Whence came the English?: exploring relationships between the Iron Age, Romano-British and Anglo-Saxon periods in Britain and Denmark : a craniometric biodistance analysis

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Whence came the English?

Exploring relationships between the Iron Age, Romano-British and Anglo-Saxon periods in Britain and Denmark: A craniometric biodistance analysis

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ABSTRACT

Many pre- and early-historic cultural transitions in Britain have been attributed to mass-migrations originating outside Britain. One of the most striking changes was the 5th century AD Romano-British / Anglo-Saxon transition, which has often been explained using models which focus on a mass migration and invasion of Angles, Saxons and Jutes from what is now Denmark and northern Germany. This explanation, based on cultural similarities between the two regions, has recently been strongly criticised on theoretical grounds. Most researchers of the late 20th and 21st centuries now view this transition in terms of elite settlement, and wide-scale acculturation. Within the last decade, however, research from the new field of archaeogenetics has reinvigorated this debate, with evidence showing that population movement between Britain and the continent may have been substantial. Despite this recent resurgence of interest, biological anthropological research in Britain has not followed suit, despite the development and relatively wide-scale application of quantitative genetic methods to anthropometric data elsewhere.

In this thesis, craniometric data, which were collected from skeletal collections, published and unpublished reports, represent over 1400 individuals from the Iron Age, Romano-British and Anglo-Saxon periods in Britain and Denmark. These data have been analysed using univariate, population genetic and matrix correlation methods, in order to investigate population structure and relationships in terms of continuity or change in Britain between these periods. The results of these analyses indicate a degree of temporal continuity and no evidence for geographical isolation, both within Britain, and between Britain and Denmark. Cultural affinities, however, are found to be significantly associated with biodistance, in some cases. Results indicate strong links between Britain and Denmark, in both the Iron Age and the early and later Anglo-Saxon periods, suggesting that substantial migration between Britain and the continent may have occurred. However, Romano-British samples appear distinct from Iron Age, Anglo-Saxon and Danish samples.

The questions remaining relate to the timing and nature of this migration, the situation in areas of Britain not sampled here, and the cause of the Romano-British distinctiveness in contrast to earlier and later samples.

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This research would have been impossible without the assistance given to me, in innumerable forms, by a great number of individuals whose roles ranged widely, and whose locations span the globe. Of these individuals, some were always available face-to-face, others at the end of a telephone, or keyboard. All have given freely of their time and knowledge, and to those who I never met – I hope one day I have the chance to say thank-you in person.

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From Tees Archaeology, Hartlepool, Pete Rowe and Robin Daniels both assisted me with locating material curated by Tees Archaeology, provided me with space in their 'bunker', and with access to both the 'grey literature' and their extensive knowledge of north-east archaeology and history. At Northern Archaeological Associates, Barnard Castle, Peter Cardwell and Paul Johnson also provided me with access to skeletal material from Spofforth, and with space to measure 'my heads'. Paul deserves special thanks for transforming me from an anthropologist with an interest in bones, into an anthropologist with experience of the 'real world' of archaeology, and an appreciation of the process that human skeletons go through before ending up in a lab, or detailed within an excavation report. Kevin Leahy at North Lincolnshire Museum, and Dave Marchant at Sewerby Hall museum both facilitated access to skeletal material, as did Martin Foreman at Hull Museums. Martin deserves particular thanks not only for providing access to material, but also for allowing me to photocopy all skeletal records cards for Wetwang & Garton Slacks – free of charge – and for his boundless enthusiasm and great coffee!

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TABLE OF CONTENTS

CHAPTER 1: INTRODUCTION

CHAPTER 2: BACKGROUND AND LITERATURE

CHAPTER 3: MATERIALS AND METHODS

CHAPTER 4: RESULTS

CHAPTER 5: DISCUSSION AND CONCLUSIONS

TABLES

FIGURES

CHAPTER 1

INTRODUCTION

> Then all the councillors, together with that proud tyrant Gurthrigern [Vortigern], the British king, were so blinded, that, as a protection to their country, they sealed its doom by inviting in among them (like wolves into the sheep-fold), the fierce and impious Saxons, a race hateful both to God and men, to repel the invasions of the northern nations. Nothing was ever so pernicious to our country, nothing was ever so unlucky. What palpable darkness must have enveloped their minds-darkness desperate and cruel! Those very people whom, when absent, they dreaded more than death itself, were invited to reside, as one may say, under the selfsame roof. [...] A multitude of whelps came forth from the lair of this barbaric lioness, in three cyuls, as they call them, that is, in three ships of war, with their sails wafted by the wind and with omens and prophecies favourable, for it was foretold by a certain soothsayer among them, that they should occupy the country to which they were sailing three hundred years, and half of that time, a hundred and fifty years, should plunder and despoil the same. They first landed on the eastern side of the island, by the invitation of the unlucky king, and there fixed their sharp talons, apparently to fight in favour of the island, but alas! more truly against it. Their mother-land, finding her first brood thus successful, sends forth a larger company of her wolfish offspring, which sailing over, join themselves to their bastard-born comrades.
> (Gildas, trans. Giles, J. A. 1891, available online at
> http://www.fordham.edu/halsall/basis/gildas-full.html)

1.1 Research problem

The long history of Britain as seen through archaeology and history involves a series of distinct cultural eras, divided and demarcated by transitional phases. One of the most ferociously debated topics in current archaeological and historical research is that of the nature of the Romano-British / Anglo-Saxon transition in Britain. The passage above, which concerns the origin and nature of this transition, was written by Gildas in the 6th century, and aptly demonstrates his disgust for both the Saxon invaders, and the rulers of Britain who invited them. This written source has informed and influenced the majority of writings and research concerning the period, although much of the ferocity and venom of Gildas' depiction has disappeared in the retelling. However, it is not solely the historical literature that indicates a major transition occurred in Britain in the 5th century AD.

The archaeological differences between the Romano-British and Anglo-Saxon periods are striking. As Lucy writes, "The Roman period was characterised by settlement evidence, monumental architecture, distinctive building styles, imported pottery and metalwork. The archaeological remains reflect the world of the living: forts, roads, villas, settlements, enclosures. Cemeteries are found in some numbers but these generally concentrate around settlement sites" (1998: 2). The dead of the late Roman period were usually buried in cemeteries lying outside town or city walls, most often with the head at the west end of the grave, and without any accompanying artefacts.

In contrast, the early Anglo-Saxon period (5th to 7th centuries AD) is notable for its cemeteries, most of which are found in the southern and eastern parts of England. The relative profusion of early Anglo-Saxon cemeteries is in stark contrast to the lack of known settlement sites of the same period. Such cemeteries can be distinguished by the number and variety of grave goods found with a large proportion of the individuals in a cemetery, as well as by the type of burials. Within this period the dead were either cremated or inhumed, those inhumed most often being buried in graves or burial pits in an extended supine position. Often the head was specifically orientated, although that orientation was much more variable than in late Roman cemeteries. In addition to the distinctive deposition of corpses, Anglo-Saxon period graves were commonly furnished with goods including jewellery, ornaments, brooches, beads, girdle-hangers and weaponry, pottery and other vessels, toilet-sets, knives and amuletic items (Lucy 2000).

Changes occurring in Britain during this period were not limited to those seen in the material culture. Events in the 5th century also had an enduring impact on the religion, language and legal systems of the period, an impact which has at times been viewed as heralding the 'beginnings of Englishness' (*ibid.*).

The dramatic transformation evident in Britain during this period leads to the problem to be addressed in this study; did a substantial migration of Angles, Saxons and Jutes have a biological as well as cultural impact on 'the Britons', or was the change due to a small number of elite invaders imposing their culture on the native inhabitants of Britain? Was the genetic as well as the cultural makeup of at least part of Britain transformed? Should this be interpreted as a period of invasion or of native continuity and adaptation? As the title of this thesis asks – *Whence came the English?*

As the coming chapters will illustrate, the question of where 'the English' came from is central not only for our interpretation of the archaeological and historical evidence, but also for our understanding of our own historical self-identity; as 'English', as 'European' (Tutton 2004), and perhaps most importantly, as products of (and perhaps also hostages to) traditional and contemporary interpretations of the evidence.

1.2 Background and justification

Whilst much work has been done within the fields of archaeology and historical research to address the questions posed at the end of section 1.1, recent perspectives and interpretations have tended to be theoretically polarised. On one 'side' are those who support models of change which invoke large-scale, or relatively large-scale, migration (e.g. Welch 1992, Burmeister 2000); on the other are those for whom such a large scale migration seems unlikely, and who emphasise acculturation models of change (e.g. Higham 1992, Lucy 1998, 2000, Tyrrell 2000). Partly because of the dominance of the latter perspective in recent times, while archaeological, historical and linguistic research concerning this period has been consistently popular, relatively little attention has been focussed on the remains of the people themselves. Indeed, the very notion of migration (with reference to almost any period of British pre- and early- history) has become so unpopular and unfashionable that those who propose large scale migration as a causal factor in cultural change, and particularly those who have used skeletal material in their research, have encountered strong ideological criticism and, in some cases, disbelief at their findings (e.g. Härke 1998). Nevertheless, recent research in the fields of archaeogenetics and isotope analysis has once again revived the 'migration question', with a growing number of researchers concluding that large-scale population movements did, indeed, take place (e.g. Weale *et al.* 2002, Capelli *et al.* 2003). Much archaeogenetic research, however, must rely on modern-day samples, while that utilising the ancient material itself (in the form of aDNA) is considered to be unreliable in many cases (Thomas 2007 pers. comm). The research relevant to the present study, and the impact of contemporary socio-political attitudes concerning all these issues, are discussed in more detail in Chapter 2.

While biological anthropology has largely neglected problems of population history in the context of cultural change in Britain, the same situation has not prevailed elsewhere, and in recent years significant advances have been made in techniques which may be applied to the study of population history, using skeletal metric data. Primary among these is the use of R matrix analyses, matrix correlation analyses, and the extension of theory and methods from genetics for use with quantitative phenotypic data (e.g. Relethford 1997). These methods have been applied, primarily in conjunction with anthropometric, craniometric, and dental metric data, to a diverse range of problems concerning population history, from the origin and spread of modern humans (e.g. Relethford 2004a), to the origins of the 'first Americans' (e.g. González-José *et al.* 2001b), to analyses of postmarital residence within a prehistoric American Indian Pueblo (Schillaci & Stojanowski 2003).

The aim of this research, therefore, is to address the questions posed toward the end of the previous subsection via R matrix and matrix correlation analyses of craniometric data. Particularly, the aim is to investigate whether the Anglo-Saxons of the 5th century AD in Britain onward were more similar to Danish populations than were the preceding Romano-British and British Iron Age populations. In this thesis, Danish samples represent the Angles, Saxons and Jutes who historically have been believed to have invaded Britain in this period, and the Iron Age and Romano-British samples both serve to represent the native, or indigenous, population of Britain prior to the Anglo-Saxon period.

1.3 Materials and methods used

In this thesis, craniometric data collected from over 1400 individuals from the Iron Age to the later Anglo-Saxon period in Britain, and from Denmark and The Netherlands, are analysed using a variety of descriptive, univariate and multivariate statistical methods. Primary among these are calculations of biodistance from the R matrix, on the basis that phenotypic distances derived from craniometric measurements can serve as a proxy for genetic distances (e.g. Konigsberg 1995, Relethford 1997). The distances derived from the R matrix are visualised in two dimensions using hierarchical cluster and principal coordinates analyses (i.e. classic multidimensional scaling), and are tested for association with geographic, temporal and 'cultural' matrices using Mantel matrix correlation tests. Finally, within-sample variation is explored using Relethford-Blangero analyses.

The results of these analyses are interpreted and discussed in Chapter 5, in the light of the research hypotheses and the previous research which has been done.

1.4 Chapter outline

In the first part of Chapter 2 an overview of the state of our knowledge about the periods involved in this research is presented, with a particular focus on historical and archaeological evidence for continuity or change, and with regard to theories from these fields concerning British population history. In the second part of Chapter 2 research from the biological sciences is reviewed, along with a discussion of factors which have influenced the popularity of such research over time.

In Chapter 3 research hypotheses and detail regarding the materials and methods utilised in this research are presented, with subsections specifying the specific samples used, the methods by which data were collected, and the means by which they were analysed.

In Chapter 4 the results of this research are presented. In the first part of this chapter, descriptive statistics for each sample are presented, along with tests for within-sample between sex differences. Analyses of variance results are presented next, followed by multivariate analyses of variance tests for the variables used in subsequent multivariate analyses. In the second part of Chapter 4, the results from the R matrix analyses are presented, firstly for biodistance, secondly for matrix correlation and finally for Relethford-Blangero analyses.

In Chapter 5 the results presented in Chapter 4 are discussed with regard to the hypotheses set out in Chapter 3. A general discussion of the findings is then presented, followed by conclusions, and suggestions for further work.

1.5 Concepts and terminology

1.5.1 Biological vs. socio-cultural theories of change

Throughout the history of research into the early Anglo-Saxon period, there has been a fundamental conflict between theories which emphasise a biological cause of change, and those which focus on social factors as the main force. Although it is really only in recent decades that the socio-cultural theories have challenged the biological theories, it is important at this stage to briefly outline the principles of both, so that what follows may be better appreciated.

