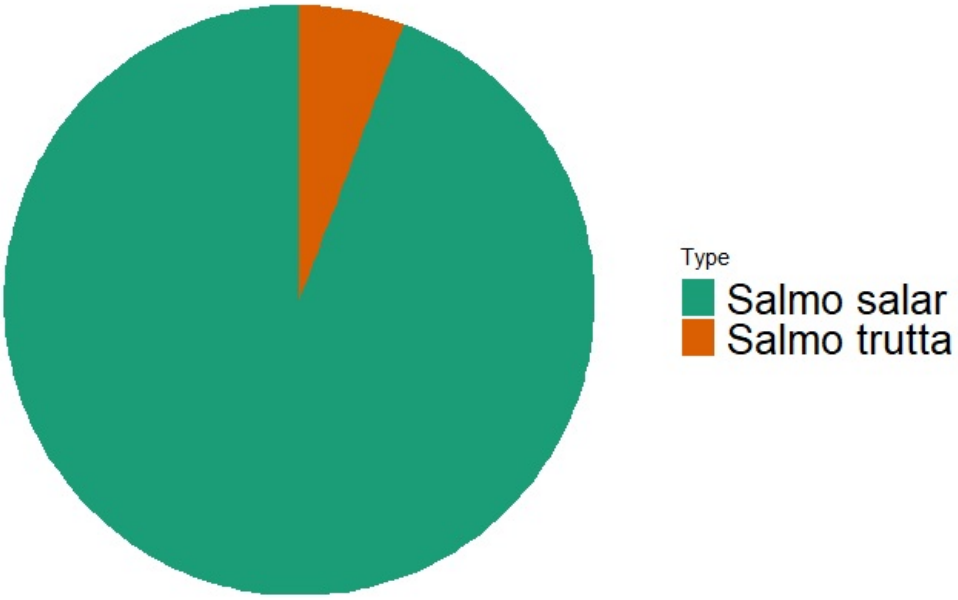
```
Values <- c(9, 14)
Type <- c("Salmo salar", "Salmo trutta")
Prop <- c(39.1, 60.9)
EB_Proportions <- data.frame(Values, Type, Prop)

EB_ecotypes <-  ggplot(EB_Proportions, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity"
EB_ecotypes <- EB_ecotypes + coord_polar(theta = 'y') + theme_void() + scale_fill_brewer(palette= "Dark2
EB_ecotypes
```

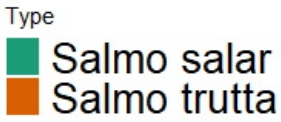


```
Values <- c(49,3)
Type <- c("Salmo salar", "Salmo trutta")
Prop <- c(96.0, 4.0)
NL_Proportions <- data.frame(Values, Type, Prop)

NL_ecotypes <-  ggplot(NL_Proportions, aes(x = 1, y = Values, fill = Type)) + geom_bar(stat = "identity"
NL_ecotypes <- NL_ecotypes + coord_polar(theta = 'y') + theme_void() + scale_fill_brewer(palette= "Dark2
NL_ecotypes
```




```
legend <- get_legend(NL_ecotypes)
as_ggplot(legend)
```




```
#remove legend

NL_ecotypes <- NL_ecotypes + coord_polar(theta = 'y') + theme_void() + scale_fill_brewer(palette= "Dark2
```

```
## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```



```
NL_ecotypes
```

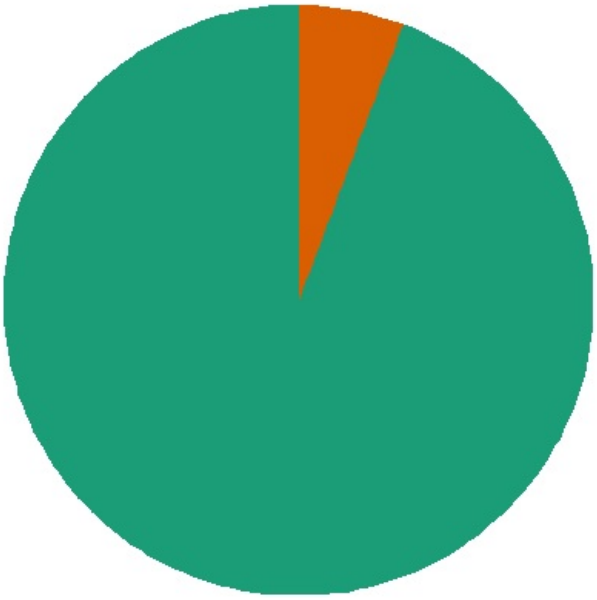
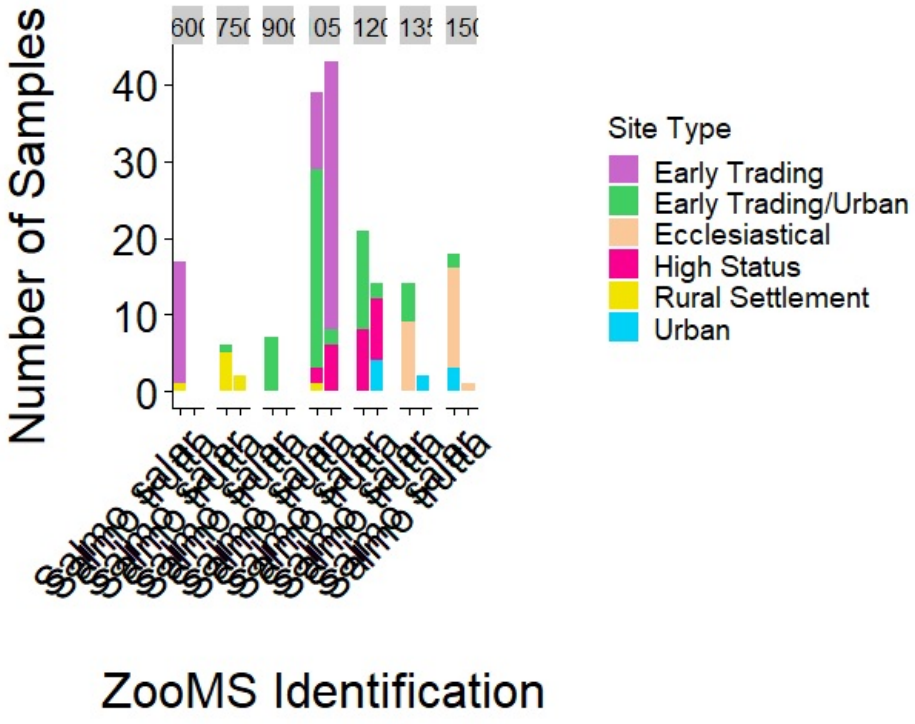


Figure 10.4 - (Plot A is a reproduction of Figure 6.15, code for Plot B below)