When attempting to account for changes in culture as seen, for example, through archaeology and language, two main models of change may be considered. The first of these, which enjoyed popularity throughout much of the past, was the assumption that any major cultural change must have been brought about by a physical movement of people carrying with them elements of the 'new' culture. This suggests that, for example, the appearance of a strikingly new form of art or language must have been due to an influx of individuals bearing these features as 'hallmarks' of their own culture. In the case of the Anglo-Saxons, the rapid replacement of Iron Age or Romano-British artefacts with those of a strikingly different nature, which became known as 'Anglo-Saxon', was initially, and for many subsequent years, interpreted as clearly indicating the mass migration of the people of those tribes considered to have made up the Anglo-Saxons (the Angles, Saxons and Jutes), replacing or overwhelming those of the 'old' Romano-British population. The important element of this approach is that it requires the large-scale movement of populations from one area to another for cultural change to occur.

Acculturation models, on the other hand, do not require large-scale population movement. Indeed, in some cases, little or no movement of populations is required between geographical areas in order to effect great cultural change. In this instance, it is suggested, even wide-scale, dramatic cultural changes may occur through only minor first-hand contact with members of a different cultural group. For whatever reason (and such catalysts may be countless), the 'new' culture is acquired, assimilated, adopted or appropriated by members of the 'old' culture, and may even replace it. Such acculturation may be so dramatic that it radically and permanently changes the rituals, dress, language, religion and so on of the 'host' population, and may result in the appearance that one culture has been entirely replaced by another. Such a transformation need not be brought about by force, and may be interpreted as evidence of a population's adaptation to changing social, political, economic or religious circumstances (e.g. Haviland 1996).

1.5.2 Terminology: periods and people(s)

When considering research into the earlier periods of Britain's history, it is crucial that certain aspects of modern nomenclature are appreciated and taken into account. In this thesis, a number of such terms must be clarified in order to make clear what meanings are intended. Primarily these concern the use of the terms 'Britain', 'England', 'Iron Age' 'Romano-British' and 'Anglo-Saxon'. To begin with, although the term 'Anglo-Saxon England' is sometimes used, it must be remembered that 'England' did not exist at the time of the Anglo-Saxons – the term was invented much later, and used to describe a political region later still (Lucy 1998). For this reason, throughout this thesis, the term Britain (or UK where a shorter form is required in coding samples) is – where possible – used in preference to 'England' in order to describe a geographical area.

Similarly, it should be noted that the 'Anglo-Saxons' would have had no concept of themselves as such, and that those individuals who made up this 'group' would have been far more heterogeneous than the label applied to them implies. As Lucy (1998: 19, and see also for example Pohl in Hines 1997) notes, "the people residing in the British Isles in the fifth and sixth centuries would have had no conception of themselves as a single political entity, let alone a racial one".

A similar caution applies to the samples in this research referred to as 'Iron Age' and 'Romano-British'. The term 'Iron Age' here refers to the mid/late Iron Age population of Britain, prior to the conquest of Britain by Rome. The British Iron Age is sometimes thought of as part of a much wider 'Celtic' population (Harding 2004), which spanned much of Europe, only part of which later came under the influence of the Roman Empire. However, it should be noted that the notion of a discrete, Europe-wide, 'Celtic' culture has fallen out of favour in recent years (e.g. Cunliffe 1991, Harding 2004). The term 'Romano-British' refers to the population of Britain, following the end of the Iron Age, but before the advent of what is known as the Anglo-Saxon period. The Romano-British, although again by no means a homogenous group, became distinct from later Iron Age populations in the north and west of Britain as a result of their inclusion within the Roman Empire.

Whilst for simplicity such terms are necessarily used to allow a discussion of the problem at hand, it should be remembered that they are not unproblematic, and must be used, defined and understood with care. In this case, while 'Romano-British' and 'Anglo-Saxon' are both used less controversially in order to describe temporal and cultural eras, they are also at times used to refer to the individuals present temporally and geographically within those eras. It is the latter use which is most difficult, as the first describes a period of cultural 'type' (though this itself is certainly neither fixed nor constant), whereas the second may risk ascribing ancestry, which is not always the appropriate or intended meaning.

In this research, the term 'early Anglo-Saxon period' is used to refer to the period in Britain in which Anglo-Saxon cultural material and rites began to appear in previously Romano-British areas, and pertains mainly to the 5th to 7th centuries AD.

1.6 Scope and key assumptions

As a first study of its kind, with regard to the methodology used to investigate the population history of Britain, the research presented in this thesis has been limited to a comparison of British and Danish samples. Because of the nature of skeletal data, in terms of absolute sample size and missing data due to poor skeletal preservation, the samples used in this study are often pooled, in order to create datasets large enough for use in the multivariate analyses. This means (as has already been noted above, and is discussed in Chapter 3) that the analyses are limited to those for which pooled samples are methodologically and theoretically acceptable, and that the usefulness of the data with regard to some of the more novel, and anthropologically interesting analyses (such as the Relethford-Blangero analysis – see above) is limited. On a related theme, the key assumption in this study, which is particularly important with regard to the pooling of disparate samples, is that the individuals present within samples are representative of the populations they are thought to represent. This involves issues of archaeological provenance, dating of sites, and the correct interpretations of these factors. These issues are discussed in Chapter 3.

With reference to interpretation of the results of this research, conclusions drawn from the results for individual or pooled samples must be set in the context of the composition of these samples, and any conclusions drawn regarding the broader nature of the population history of Britain between the Iron Age and later Anglo-Saxon periods can, therefore, only be considered tentative.

1.7 Conclusion

Within this chapter, the background to the research has been introduced, and the research questions stated. The current state of research into the Romano-British / Anglo-Saxon transition has been outlined, and the contribution which will be made to this body of knowledge by the present research stated. An outline for the remainder of the thesis has been presented, and notes have been made regarding terminology and concepts central to this research.

CHAPTER 2

BACKGROUND AND LITERATURE

2.1 Introduction

This chapter provides an introduction to the research done on Britain from the Iron Age, through the Romano-British and Anglo-Saxon periods, up to and including the Viking period. This review is divided into three main parts:

Section 2.2 describes archaeological and historical perspectives on the Iron Age, Romano-British, Anglo-Saxon and Viking periods in Britain, and addresses these in chronological order. Since the major aim of this work is to elucidate what happened between the Romano-British and Anglo-Saxon periods (and indeed much more work has been done anyway which concerns this period), the section dealing with the Anglo-Saxons contains considerably more detail in terms of both the evidence and critical debate than any of the others. Although it is slightly later than the major focus of this work, a section is also given over to the later Anglo-Saxon / Viking period. Theories regarding socio-cultural change are presented alongside evidence concerning environmental and economic continuity and change for each period. Section 2.3 summarises the research presented in section 2.2.

Sections 2.4 - 2.6 deal with the biological evidence for the population of the British Isles (again with greater emphasis on England and the Anglo-Saxon period) from a number of fields – biological anthropology, craniometrics, archaeogenetics, and isotope analysis. As many of these studies do not focus solely on one period of history, this section is divided by discipline rather than by archaeological period. Section 2.7 summarises the research presented in sections 2.4 - 2.6.

Sections 2.8 and 2.9 briefly discuss issues which may have affected both the research reviewed, and also the present study. These include a discussion of the impact of our knowledge of cranial plasticity on craniometric research, and of changing fashions in archaeology and the social sciences on the research conducted.

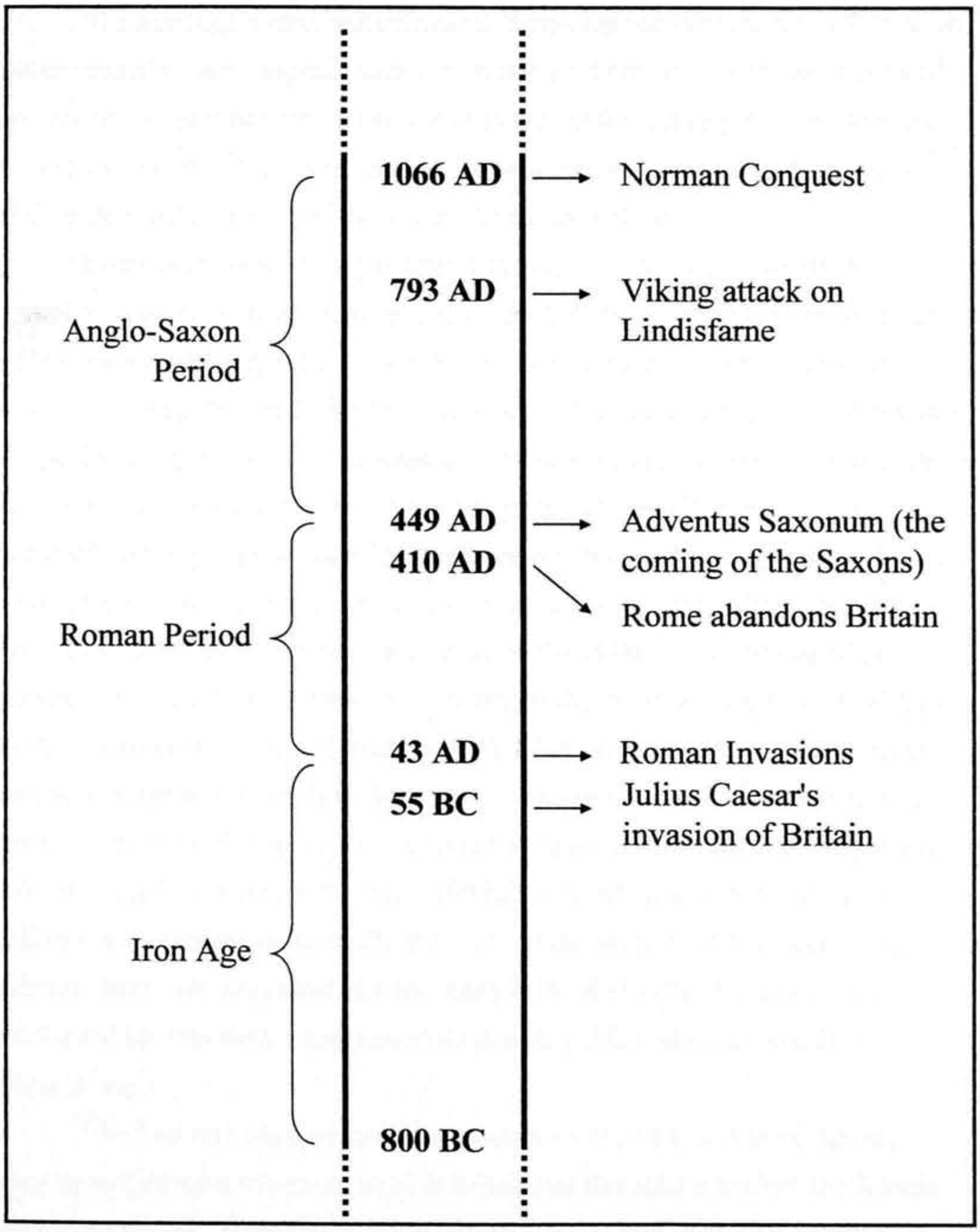
Lastly, section 2.10 summarises the review as a whole.

2.2 Historical and archaeological research

The history of Britain and Europe, in both historical and prehistoric eras, has been complex, with biological and socio-cultural changes occurring throughout. Some of the most notable changes involved the migration of people – the scale of which is variously accepted or disputed by academics, depending on the period in question, and the theoretical inclinations of those debating the issue. Alongside possible migrations (and arguably, in some cases, in testament to them) are changes in social structure, population size, subsistence strategy, settlement characteristics, political climate, material culture and language. When examining the biological characteristics of 'a population in time', it is necessary that we have some understanding of the changes occurring in all these aspects of an individual's (and by extension a population's) biological and socio-cultural environment. Without this broad understanding of the changes which took place throughout the history of the periods under study in this research, interpretation of any biological changes observed within and between time periods would be severely limited.

The history of Britain has traditionally been divided into time periods which correspond with these changes, and this section is intended to provide an overview of those periods with which this study is concerned. This overview commences with the Iron Age, and continues through the Roman period, the Anglo-Saxon period, and considers the impact of the Vikings in the latter portion of the Anglo-Saxon period preceding the Norman Conquest. The details given in this review, and the theories of change, rely mainly on the accepted historical record (where such records exist) and archaeological features of the period. They also (briefly, as a detailed description would be beyond the scope of this thesis) consider Britain in the context of its relationships and contacts with the continent. Details specific to sites and samples used in the present work are given in Chapter 3, section 3.3. On the following page, a timeline (figure 2.1) outlines the chronology of the periods in question, with some of the most important dates (in transitional terms) also given.

Figure 2.1 Timeline of periods examined in this research



2.2.1 The Iron Age

The Iron Age, within and between different regions of modern-day Europe, is not consistently chronologically defined. In Britain it runs from at the earliest the 8th century BC to the time of the Roman invasion in the first century AD. (In Denmark, in contrast, the term 'Iron Age' is applied to a much longer time period, from the fifth century BC to the end of the Viking Age in around 1050 AD.)

Partly because of its long temporal duration the Iron Age in Britain is complex, in terms of its regional variability (the population being distinct from that of later periods in being made up of relatively discrete tribal regions) and also in terms of its temporal variability. Over the course of research into this period this has resulted in many different chronological schemas being applied to it by researchers. During the earliest period of research, when migration models were more easily accepted, Iron Age 'sub-cultures' were named with respect to their proposed links to the continental Iron Age (e.g. La Tène). However, the difficulty of exactly matching British and continental material cultures led, in the 1930s, to the division of the British Iron Age into three materially and temporally defined groups: A = Hallstatt, B = La Tène and C = Belgic (Stead 1965: 1). More common in recent work on the period, is division of the British Iron Age into two (early = 8th – 4th centuries BC and later = ~300 BC – 1st century AD) or three/five (earliest = 800-650 BC, early = 650-400 BC, middle = 400-100 BC, late = 100 BC - ~43 AD and latest = ~43 AD - ~100 AD) temporal categories (Cunliffe 1991: 26). In the intervening time, many other schemas have been suggested (see for example Hawkes 1959), which results in earlier and later research being based on often very different chronological perspectives.

The Iron Age takes its name from the development of iron smelting and forging technologies which occurred in Britain and throughout modern-day Europe during the period. Unlike many of the later transitions discussed in this section, however, there is no clear historical or archaeologically recognisable division between the end of the Bronze Age and the start of the Iron Age in Britain (Haselgrove 1999: 113). Iron use was, in fact, of limited importance at the start of the period, and major socio-economic changes are not seen until the later Iron Age (*ibid.*). Nevertheless, the use of iron during this period does provide a unifying characteristic that justifies the distinction of this period in British (and indeed European) prehistory from that which went before (Ralston 1999: 501). Additionally, defining the end of the Iron Age is complicated by the fact that the Roman conquest of Britain took some time to complete, and in any case did not affect the whole of Britain (Haselgrove 1999).

Significant geographic and temporal variability is seen in Britain during the Iron Age, with changes through time in the types and density of settlements and cultural traditions (Ralston 1999). It has been suggested that climatic deterioration, persisting through to the Iron Age from the Bronze Age, led to a retreat from the upland areas of Britain and increasing competition for lowland land; this perhaps being responsible for the initial phase of hillfort-building during the earlier part of the period (Haselgrove 1999: 128). Hillforts were initially constructed in the south of England during the 6th and 5th centuries BC and gained a locally dominant role during the 4th and 2nd centuries BC (*ibid.*: 120). Throughout the rest of Britain settlement types included strongly defended homesteads, enclosed homesteads (notably in the north-east) and villages and open settlements (Cunliffe 1991).

Around 400 BC the climate improved once again, and by the end of the Iron Age Britain's climate is thought to have been similar to that of the present day, leading to wide-scale settlement expansion and the intensification of agriculture (Haselgrove 1999: 129). Iron smithing and smelting became increasingly important in the later Iron Age, and there is evidence for some level of standardisation in its production. There is also evidence that salt was an important commodity for trade, and that during the late Iron Age it was transported via a network of distribution from the west Midlands as far north as the Tees valley (*ibid.*: 125-6).

The archaeological perspective on the Iron Age in Britain is dominated by plentiful settlement evidence, from the hillforts of Scotland and the south and west of England, to the open village sized settlements found in eastern England during the later Iron Age. Burials, however, are rare – excarnation or scattering of cremated remains being the favoured methods for disposing of the dead – and are concentrated in a few regions (Cunliffe 1991, Haselgrove 1999).

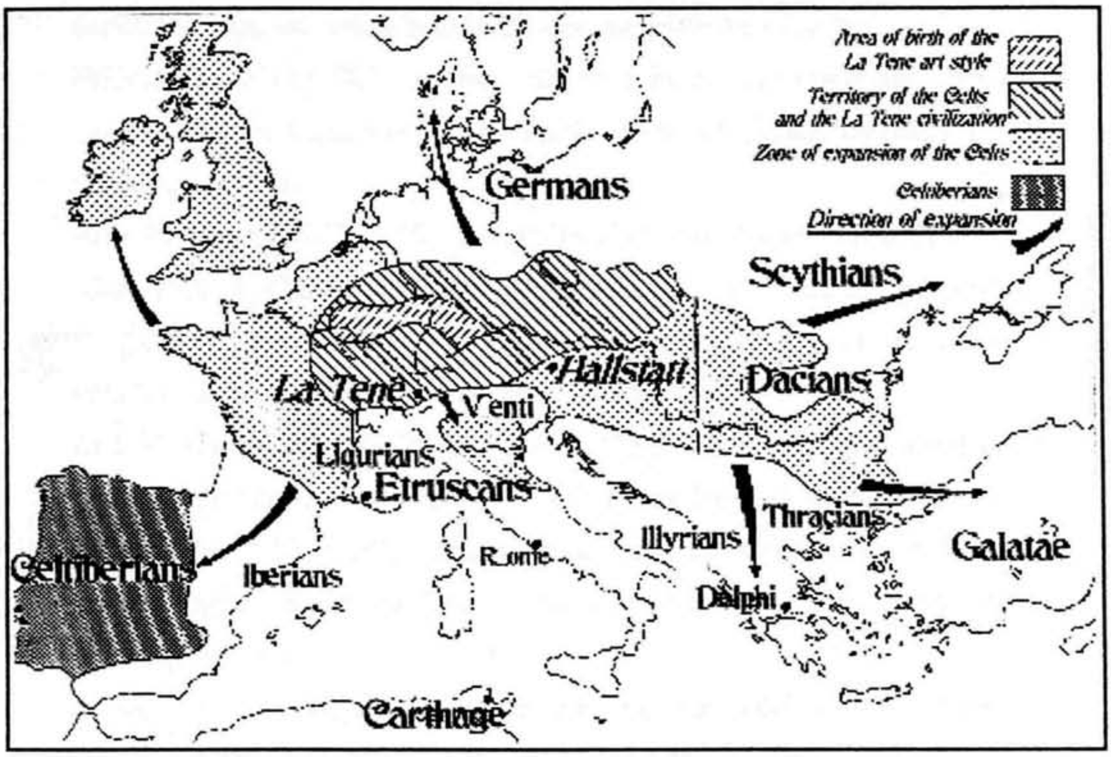
Exceptions to the 'rare burials' rule occur in areas which appear to have strong continental affinities, notably the Arras culture area of East Yorkshire, where individuals were inhumed under small barrows, within rectangular ditched enclosures, often grouped into large cemeteries. Some cemeteries also contain one or more high-status burials accompanied by two-wheeled carts (for example at Wetwang Slack, East Yorkshire). The strong similarities between Arras culture burials in eastern England and those on the continent have long been considered evidence for mass migration from northern France and Switzerland, possibly from as early as the 4th or 5th centuries BC (Stead 1965, 1991, Cunliffe 1991). This 'folk movement' brought new material culture, and ways of burying the dead which, although modified and mediated by local indigenous traditions, remained distinct in Britain for a considerable period of time. Whilst acknowledging arguments that emphasise local change rather than the role of migration, along with the difficulties involved with identifying first generation immigrants in the archaeological record, Cunliffe (1991: 78) writes

> …the Yorkshire evidence is impressive. It suggests small bands arriving [around 400 BC], with little more than their personal equipment, and settling down among the natives in whose pottery traditions they shared. When time came for burial they maintained their own rituals, using a mortuary cart to bring the body to the grave and sometimes burying it with the dead. So strong were these religious practices that they remained dominant for several hundred years.

In recent times, however, many researchers (as is the case with other transitional periods), prefer to suggest that, as with changes in the material culture of the rest of Britain throughout the Iron Age, a wide-scale folk migration is unlikely to have been the cause – it is more likely that a ruling group or 'missionaries' with foreign connections imported the exotic style which was then adopted by the indigenous population (Haselgrove 1999: 123-4, Harding 2004: 35-7).

The general trajectory of the development of the Iron Age throughout Britain, and its linguistic, cultural and technological parallels with continental Europe, has for many years been linked with an outward migration of 'Celts' from the so-called Celtic homelands of central Europe (see figure 2.2). As with so many such cultural movements, however, the reality of this 'folk movement' has recently been cast into doubt; a picture of continuity and trade, or elite driven change, currently being favoured by the academic community at large (see Cunliffe 1991 for a full and comprehensive account of the archaeological and historical evidence, and of changes in explanatory models over time).

Figure 2.2 Celtic homelands and expansion in Europe



(http://www.glamoury.50megs.com/intro.html)

Nevertheless, while the idea of a large-scale invasion is currently unpopular for the Iron Age in general, there is evidence for established trade routes and contact with far-flung regions of the continent – including France, Switzerland, Iberia and the Mediterranean – from even the earliest part of the Iron Age in Britain. This contact seems to have gone into decline for a time in the 3rd and 2nd centuries BC, before reintensifying once again in the 1st (Cunliffe 1991: 442-3).

The evidence supporting migration / invasion models of change appears strongest for the Arras area of East Yorkshire (see above) and also perhaps for parts of southern Britain, where there is some evidence to suggest that one or more migrations of Belgae from northern France may have occurred in the late Iron Age (*ibid.*: 108-110). Others, however, have regarded the evidence for such a migration, and its distribution, with scepticism (e.g. Todd 1985: 28-30).

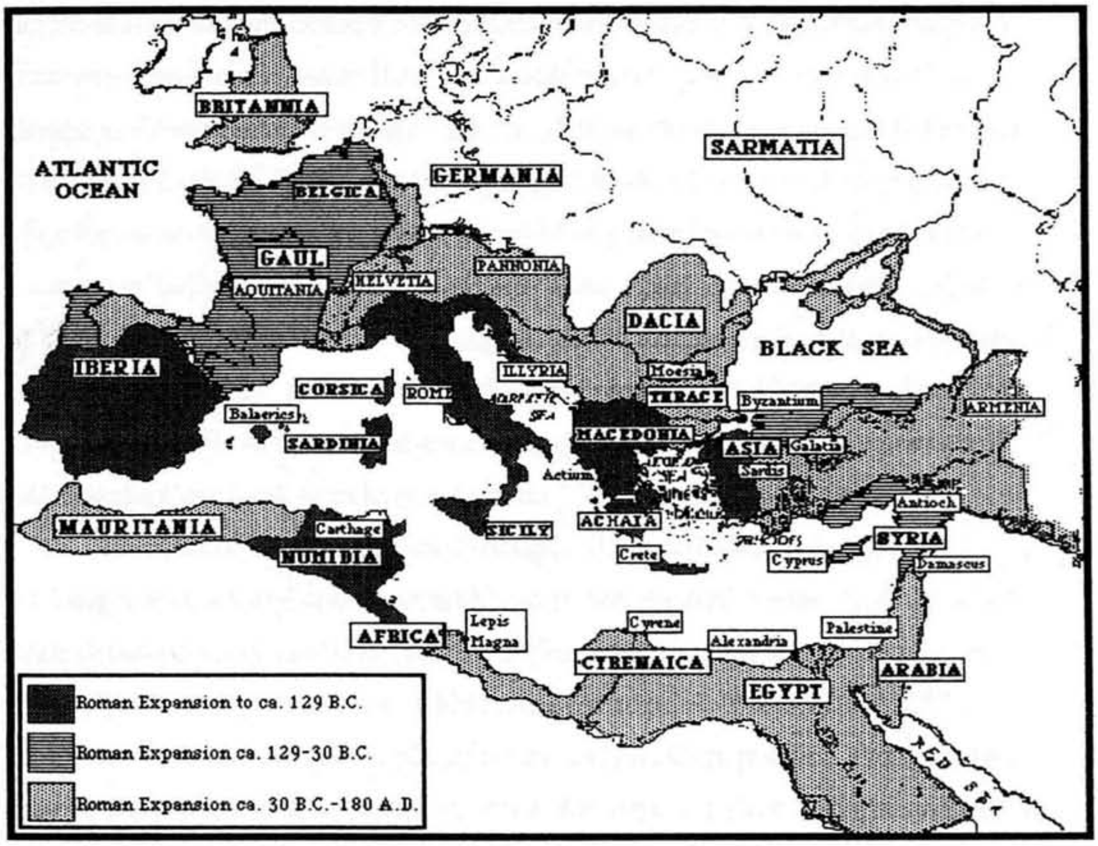
Bearing in mind the earlier points made regarding chronological and regional variation, within Britain archaeological relationships with periodic changes in continental Europe may be summarised thus (Haselgrove 1999: 131):

- Hallstatt C (750-625 BC) – a sudden decline in hoarding and the ritual deposition of metalwork is seen in Britain and north-west Europe.
- Hallstatt D (625-450 BC) – southern British and continental weaponry follow similar fashions, daggers replacing swords, and bow brooches are used for fastening clothing.
- Early La Tène (450-325 BC) – in both Britain and continental Europe the reintroduction of the sword is seen, along with a new style of art. There appear to be close continental links with East Yorkshire, and pottery indicates links between southern England and northern France.
- Middle La Tène (325-150 BC) – evidence of links between Britain and the continent diminish, as a Europe-wide period of regionalism flourishes.
- Late La Tène (150-20 BC) – cross Channel exchange re-intensifies, as Roman imports begin to be seen in Britain, perhaps arriving via an indirect route of exchange networks.
- 20 BC on – Increasing Roman influence is seen, especially in south-eastern England, with increasingly diverse imports and, possibly, early signs of literacy.