```
#Multivariate stacked/grouped bar charts showing the Fish NISP and Salmonid NISP by period

ZooMS_Period <- read.csv("ZooMS_Periods.csv")

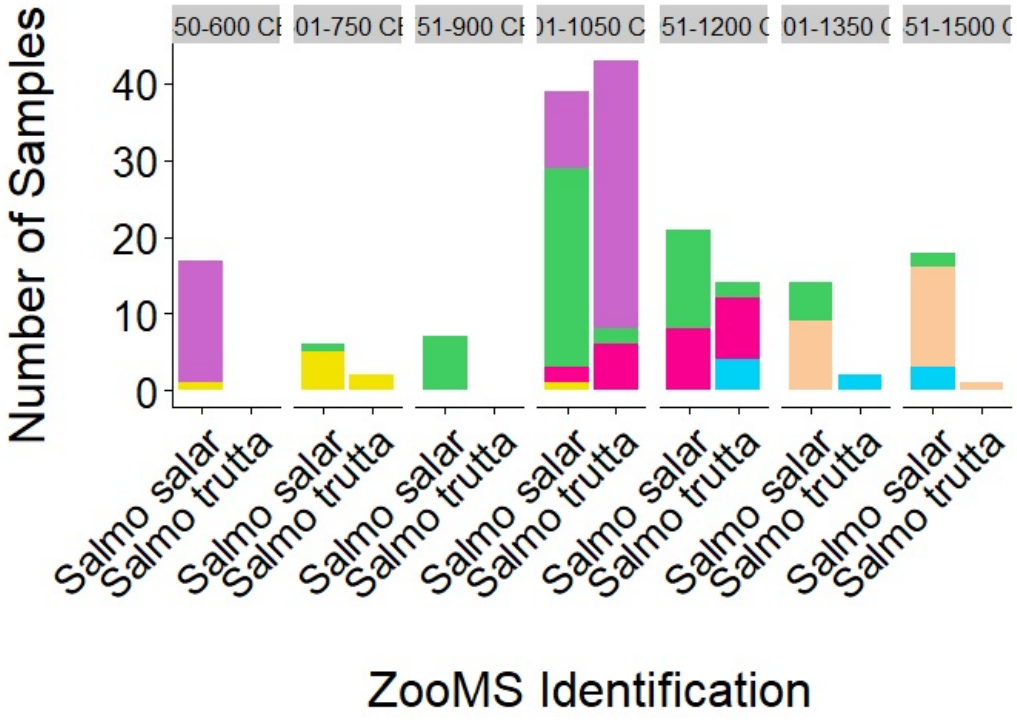
ZooMS_Time<-ggplot(ZooMS_Period, aes(x = ZooMS_ID, fill = Site_Type)) +
  geom_bar(stat = 'count', position = 'stack') +
  facet_grid(~factor(Period,levels=c("450-600 CE", "601-750 CE", "751-900 CE", "901-1050 CE", "1051-1200
  scale_fill_manual(values=Liz_PhD)+
  theme_cowplot() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1),
        axis.text = element_text(size=20),
        axis.title = element_text(size=24),
        legend.text = element_text(size=14),
        legend.box.margin = margin(50,50,50,50),
        legend.margin=margin(0,0,0,0))+
  xlab("\nZooMS Identification") + ylab("Number of Samples\n") + labs(fill="Site Type")
ZooMS_Time
```




```
legend <- get_legend(ZooMS_Time)
as_ggplot(legend)
```




```
#remove legend
ZooMS_Time<-ggplot(ZooMS_Period, aes(x = ZooMS_ID, fill = Site_Type)) +
  geom_bar(stat = 'count', position = 'stack') +
  facet_grid(~factor(Period,levels=c("450-600 CE", "601-750 CE", "751-900 CE", "901-1050 CE", "1051-1200
  scale_fill_manual(values=Liz_PhD)+
  theme_cowplot() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1),
        axis.text = element_text(size=20),
        axis.title = element_text(size=24),
        legend.text = element_text(size=14),
        legend.box.margin = margin(50,50,50,50),
        legend.margin=margin(0,0,0,0),
        legend.position = "none")+
  xlab("\nZooMS Identification") + ylab("Number of Samples\n") + labs(fill="Site Type")
ZooMS_Time
```


50-600 CE
01-750 CE
51-900 CE
01-1050 C
51-1200 C
01-1350 C
51-1500 C
Number of Samples
40
30
20
10
0
Salmo salar
Salmo trutta
ZooMS Identification