2.2.2 The Roman period

The beginning of the first millennium AD brought with it significant and pervasive change to much of Britain when, from 43 AD it became one of the last additions to the then all-powerful Roman Empire (see figure 2.3). Rome (or Roman culture) had been in contact with the British Isles from well before the end of the Iron Age (Haselgrove 1984), and the island had suffered an invasion attempt nearly a century earlier, by Julius Caesar in 55 BC. It was the invasion of 43 AD under the Emperor Claudius, however, which brought at least partial success for the Roman Empire, and substantial change in the political, social, economic and cultural life of the Britons (Todd 1985).

Figure 2.3 The spread of the Roman Empire



(http://www.shsu.edu/~his_ncp/370-11.GIF)

The Roman period is usually dated from the Claudian invasion of 43 AD until some time in the beginning to middle of the 5th century AD. Defining the exact end of the period brings some problems as, theoretically, a number of different 'ends' can be identified (Esmonde Cleary 1999: 173). These include a political and administrative end in around 411 AD when the Roman empire could no longer maintain control in Britain, followed by an economic and military end as the Roman economic system broke down, and finally a material cultural end in the mid 5th century, when Germanic cultures appeared and became dominant (*ibid.*). By 450 AD at any rate the Roman towns were no longer; villas had been abandoned, and Roman pottery and coinage was no longer being made (*ibid.*).

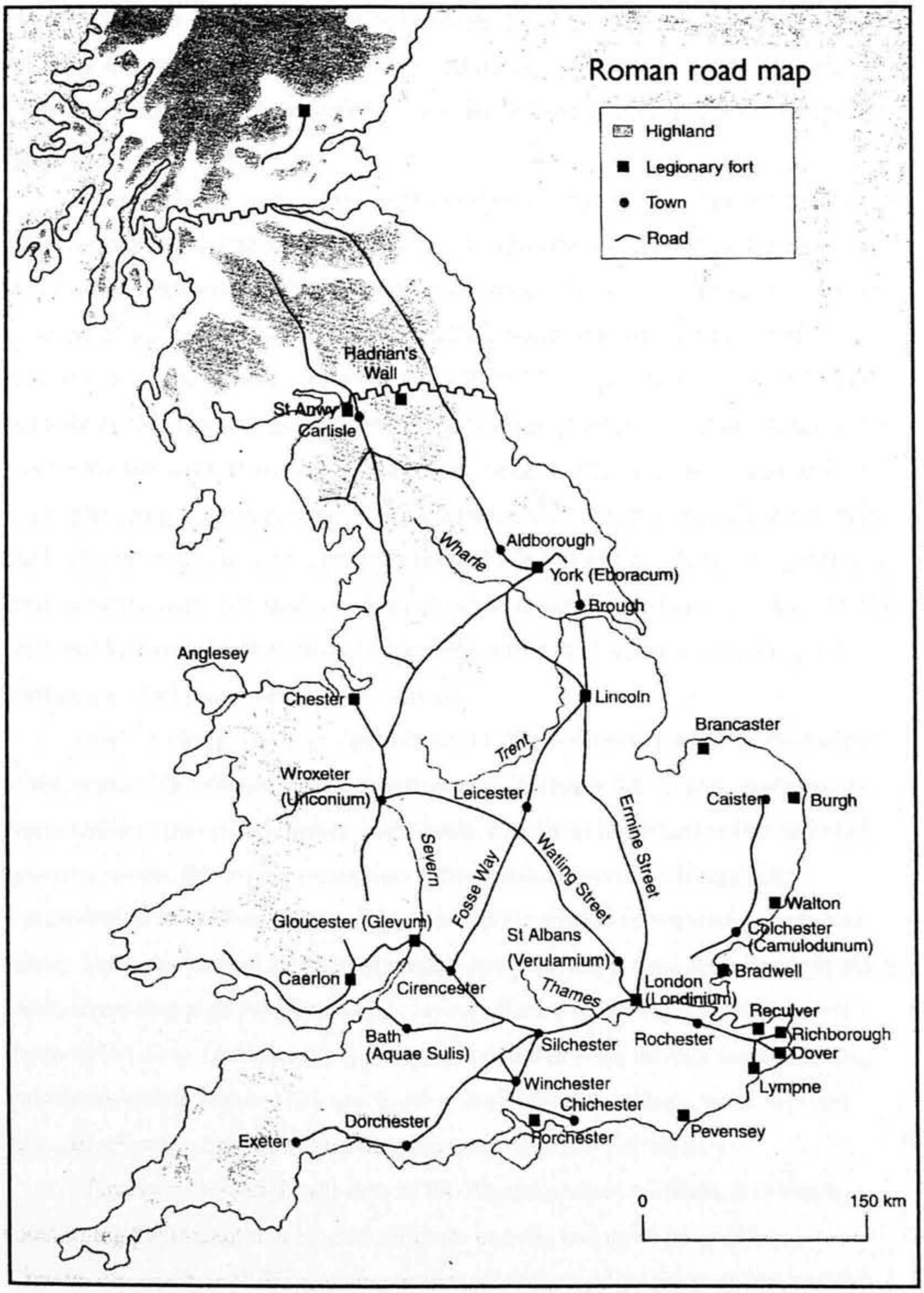
The Roman period may be divided into two parts, which are related to differences in the tempo and direction of cultural change within the period. The earlier part spans the period 43 AD to the end of the 2nd century, and the later from the third century to the collapse of Roman rule and Roman material culture in the middle of the 5th century A.D (*ibid.*: 158). The earlier part may be characterised as a period of conquest and of the Romanisation of the indigenous population and socio-economy from outside, via military and adaptive processes. The later period sees change in Romano-British culture via internal processes and in response to the wider Roman world (*ibid.*). The role of the military in Roman Britain is an important one, often focussed on by archaeologists, however only four legions were used in the conquest of Britain, and by the 80s AD only three remained in permanent fortresses at York, Chester and Caerleon. The majority of the Roman garrison was composed of auxiliary 'non-citizen' soldiers, drawn from the provinces and housed in forts. Over time, the army would have become increasingly Romano-British, via processes of intermarriage and local recruitment (Hanson 1999: 139-147).

The start of the Roman period brought with it significant changes in landscape, monumental and urban architecture and material culture, with the wide scale development of roads, towns, new styles of building and an intellectual and literary phase, many elements of which remain recognisable today (*ibid.*: 157). However, when an emphasis is placed on the indigenous population, these changes may be seen almost as a continuation of the Iron Age, via a Roman influence; the indigenous population making choices about how to adapt to the imperial governance through the adoption of Roman-style behaviour and material expression (*ibid.*).

A key feature of the Roman period in Britain is the emergence of towns (see figure 2.4), and this development is in stark contrast to urban/rural development in Scandinavia, where towns did not develop until the Viking age (Hayward 1995).

Towns were centres for administrative governance, but they were also centres for leisure and social activity, and during the early part of the Roman period were dominated by large public buildings (administrative, baths, theatres, temples). These would have been paid for (and used) not by the Roman authorities, but by the local elites, partly functioning therefore to demonstrate their acceptance of Roman customs and behaviour (Hanson 1999: 161). Although towns were used administratively and socially by the local elite, until the late 2nd century they were occupied mainly by traders and artisans involved in local, national and international commerce, and the dead were buried in cemeteries outside the walls of the town – separating the dead from the world of the living (Lucy 1998). During this time the elite tended to live outside the towns in another distinctive feature of the Roman period – villas. From the late 2nd century, however, the elite began to move into the towns, occupying large town-houses, at which point the public buildings began to fall out of use and the commercial function of towns declined (Hanson 1999: 162).

Figure 2.4 Roman forts, towns and roads



(http://www.nuffieldfoundation.org.uk/fileLibrary/jpg/Romanroadmap.jpg)

Following the decline of the larger towns as centres of trade and industry, there was an increase in the preponderance of 'small towns', which grew up alongside roads, or at important crossroads of communication. These small towns appear to have assumed the role of centres of trade, and to have acted as local 'market-centres'. In contrast to the large towns, these small towns lacked formal planning and public buildings, and were composed largely of shops and workshops. Burials are seen both in cemeteries and within the towns, amongst the dwellings of the living (*ibid.*: 163-4).

As previously noted, villas were an important part of the Roman settlement structure in Britain. The term 'villa' is used to describe any rural building in the Roman style. However such structures vary considerably in size, and date – from the 1st to the 5th centuries AD, suggesting that their social significance, form and function varied substantially through time (*ibid.*: 166). Apart from towns and villas (significant, but relevant only to a minority of the population of Roman Britain), the most important settlement type in this period remained the rural farmstead, as it was in the preceding Iron Age. Most of these settlements were small and dispersed as in the Iron Age, although some appear to be structured in nucleated, linear, village-like arrangements. Although there is evidence for some continuity from the Iron Age, it is clear that settlements were subject to periodic shifts in location and the design of boundaries and field-systems (*ibid.*: 164-6).

Also as in the Iron Age, agriculture was the main occupation for the majority of the population with considerable Iron Age to Romano-British continuity evident, many staple crops (wheat, barley, oats) being equally as important in this as in the previous period. Some new crops were introduced, however, reflecting the Romanisation of cuisine, and these included new varieties of vegetable, herbs and spices. Domestic animal species also reflect the previous period, with an emphasis on cattle, sheep and pigs, but with an increasing reliance on cattle, at the expense of sheep (*ibid.*: 171). Gold, lead, copper and tin deposits were heavily worked during the Roman period (*ibid.*: 172), and trade – of metals, salt, pottery, wine, oils and agricultural products – was extremely important (Todd 1985: 192-3).

Finally in this brief overview of the Roman period in Britain, it is worth mentioning the impact that Roman religions or cults had on the population. Christianity was one of the most important cults imported by the Romans, and there is evidence for it being relatively important for the urban elite and rural land-owning classes by the 4th century AD. Its impact on the general population, however, is less clear, as the east-west burial orientation without grave goods, often cited as evidence of Christianity, appears merely to reflect a general late Roman burial rite, and is not necessarily related to an adoption of Christianity by the masses (Hanson 1999: 168).

Unlike the Iron Age and the Anglo-Saxon period in Britain, very little attention has been given to population change and the movement of people(s) in the Roman period. Research has focussed on military and civilian life, and any attention to the role of the movement of people has been aimed at unravelling details of the interaction between these two groups – the Roman soldiers and the indigenous inhabitants of Britain. The same changes in academic focus have nevertheless had an effect in this period as in others, in that the emphasis has shifted away from external causes of social and cultural change, toward a focus on internal indigenous processes and continuity (Esmonde Cleary 1999, Hanson 1999).

In terms of burial archaeology (and cemeteries are plentiful in this period), even identifying soldier and civilian is problematic, as in most urban areas, civilians and military individuals appear to have been buried in the same cemeteries, with little distinction made between the two. This is usually taken to indicate the integration of Roman military personnel into Romano-British society (Jones 1984: 223) – a process which would also lead, as has already been noted, to intermarriage and the Romano-British-isation of the military. From the perspective of the present research, therefore, while there is no reason to suspect any large-scale biological change in the population of Britain in general during this period, it must be noted that the urban samples may be made up of an unknown combination of local indigenous civilians and military personnel, whose continental origins were potentially diverse. Further comments on the specific samples used in this study are made in Chapter 3.

2.2.3 The Anglo-Saxon period

As the central focus of this research, the Anglo-Saxon period will be considered in more detail than other periods considered here, and sections 2.2.3.1 and 2.2.3.2 are given over to the historical and archaeological evidence respectively.

Following the early 5th century collapse of Roman rule in Britain, changes began to take place, especially in terms of the decay of towns, and the disappearance of distinctively Roman material culture, as described in the previous section. In the middle of the 5th century, a dramatic transformation occurred, with the sudden appearance of an apparently entirely intrusive Germanic culture. This influenced all spheres of Britain's culture and settlement, but especially (and most visibly in the archaeological record) the manner in which the dead were buried.

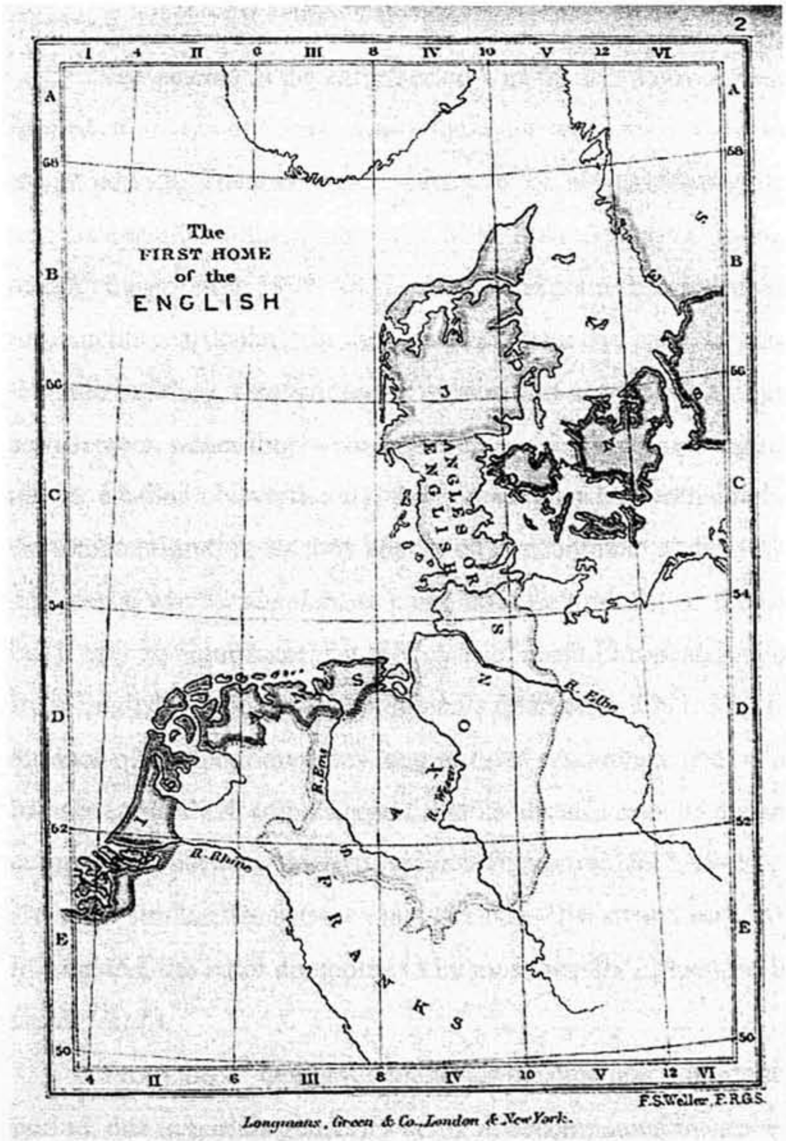
Many different names have been given to this period, including the Dark Ages, the Anglo-Saxon period, the early historical period, the early medieval period, and the migration period. Many of these terms have connotations which reveal inherently particular perspectives, and some are plain misleading as to the nature of the period (Hills 1999: 176-178). In this thesis, the term *Anglo-Saxon period* is used. The period spans around six hundred years, the 'start' date usually coinciding with the *adventus Saxonum* recorded in historical documents as occurring in 449 AD, and ends with the Norman conquest in 1066 AD, thus overlapping with the Viking Age in Britain (see following section). The term 'Anglo-Saxon England', however, is only really applicable to the east and south of Britain in this period, as in the north and some parts of the west the Germanic impact was less (as indeed was Roman influence), and there is much more evidence for Iron-Age or sub-Roman continuity. The period may be divided into at least two phases; an early (pagan) phase dating from the mid 5th century AD and a later (Christian) phase from the 8th century AD up to the Norman conquest. Some scholars prefer a three-phase division covering early (~450-650 AD), middle (650-800 AD) and late (800-1066 AD) phases (*ibid.*: 176).

In contrast to the earlier periods examined in this section, there are a few major narrative sources available for the Anglo-Saxon period (particularly Gildas' *De Excidio* and Bede's *Historia Ecclesiastica* – see section 2.2.3.1 for a more detailed discussion of these sources) which tell the story of a mass Germanic invasion, migration and settlement of the eastern portion of the British Isles in the middle of the 5th century. Three main tribes, the Angles, Saxons and Jutes were involved, and are described as originating from homelands in modern-day north Germany, Denmark and The Netherlands (figure 2.5).

Rather than representing an indigenous development, early Anglo-Saxon burials strongly resemble those from parts of northern Germany and Denmark. Particularly, the large cremation cemeteries in the east of England (principally in Norfolk, Nottinghamshire, Lincolnshire and Yorkshire) contain pottery and grave goods which appear very closely related to those from Schleswig Holstein and Lower Saxony (e.g. Welch 1992, Hills 1999). However it is unclear whether these burials represent a large number of intrusive migrants from the continent, or rather indigenous peoples who, through contacts with the continent, had adopted customs relating to religion, goods, ideas and so on for social or political reasons.

In southern parts of England cremation cemeteries are not so significant, and the practice had been abandoned by around 600 AD. Inhumations were, however, richly furnished in many cases, with weapons, brooches and jewellery. It has been noted that regional variations in dress-fasteners appear to reflect the ethnic divisions between Angles, Saxons and Jutes described in the narrative sources, although these variations may well be more complex than they first appear and are possibly not solely due to the impact of early 5th century events (Crawford 1997, Hills 1999: 184).

Figure 2.5 The historical settlements of the Anglo-Saxons



(Map after http://www.livgenmi.com/gardiner2.htm)

In terms of the archaeological evidence, most weight has been placed on early Anglo-Saxon cemeteries, visible as they are, and comparably little on Anglo-Saxon settlements which, given the decline in the use of towns following the collapse of Roman rule in Britain, are rural and, until recently, rarely located or excavated. However, the locations of many are now known through survey and aerial reconnaissance and a handful have been extensively and thoroughly excavated and assessed (e.g. at West Heslerton, East Yorkshire; Powlesland 1987). Archaeological evidence indicates a relatively high population density in lowland areas during the early Anglo-Saxon period and, apart from the changes in building style and settlement planning noted below, there is considerable continuity apparent in terms of land use and agricultural techniques from the Roman period (Crabtree 1989, Hamerow 1997, Hills 1999).

Settlements in the early period – as far as is known – seem to have been formed of groups of farms, whose locations were subject to periodic shift, as in earlier periods. There is some evidence from West Heslerton that the settlement there was designed on a functional basis, with a planned layout more like that of a town than a village (Hills 1999: 187). One of the main features of Anglo-Saxon settlements (particularly in the east of the country) is the *Grubenhaus*, or sunken featured building. *Grubenhauser* were in fact not the most important buildings within a settlement, rather they were subsidiary to the large, rectangular 'halls', which did not have cellars. Nevertheless, their appearance has been cited as evidence for Germanic migration, as they appear on the continent as early as the 2nd century. It is not known why *Grubenhauser* came into use initially, on the continent or in England, but it may be significant that the 'classic' north European longhouse is not known from English Anglo-Saxon settlements (Hamerow 1997: 37, Hills 1999: 187). The absence of the longhouse has long puzzled researchers and, while no firm answers have been reached, some suggest that its absence may be due to differences in social composition between the two regions (Hamerow 1997: 39-40). However, while there are some similarities between late Romano-British and early Anglo-Saxon 'houses' in England, the latter do appear to be most heavily influenced by continental building styles (*ibid.*).

From the 7th century, cemeteries become less important as evidence for the period, due to burials generally being unaccompanied by grave goods in a Christian fashion, and more emphasis is placed on the manuscripts, churches and sculpture of the period, and the re-emergence of towns as an important factor in trade, the economy and the administration of Anglo-Saxon kingdoms (Hills 1999: 179).

There is evidence that trade continued at some level during the early Anglo-Saxon period, and Mediterranean pottery, ivory, glass and bronze are all known to have been imported. However no permanent market sites are known from this period, and it is only from the 700s onward that trading places once again emerge on both sides of the North Sea. Coins, which had also gone out of use at the end of the Roman period were reintroduced in the late 7th century, with the introduction of the Northumbrian *sceattas* (*ibid.*: 191).

2.2.3.1 Historical sources: interpretations

> The race of the Angles or Saxons, invited by Vortigern, came to Britain in three warships… They came from three very powerful Germanic tribes, the Saxons, Angles and Jutes. The people of Kent and the inhabitants of the Isle of Wight are of Jutish origin, and also those opposite the Isle of Wight, that part of the kingdom of Wessex which is still today called the nation of the Jutes. From the Saxon country, that is, the district now known as Old Saxony, came the East Saxons, the South Saxons, and the West Saxons. Besides this, from the country of the Angles, that is, the land between the kingdoms of the Jutes and the Saxons, which is called *Angulus*, came the East Angles, the Middle Angles, the Mercians, and all the Northumbrian race (that is those people who dwell north of the river Humber) as well as the other Anglian tribes. *Angulus* is said to have remained deserted from that day to this. (Bede, *Historia Ecclesiastica* I. 15. In Frazer and Tyrrell (eds) 2000: 28)

This famous passage was written by the monk known as the Venerable Bede in the *Historia Ecclesiastica*, which was completed in 731 AD. Its message is clear – Britain was invaded by the Angles and Saxons, who arrived *en masse* in the mid 5th century AD. Bede's writings are one of the major sources of historical documentation of the time (although he was writing some 300 years after the supposed events took place) and were heavily influenced by the works of Gildas, whose *De excidio Britannae et conquestu* begins covering events in Britain in the 4th century AD, and continues into Gildas' own day, thought to be sometime in the 6th century AD. According to Gildas, in the 4th century AD the people of Britain came under repeated attack by the Picts and Scots, at a time when the Roman armies had withdrawn from Britain. Saxon mercenaries were invited to defend Britain, however the visiting mercenaries became more and more demanding of their hosts, eventually turning on the British, breaking their protective stance in favour of a savage attack on the towns, villages and inhabitants of the land. Many indigenous Britons were slaughtered, the survivors turning tail, and making for the safety of the mountains, only to be captured and enslaved (Winterbottom 1978 cited in Lucy 2000: 156).

While neither of these two writers provides a contemporaneous account of the events happening in Britain in the 5th century AD, these are the earliest and most detailed historical records available, and have thus been extremely influential in shaping our understanding of this period. Their perspective is still taught to the schoolchildren of the 21st century, and provides a starting point for most researchers interested in the Romano-British / Anglo-Saxon transition.

The descriptions of events given by Gildas and Bede were for many years taken as fact, and early researchers endeavoured to fit the archaeological evidence to the historical sources. In recent decades, however, academic and socio-political emphases have changed, and the historical sources have been re-examined in the light of their contemporary socio-political and cultural influences. Whilst not dismissing the value of the documentary sources entirely, researchers now understand them to be products of a very specific period in Britain's history, imbued with the writers' own morals and motives (but see section 2.9 and Hamerow 1997 for a review of the impact of researchers' own subjectivity in shaping the Anglo-Saxon debate). For example Higham (1992: 157) writes "Does Gildas' account deserve any credence? […] Gildas was uninterested in history for its own sake but he used his own expurgated and partial account of the recent past to underline the sinfulness of the Britons and the plenitude of God's power, so as to reinforce and make terrible his strictures concerning the present."

As a result of this recent reinterpretation, the historical sources are now considered (by many but by no means all) to be of little use as strictly factual sources, but of more use in teaching us about the social and political climate of the periods in which they were compiled. As such, some researchers regard them as little more than records containing first-hand information about the origin myths, legends and traditions of the British (e.g. Lucy 2000).

That Gildas' *De Excidio*, Bede's *Historia Ecclesiastica*, and the *Anglo-Saxon Chronicles* are less than reliable accounts, as regards the actual events of the early Anglo-Saxon period in Britain, is nowadays considered beyond doubt. Despite this, they represent extremely important documentary sources regarding the Romano-British / Anglo-Saxon transition, and have, as noted above, for many centuries been treated as factual documentary evidence. As John Moreland comments (2000: 28), regarding the impact of the passage by Bede quoted above, "This is the account of the Anglo-Saxon settlement which has so beguiled generations of archaeologists, historians, politicians and Churchmen. It provides the historical context within which many archaeologists have sought to situate their evidence". The documentary sources, then, are largely responsible for the long-standing assumption that the Romano-British / Anglo-Saxon transition was biologically based, the Anglo-Saxon immigrants / invaders producing the change subsequently seen in archaeological material culture, which will be discussed next. This, perhaps unconscious, assumption has impacted greatly on the ways that other historians have represented the history of Britain, and the ways in which researchers in other disciplines have gone about collecting and interpreting evidence regarding this period. As Lucy notes, "The 'Coming of the Saxons' is now so much a part of our national mythology that it is often not realised that the origins of the people who lived in the eastern and southern part of Britain, now known as the English, have not always been traced back to Germanic invaders or migrants from the continent" (2000: 158).

2.2.3.2 Archaeological material: interpretations

As noted previously, for many decades (indeed for centuries), archaeological evidence was situated within the frameworks for the Anglo-Saxon transition provided by the writers discussed above. In the latter half of the 20th century, thinking about these sources changed fundamentally, and archaeological research began to focus on context, process and patterning, rather than on 'fitting in' with historians' views of events. The argument over the biological identity of the people of 5th century Britain has since been played down, in favour of the more 'anthropological' (and arguably less controversial) aim of identifying and understanding evidence for the construction and maintenance of social identity in the early medieval period.

The 'mass migration' described by Gildas and Bede remains important to some researchers, however, and archaeological perspectives on the Anglo-Saxon transition may still be split into two main camps; those who maintain that the transition was caused by a mass migration of Angles and Saxons from continental Europe (biological, population movement based change) as per Gildas and Bede, versus those who propose an 'acculturation' process, perhaps involving only the migration into Britain of warriors and, perhaps, elite individuals. Both sides of this debate remain reasonably well represented, although the latter is currently (despite advances being made in recent archaeogenetic work) far more popular.

From a 'pro-migration' perspective, Martin Welch states in his introduction to *Anglo-Saxon England* that "the first three centuries (c. 400-700) [of the Anglo-Saxon period] is the crucial period of settlement and conquest by Angles, Saxons, Jutes and other peoples from north Germany and south Scandinavia. They created England, the land of the Angles, from Lowland Britain" (1992: 9).

Despite acknowledging the problems associated with the historical sources, and with certain interpretations of the archaeology, Welch criticises some archaeologists for refusing to believe that more than a few immigrants from Germany and Scandinavia were involved in the transition. Such archaeologists, he suggests, prefer instead to favour those interpretations which emphasise the role of small warrior bands successfully gaining control of British regional kingdoms (*ibid.*: 11). Welch's criticisms are based on the viewpoint that, whilst historical sources should be treated with care, the 'small-bands' theory "argues that we know much better than both contemporary and slightly later commentators who wrote about events in Britain" (*ibid.*). He argues additionally that pottery and brooches found in Anglo-Saxon contexts in Britain "can be matched precisely back to those regions of north Germany and south Scandinavia which were their continental homelands according to Bede" (*ibid.*).

Welch continues his argument by suggesting that the presence of regional continental 'folk-costumes', as seen in female Anglo-Saxon graves, does not tie in with the argument that it was small warrior groups who instigated the cultural transition; rather it indicates that "many Anglo-Saxon men brought their wives and families with them across the North Sea" (*ibid.*). He does go on to note, however, that such artefacts may not be used to determine the biological proportion of Britons in Anglo-Saxon cemeteries. Welch also sees the introduction of cremation cemeteries in Britain as an undeniable indicator of the presence of Anglo-Saxons, suggesting that comparisons between the vessels and goods involved in cremations in England, and those on the continent, indicate a clear match. "Surely this must suggest the movement of complete families and communities across the North Sea, rather than rapid adoption by the native population of burial practices introduced by a few newcomers" (*ibid.*: 12). Welch reinforces his argument by citing linguistic and place-name evidence as indicative of a large-scale migration. That the language of the Britons (Celtic) was replaced by English (related to Germanic languages), and that this replacement extended to place-names, he suggests, indicates that Anglo-Saxon settled in some numbers as farmers, rather than simply as land-lords (*ibid.*).

Welch's reasoning and hypothesis, while remaining popular amongst some academics and in popular thought, have been strongly criticised on a number of grounds, most notably on those which condemn the equation of cultural artefacts with biological ancestry. John Moreland (2000: 28) notes that Welch's approach is essentially the same as that used by the typologists of the 19th and early 20th centuries, in which matches between English and continental material are sought and found, and subsequently labelled according to the 'ethnic names' derived from the historical sources. This approach has the unfortunate effect of ascribing – intentionally or otherwise – a homogeneity to these 'ethnic' groups which, to many theoreticians, is entirely inappropriate. As Moreland (*ibid.*: 35) remarks, "Contrary to common understanding, it would be a gross error to assume that the Angles, Saxons and Jutes possessed discrete identities in their so-called homelands and maintained them in the early part of their settlement in England."

Welch's approach to the problem, suggests Moreland, is trapped within the 'culture-history' approach, which seeks to match archaeological evidence to historical sources, serving to construct "a racial and ethnocentric view of early English history" (*ibid.*: 29). Moreland also notes that, while it is often implied that clear cultural divisions may be seen regionally in the material culture of the Anglo-Saxon period (which are associated with the 'tribes' of the *adventus*) such distinctions may in fact be far less important than has previously been suggested (*ibid.*: 33). He supports this assertion by pointing out that "While it is the case that there are parts of England where so-called Anglian or Saxon material predominates, this is not always true" (*ibid.*). The presence of 'Saxon' material from north of the Humber to Sussex, and the mixture of Saxon types with Anglian material in East Anglia suggests that the idea of (and the search for) bounded regional identities may be, indeed should be, dismissed from the interpretation of the archaeology (*ibid.*).

Opposing the theories involving substantial migration, such as those proposed by Welch, are those which suggest that the Anglo-Saxon transition was brought about by the impact of a relatively small number of immigrants. In *Rome, Britain and the Anglo-Saxons*, for example, Higham proposes a hypothesis that "allows for massive ethnic continuity from late Roman Britain to Anglo-Saxon England [...] from the weighing of evidence of different kinds so as to arrive at a balance of probability" (1992: 209). Higham suggests that at the end of the Roman period in Britain, falls in production and population, and the 'onerous scale' of taxation, led to the decline, in the first half of the fifth century, of the material culture which had been characteristic of Roman Britain (*ibid.*: 214, 216). Increasing threats from the Scots and Picts led to the involvement of Barbarian warriors in the defence of the British elite, which subsequently, just as Gildas suggested, turned sour. Higham (*ibid.*: 223-4) goes on to suggest that

> ...the fight back by the Britons was too little and too late to save the British lowlands for an indigenous society and culture which had been heavily influenced by Romanisation and which thereafter failed to adapt sufficiently rapidly to the radically changed circumstances of the fifth century. Anglo-Saxon warriors rolled up the more westerly areas of the lowland zone during the sixth and seventh centuries, without meeting effective military opposition. [...] When pressurised by raiders or settlers from outside, local societies could not rely on the levels of social and cultural cohesion which already existed or were now developing in upland societies. Without a cohesive ideology, language or culture, and exposed to incomers by the accidents of geography and a long history of cultural receptiveness, the lowlanders were ill-placed to resist even small bands of determined and competent warriors.

Regarding the mortuary evidence, Higham proposes that the distinctive forms of cremation and inhumation seen in the cemeteries of the early Anglo-Saxon period were indeed imported by immigrants and invaders. The success of these forms of burial throughout the wider population, however, owed more to the efficiency with which they advertised the social and ideological affinities of the deceased – useful indeed for those Britons attempting to 'fit in' with their new Anglo-Saxon rulers (*ibid.*: 225). Links between settlers in Britain, and their counterparts on the continent, encouraged the transfer of fashions, ideology, weapons and other cultural artefacts; a process that Higham describes as 'characteristic' of the Germanic societies in question (*ibid.*).

The adoption of the language, material culture and traditions of the new Anglo-Saxon elite, "by large numbers of the local people seeking to improve their status within the social structure, and undertaking for this purpose rigorous acculturation" (*ibid.*: 229), is the key to understanding the Romano-British / Anglo-Saxon transition, according to Higham. The progressive nature of this acculturation, and the 'retrospective reworking' of kinship ties to the dominant group led, ultimately, to the "myths which tied the entire society to immigration as an explanation of their origins in Britain" (*ibid.*: 230). This explains the conviction of later medieval historians (such as Bede) that their ancestral origins were not with the British, but rather with the Germanic invaders of the early Anglo-Saxon period.

Through this hypothesis, then, Higham seeks to account for the demise of the Romano-British material culture in Britain, the adoption of Anglo-Saxon culture and language, and the belief of Bede that the people of England largely derived from earlier settlers, *without* requiring large scale invasion or migration.

Such theories, whilst gaining considerable appreciation over the biologically based theories of mass migration described previously, are still debated by those seeking to theorise approaches to the Anglo-Saxon period. There remains, even in Higham's approach, a strong emphasis on the historical sources in order to interpret the archaeology of the period, and, perhaps just as problematic, a continued reliance on the nature of the incoming cultures as representing 'bounded', homogenous, and cohesive ethnic identities (Moreland 2000: 42).

More recently, and in an academic atmosphere which is becoming once again more amenable to models which invoke migration and invasion as instigators of change, Stefan Burmeister (2000) applied his 'approaches to an archaeological proof of migration' to the Romano-British / Anglo-Saxon problem. Burmeister takes on board the 'new' approach to investigating prehistoric migrations (see section 2.9 and, for example, Chapman & Hamerow 1997) which rejects the 'retreat from migration' seen in archaeology since the 1960s on the basis that it was founded on untenable premises.

Burmeister notes not only the similarities between British and continental material culture, but also evidence for the abandonment of regions of northern Germany and Denmark from the 2nd century AD, and for a decline in the number of men overall, and of individuals in the 20-40 age group, in these continental regions. This evidence, along with an analysis of the 'push factors' of flooding and climate change, evidence of declining health (indicated by an increase in Harris lines – markers often interpreted as indicative of periods of physiological stress, resulting in arrested growth – in the skeletal material), changes in status and hierarchy structures on the continent and "evidence of a [limited] cultural reflux from England for the second half of the 5th and the beginning of the 6th century" (2000: 549) add up to compelling support for models proposing a substantial migration out of northern

Germany and Denmark to Britain in this period. Added to the evidence from continental Europe, Burmeister suggests that a long-term history (i.e. a tendency for) of migration, and the abandonment of Britain by the Romans in the 5th century may have been deciding factors in triggering the migration.

Despite the rather compelling evidence for the migration of kinship groups (i.e. families, not just elite individuals or warriors), Burmeister does advocate caution, in that the picture drawn by the evidence from the relevant parts of the continent is constantly changing, as more discoveries are made which emphasise continuing settlement rather than complete abandonment of some regions.

Also in 2000, and emphasising the likelihood of extensive migration (although certainly not complete replacement of the indigenous population) in the Anglo-Saxon period, Ward Perkins asks "why did the Anglo-Saxons not become more British?" Ward-Perkins is, at least partially, asking one of the questions which has most vexed researchers of this period, which is how and why, if the migration / invasion was less substantial than was at one time thought, did Anglo-Saxon culture, language and social structure so completely replace the native Romano-British culture, language and social structure? He notes that in contrast to similar 'invasions' or influxes of Germanic peoples to other areas of continental Europe (in particular with regard to the invasion and settlement of Gaul by the Franks), the incoming Anglo-Saxons in Britain were particularly notable for their almost complete failure to absorb any of the native culture or language of the indigenous population. Instead, and "by an act of supreme arrogance, they even termed the Britons '*wealas'*, or 'foreigners' in their own island" (2000: 514). Their own pagan religion was retained for a considerable time, and British and Anglo-Saxon genealogies when eventually written were kept distinct.

The explanation, suggests Ward-Perkins, lies in the nature of the process of the Anglo-Saxon invasion, and also in those factors which would have encouraged the native Britons to appropriate Anglo-Saxon identity so fully. Firstly, the abandonment of Britain by Rome and the complete disappearance of the Roman way of life predisposed the Romano-British population to being receptive of the incoming culture. In addition, Anglo-Saxon laws and systems of taxation favoured those who had at least appropriated the new identity, and would have provided an incentive favouring acculturation. Secondly, British culture was seen as inferior; "When invaders find a native culture that they feel to be superior to their own, they borrow heavily and readily from it, as happened among the Franks in romanized Gaul; but when, as in Britain, they find a culture that they, rightly or wrongly, perceive to be inferior, the story is very different" (*ibid.*: 530). Thirdly, and perhaps most importantly, the de-Romanisation of Britain seems to have led to an at least partial return to tribalism, which in itself may have meant that native resistance to the Germanic invaders was relatively strong. The strength of this resistance, and the long-standing antagonism that would have ensued, could explain why Anglo-Saxon identity was so important – it provided a cultural, social and linguistic unity that with very few exceptions totally excluded and devalued the native Romano-British traditions.

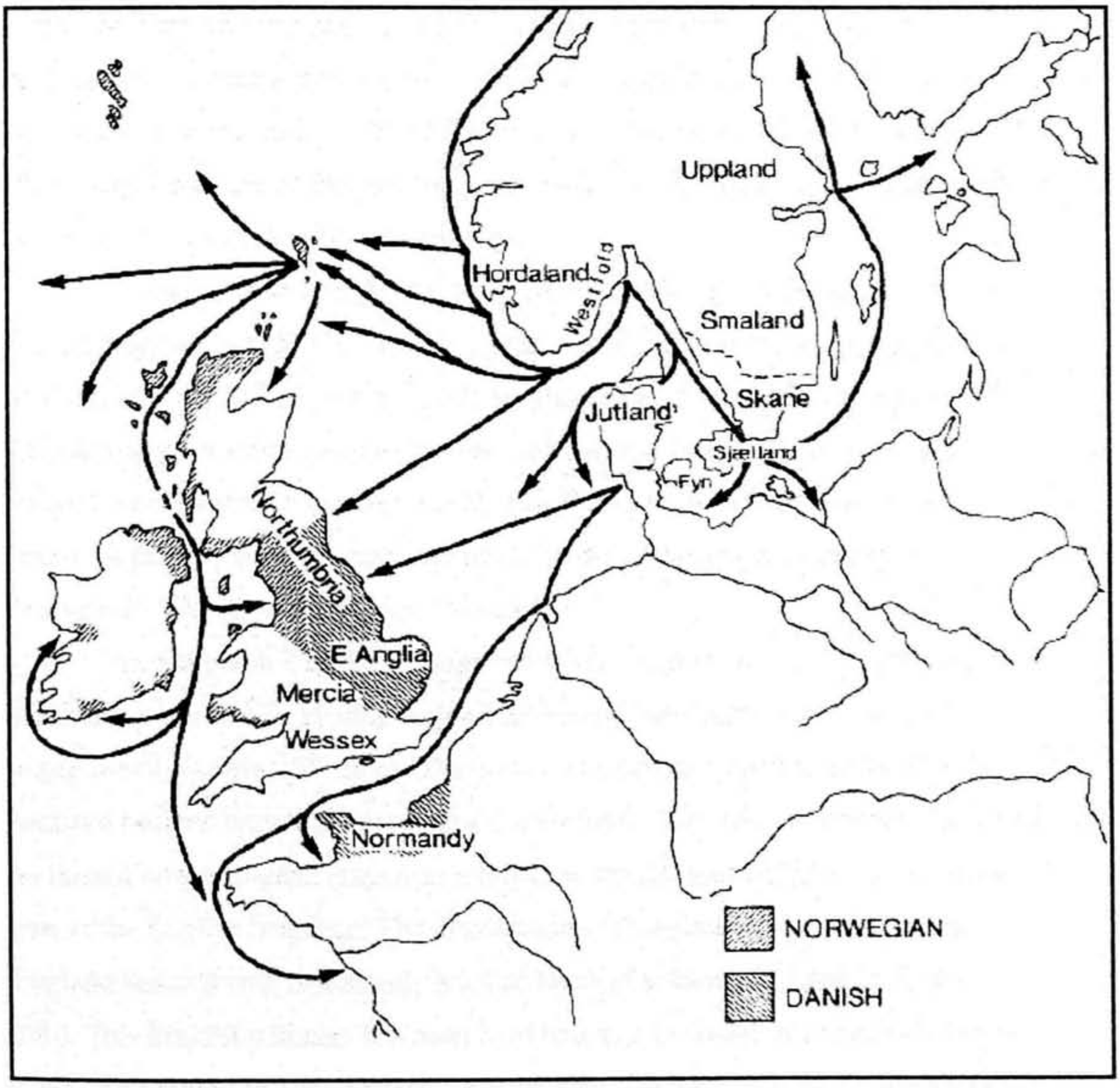
2.2.4 The Viking period

The word 'Viking', now used to refer to both Scandinavian invaders in the 9th to 11th centuries, and a concomitant period of time in British history, is thought to derive from the Old Icelandic verb *vikya* meaning 'to turn aside' – possibly used to describe individuals or groups who were away from home (Richards 1991: 9). *Víkingr* came to be used to describe a warrior, or pirate, and *víking* referred to an expedition. Those Scandinavians who went 'a-viking', therefore, were probably the original (and true) Vikings of the period (*ibid.*: 10). Originally, the term '*wicing*' appears to have been used to describe small raider bands, as opposed to large-scale invasion or settlement forces (for example in the Anglo-Saxon Chronicle), and the term as it is used nowadays only came into common use to describe Scandinavian settlers in the 19th and 20th centuries (*ibid.*: 10). Contemporary chroniclers referred to the invaders by various names used, seemingly, interchangeably, such as 'Norse', 'Danes' or 'heathens' (Richards 1999: 195).

'The Vikings' as we understand them currently, probably comprised individuals from many countries, predominantly originating from Sweden, Norway and Denmark. Their most remarkable feat may be considered to be the astonishing geographical extent of their cultural domination, from the coast of Newfoundland, to Greenland, Iceland, Britain and into eastern Europe. Danish Vikings are thought to have been predominantly responsible for the invasion and settlement of eastern England, while Norwegian invaders settled in the west of England, and the north of Britain (see figure 2.6) (*ibid.*: 207).

The precise cause of the 'Viking expansion' is not known, although theories abound, focussing on Scandinavian population pressure, worsening climate and/or the ship-building skills of the Viking Age population of Scandinavia (*ibid.*: 207). According to Richards the most likely reason might include elements of all the above, but may centre on the structure of Viking Age society, and the importance of wealth and resources in terms of 'gifts' given and received for the purpose of maintaining the hierarchy of social and political status (*ibid.*: 207).

Figure 2.6 Viking expansion 800-1050 AD



(Richards 1991: 10)

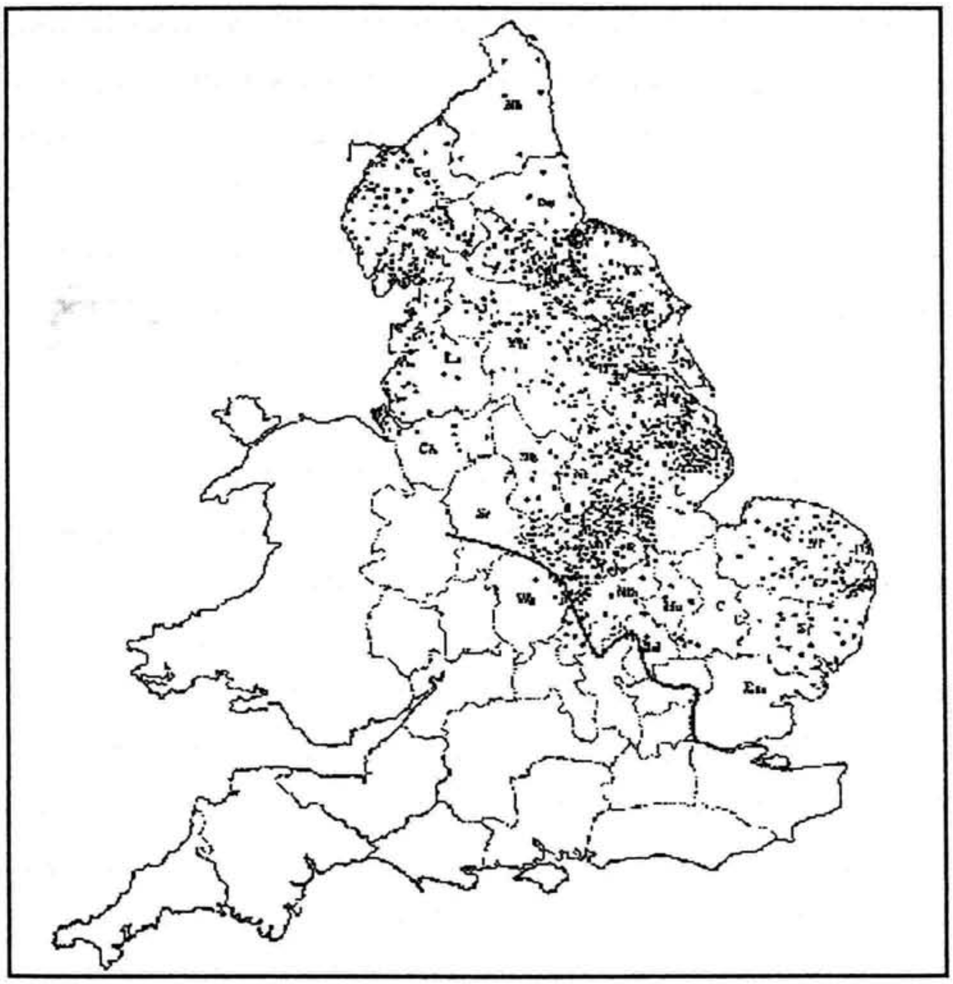
Richards' thesis is that dwindling resources led to internal pressures within Viking Age society, causing some members of the population to look elsewhere for sources of wealth. The wealth of the Anglo-Saxon monastic community may have been an initial draw to the shores of Britain, only later developing into a desire for territorial (taxable) control (*ibid.*: 207).

Whatever the draw, the Vikings became part of life in Britain in spectacular fashion when, in 793 AD, the monastery at Lindisfarne (Holy Island) was raided and ransacked by Viking plunderers, many monks being killed or captured in the process. Four years earlier three Viking ships from Norway had raided Portland – however the raid on Lindisfarne was particularly fear-inducing as it had been against one of the most holy sites in Britain. If God had not been able to protect Lindisfarne, what hope was there for the rest of the country?! (Hayward 1995: 50-51) A period of raiding by small fleets in uncoordinated attacks on the British Isles ensued, and continued for some time following the attack on Lindisfarne, but in the middle of the 9th century the nature of the incursions changed, and the conquest and subsequent settlement of Britain by the Vikings began.

According to the Anglo-Saxon Chronicle, a Danish 'great army' invaded eastern England in 865 AD, capturing York in 866, and eventually conquering (and settling) territory including Northumbria, Mercia and East Anglia during the 870s. This territory became known as the Danelaw (Richards 1999: 194). Elsewhere, Iceland was simultaneously being settled by the Vikings in what appears to have been a largely peaceful process, and north-western England was settled by Norwegian Vikings from around 900 AD.

The appearance of the Vikings had a huge impact on Britain; existing power structures were broken up, and Anglo-Saxon kingdoms eliminated (with the exception of Wessex), When the Danelaw was ultimately conquered by Wessex, England became united under a single crown for the first time. The settlers also had an impact on the English language; many loan words from Old Danish becoming part of the English language. The distribution of Scandinavian place-names in England accords with historically attested areas of settlement (figure 2.7) (*ibid.*: 196). This linguistic impact has been used to argue in favour of a relatively large-scale immigration of Scandinavian settlers, although there is some debate about just how many individuals are required to effect linguistic change, given the differences in status which may have existed between locals and (politically and economically dominant) incomers (*ibid.*: 196).

Figure 2.7 Scandinavian place names in Britain



(http://www.sharp.arts.gla.ac.uk/issue2/yokota.htm)

It is also probable that the presence of the Vikings encouraged the development of urbanisation alongside increased and developed trade relationships (Hayward 1995: 52-53, Hall 2000). Viking-Age York (Yorvik), for example (which along with many urban centres in Britain had fallen into disrepair following the collapse of Roman rule in England), was subject to Danish settlement from around 886 AD, and by 1000 AD probably had a population of around 10,000 – a large population by the standards of early medieval Europe – and was the administrative and economic centre of a kingdom encompassing most of the old kingdom of Northumbria south of the Tees (Hayward 1995: 70).

In Scandinavia, the Viking Age also brought a period of profound change. There were no true towns in Scandinavia before the Viking Age, however during this period (as elsewhere in many parts of Europe) urban centres began to develop, primarily – as in England – as centres for controlling trade and as foci of administrative and ecclesiastical power. By 1100 A.D there were 15 towns in Denmark (Hayward 1995: 42). Prior to (and during much of) the Viking Age, however, farming was the major occupation in much of Denmark and wider Scandinavia, with both animal husbandry and arable cultivation playing important roles in the subsistence economy of the region, arable being most important in Denmark and southern Sweden, where barley, rye, oats, peas, beans and cabbage formed the staple crops. Settlements took the form of small villages, but these tended to shift location every few decades, and there were few permanent village sites until after the end of the Viking Age (*ibid.*: 36).

Paradoxically, despite the Scandinavian impact on the material culture and language of the Viking Age, the physical remains of such settlers are almost invisible archaeologically (although other archaeological remains such as metal artefacts, sculpture and hordes exist in some regions of England). Only around 30 pagan Viking burials are known from England – suggesting to many that the settlers must have been either very small in number, or very adept at 'blending in' with the indigenous culture they found in eastern England. Indeed Richards (1999: 207) proposes that the ability to alternatively blend in (e.g. in the Danelaw), or impose a highly distinctive and visible identity (e.g. northern Britain), could be the key to the geographically wide success of 'the Vikings'. Additionally the burials which are known were discovered and excavated mostly in the 19th century, so details regarding the exact provenance of these remains must remain dubious (Hall 2000).

The scale of the Viking migrations and settlement has not been the subject of such wide debate as has been applied to the Anglo-Saxon period, and it is not known whether this period saw a reasonably large settlement, or simply the immigration of a small number of elite, ruling individuals. Hall notes, however, that recent evidence "suggests that there was more direct and continuing Scandinavian contact in the tenth century than previously thought, and that there were many peasant farmers of Scandinavian origin and not just a ruling elite" (*ibid.*: 153).

Even in these more recent times, the problem of accurate dating remains – which means the question of exactly when Viking and Viking-related activities began may not be as clear cut as it once appeared. Hall (*ibid.*: 151) further proposes that evidence from Ingleby in Derbyshire suggests there may be reason to believe that Viking bands were settling in England some time before the "historically attested land-taking by the Great Army in 876-80". "If such a band was resident at or near Ingleby at a sufficiently early date to allow them to establish an 'ancestral cemetery' before the great army arrived, it would raise the possibility of the other 'early' groups of Viking settlers, and would suggest the need for a major reassessment of Scandinavian settlement in England."

The Viking Age in England did not come to an abrupt end – rather it faded away around the time of the Norman Conquest in 1066 AD (Hayward 1995: 115), although parts of Scotland and the Isle of Man remained under Scandinavian rule until the 13th century – and Orkney and Shetland under Norwegian rule until the 15th century (Richards 1999: 195).

2.3 Historical and archaeological summary

This review has shown that relatively recent approaches to the study of cultural change in Britain, particularly with regard to the Anglo-Saxon and Viking periods, have made some headway in attempting to transcend the theoretical limitations and anti-migrationist perspectives which have dominated research for the last few decades (e.g. Burmeister 2000, Hall 2000). However, the prevailing attitude within archaeology is still dominated by an anti-migrationist perspective, which stresses models of change caused by very small, usually elite, population movements, in concert with swift and pervasive acculturation.

This shift in attitude has led not only to a dearth of theory involving migration, but also to a comprehensive repositioning of researchers' perceptions with regard to what is *important*, in terms of topics warranting serious academic study.

'Small band' theories currently have an advantage over theories of mass migration, not only because, in the eyes of some, they fit the available evidence better, but also because they allow the focus of archaeological debate to rest on the more anthropologically oriented study of acculturation, and the construction and nature of early medieval identities. Lucy's attitude, for example, is bluntly stated in *The Early Anglo-Saxon Cemeteries of East Yorkshire* when she dismisses questions regarding the extent of any biological or population movement during this period as "irrelevant" (1998: 20). She goes on to state that what *is* important is what mortuary evidence, material culture and settlement evidence can reveal about the *society* in question, rather than about the ancestry of the people in question (*ibid.*).

This 'retreat from migration' (see Adams 1978, and section 2.9 in this chapter) has greatly impacted on the way almost all cultural transitions in the British Isles are now viewed, and has not by any means been limited to perspectives on the Romano-British / Anglo-Saxon transition. The cultural and social changes between the Bronze and Iron Ages, the Iron Age and Romano-British period, and the impact of the Viking period have all received the same reinterpretation, ultimately to the point where, if the greater body of recent research is to be uncritically accepted, almost no population movement into Britain would have occurred, certainly between the Bronze Age and Norman periods and, in the eyes of some, for a long time before that. What this means in practical terms, is that the general body of recent research and opinion sees continuity in Britain's genetic make-up dating back as far as the Mesolithic – if those who also question the Neolithic spread are to be included.

Regrettably, at least for those hoping to pursue a multidisciplinary approach to the problem, this has resulted in an attitude seemingly held by many, that biological identity or indeed anything biological is entirely unimportant. Despite the often-stated concern for contextualising evidence and theories, many otherwise comprehensive accounts of the Anglo-Saxon period now have a gaping hole where once would have been theories about the biological, or indeed geographical, origin of individuals and groups. Higham's *Rome, Britain and the Anglo-Saxons* represents an excellent example of a work which aims, through a synthesis and interpretation of all the evidence concerning the Anglo-Saxon period, to elucidate a hypothesis regarding its origins. Higham nonetheless almost entirely neglects the issue of biological identity, as seen through the remains of the people themselves, allowing such studies just half a page of text in his 236 page book. Within these 25 lines, Higham (whilst not, at least, proclaiming such studies are irrelevant) states that the pursuit of knowledge about the biological ancestry of individuals in Anglo-Saxon cemeteries is futile, and will remain so despite the best efforts of biological anthropologists until such time as 'genetic fingerprinting' may be used on a vast scale. In fairness, at the time Higham was writing (1992), modern studies on the skeletal remains of the 'Anglo-Saxons' were almost unheard of, and archaeogenetics (see section 2.5) had not yet been born, a situation which is only beginning to change today.

As a biologically *and* culturally trained anthropologist I would suggest that, whilst perhaps not the decisive factor in shaping identity, biology is at least *a* factor, and as such it would certainly be of benefit to continue to pursue knowledge about the biological component, if any, involved in the origin of the Anglo-Saxon period in Britain. To decide to ignore the issue, perhaps because it appears to be unanswerable at the current time in archaeology, and to decide that the issue itself must therefore be considered unimportant, or worse, irrelevant, seems to me to be evading the issue somewhat. This is particularly relevant for those works, like Lucy's, which attempt to synthesise the evidence alongside a critical history of thought about the period, and perhaps more surprisingly Higham's, which aims not only to synthesise the evidence, but also to develop theory. (It may be that the reasonably new focus on reflexive critical analysis, and the contextualisation of research and theory-building could, perhaps, be usefully applied in the case of these modern syntheses also.)

Surely a more appropriate response would be to ask how, then, do those fluid social identities (as seen through modern archaeological interpretations) relate to biological identity, both locally on the scale of individual kinship groups and on the larger scale of European population and cultural dynamics? And to answer *that* question, we must learn more about the biological make up of the period.

While the use of archaeological material, including funerary remains, to investigate ancestry in relation to ethnicity and identity is facilitated by the ever-increasing quantity of such material, using it to answer questions regarding population change is made difficult by the nature of cultural (or ethnic) material. It is difficult at best, and certainly inadvisable, to draw simplistic conclusions about an individual's complex and culturally subjective social and biological identity, on the basis of the artefacts with which they were buried (e.g. Tyrrell 2000). Similarly, it is necessary to be aware that those individuals within a cemetery (and moreover, those sampled) are not necessarily truly representative of a society in life. There are many examples in the anthropological and ethnographic literature of societies in which either the males or the females of the society remain in their 'ancestral' community, while the other leaves in order to marry and reproduce. In some cases, the 'leavers' are returned for burial at the end of life. As a result, the only way to address the questions that have recently been abandoned, and to assess the degree of biological change and population movement in pre- and early historical periods is to examine the remains of the people themselves.

Despite the problems involved, and (with regard to more recent work) given an awareness of them, there have been – and still are – researchers, mainly in the diverse field of biological anthropology, and the biological sciences in general, who (whilst still few and far between) have considered the possibility of biological change and population movement playing a significant role in the Anglo-Saxon transition to be pertinent, and their research is reviewed in the coming sections.

2.4 Biological research

In recent years, there has been a resurgence of interest in the nature of the Romano-British / Anglo-Saxon transition, from within the broad remit of biological anthropology (although the Iron Age in Britain has not received similar attention). Biological anthropological approaches can add a valuable perspective to debates about identity via direct examination of the remains of the people themselves. The combination of biological and cultural / archaeological approaches has the potential to add an additional dimension not only to debates about the extent of population movement as in this case, but also to those which are concerned with the way in which 'identity' itself is constructed.

Until very recently, there has been a notable lack of research done, in the field of biological anthropology, with the aim of examining cultural / biological transitions in the United Kingdom. There are various reasons underlying this neglect, relating to the misuse of biological anthropological research in the past, and an emphasis by anthropologists on, for example, diet and disease in archaeological populations (Mays 1997, see also e.g. Cox & Mays 2000; Härke 1998; Larsen 1997). While more recent research in Britain has employed non-metric data, metric approaches, such as craniometry, have the potential to identify patterns over a large geographic area which may indicate population relationships in a way that other biological anthropological approaches may not. However, such research has only recently begun to regain popularity, and there are only a handful of recent studies which address the Romano-British / Anglo-Saxon problem specifically.

In this section, research from biological anthropology is reviewed. In sections 2.5 and 2.6 research from archaeogenetics and isotope analysis are reviewed, and research from all three is summarised in section 2.7. Some of the likely reasons for the general lack of recent craniometric / biological anthropological research are discussed in sections 2.8 and 2.9, which focus on the heritability of cranial traits, and the rise and fall in popularity of 'migration theories' in recent years. Finally, the whole literature review is summarised in section 2.10.

2.4.1 Craniometric Research

Studies using craniometry, which address the Iron Age, Anglo-Saxon and/or Viking periods in Britain are few and far between, even when the whole range of such research over time is considered. The major early study in this area was *A first study of the craniology of England and Scotland from Neolithic to early historical times, with special reference to the Anglo-Saxon skulls in London museums* published in 1926. In this study, Morant examined Anglo-Saxon skulls from the British Museum, the museum of the Royal College of Surgeons and the London Museum. Using Pearson's Coefficient of Racial Likeness, he compared Anglo-Saxon skulls with series from the Neolithic, the Bronze Age and the Iron Age. Morant found that the Anglo-Saxon skulls, associated with 'Anglo-Saxon' artefacts, which all dated between the 5th and 10th centuries AD, formed

> …a perfectly homogenous population, and the type is clearly distinguished from that of the British Iron Age by its greater calvarial height, though the lengths, breadths and cephalic indices of the two are almost identical. The ♀ Anglo-Saxon skulls are of precisely the same shape as the ♂ suggesting that the earlier and later invaders lived side by side without intermixture for some centuries. From other evidence we know that the former were not exterminated, but that they were in all probability, far more numerous than the Anglo-Saxon during that period. (1926: 57)

Morant also divided his Anglo-Saxon sample geographically, with reference to the divisions made by Bede, into four groups; the West Saxons, the South Saxons, the Angles and the Jutes. He found, however, that these four groups "represent populations which are extremely similar, if not absolutely identical […] only one – that between the Angles and the West Saxons – suggests any real difference of type" (*ibid.*: 77). The differences between the Anglo-Saxons and the Iron Age samples, suggests Morant, lie mainly in the greater basio-bregmatic height, and the greater basi-nasal length of the Anglo-Saxon skulls (*ibid.*: 85), while the cranial length-breadth index of the two groups is almost identical.

The reference to 'earlier and later invaders' demonstrates that Morant considered both his Iron Age and Anglo-Saxon samples to be representative of immigrant populations in Britain in these periods. Interestingly, he also considered Romano-British populations (which he does not compare directly with any other groups), to be representative of the later Iron Age, indicating that the impact of Roman immigration would have been so small as to be invisible. Unfortunately the exact nature of his pooled Iron Age sample is unclear – although he notes that the sample from Danes' Graves, East Yorkshire, was not included in the sample, because of cultural evidence that distinguishes this area from the rest of Britain (see also section 2.2.1). He does observe, however, that the Iron Age sample appears morphologically intermediate between British Neolithic and Bronze Age samples.

Later research using this sample (Goodman and Morant 1940) additionally found that there was no difference between this Anglo-Saxon sample and an Iron Age sample from Maiden Castle, Dorset.

Since Morant's study, other work has sporadically been done with regard to the cranial morphology of various populations in British history and pre-history, either across time periods, or with a focus on a particular era. In 1968, for example, Ian Tattersall carried out his *Multivariate Analysis of Some Medieval British Cranial Series*, in which he examined a series of remains from an excavation at Clopton, south-west of Cambridge. Romano-British, Saxo-Norman and Medieval remains were all found, and the graveyard appeared to have been established in the 12th century. Most material dated to between the 12th and 14th century. Tattersall compared this series with series from Hythe, Dunstable and Scarborough, all of which were to some extent insecurely dated, or over which were uncertainties about the ancestry of the individuals concerned.

Tattersall applied principal coordinate analysis, and compared individual measurements of the Clopton individuals with the means of measurements from the other three series. His findings indicated that all four populations were generally homogenous, although the Hythe series exhibited differences from the others in its shorter cranial length. Thus he stated that many of the explanations for the other series, in terms of their morphological characteristics, which had described them as to some degree aberrant, or which had invoked migration theories, were unsustainable.

A somewhat broader-scale study was conducted by Brothwell and Krzanowski in 1974. In their research, they aimed to use cranial measurements collected by themselves or others, to examine how well a limited number of measurements could expose differences existing between British populations from a number of periods. The periods represented in their study were early Neolithic, late Neolithic/Bronze Age, Iron Age, Romano-British, Saxon and contemporary groups, Anglo-Norman (medieval), Norse and insecurely dated series. The focus on 'commonly available measurements' reflects the fact that archaeological human remains are more often than not imperfectly preserved, hence in most studies the measurements available for use are constrained by patterns of skeletal preservation. In Brothwell and Krzanowski's study, all measurements 'most commonly available' were those which could be taken from the vault of the cranium, presumably as the authors state, because the vault is less susceptible than the bones of the face to factors which induce skeletal decay or fragmentation (1974: 250).

Canonical variates analysis was used to analyse group differences in the sample, and the results presented using chronological groupings. It was found that early Neolithic and late Neolithic/Bronze Age groups were clearly separated, and groups within these samples were distinguished from one another in ways which supported previous theories regarding group differences. As in Morant's (1926) study, Iron Age samples appeared intermediate between Neolithic and Bronze age samples although Iron Age and Roman samples were not clearly differentiated, perhaps suggesting that the 'Roman' samples predominantly comprised indigenous Iron Age people (*ibid.*: 256). Saxon samples were found to be clearly separated from the medieval samples, although regional differences may also have been apparent, and, although the comparison is not discussed in detail, Saxon samples seemed to cluster with both Iron Age and Roman samples. As with Morant's study, however, Brothwell and Krzanowski do not detail the exact composition of the samples which are ultimately used in the multivariate analyses, and additionally do not consider regional groupings of Iron Age samples separately.

Dawes and Magilton (1980) examined medieval material from St Helen-on-the-Walls, Aldwark, in comparison to a range of samples (mostly derived from the north of England) spanning the Neolithic through medieval periods in Britain, performing cluster analyses on the sample means. Of relevance to the present research, generally, they found that while medieval samples appeared relatively homogenous, they were separated from the earlier samples which in some analyses similarly clustered together. A major cluster included Yorkshire Iron Age, Wetwang, Yorkshire Roman (mainly Trentholme Drive), Yorkshire Anglian and Anglo-Scandinavian, and Orkney Norse. Separate from both clusters were Danish Neolithic, Yorkshire Bronze Age, and British Neolithic samples. Dawes and Magilton's findings therefore suggest that samples were loosely arranged in terms of similarity associated with temporal period, and also that (relatively) there was little difference between Wetwang and other Yorkshire Iron Age samples, and between these, Yorkshire Roman and Anglian / Anglo-Scandinavian samples. However, these associations also varied by sex, and by the number and type of variables on which analyses were based.

A similar conclusion regarding the Iron Age in Britain was reached by Leese (1991), who found that Iron Age samples from Yorkshire (including Wetwang) and elsewhere (including Maiden Castle), appeared reasonably homogenous.

Recent research, such as that described toward the end of this subsection, which employs craniometric methods, is very unusual in modern archaeology and anthropology, and (at least at the present time) does not appear to signal a significant general resurgence in the popularity of applying the techniques of craniometry to questions surrounding potential 'migration periods' in Britain.

2.4.2 Non-metric skeletal research

In *Warrior Graves?* (1990), Heinrich Härke attempted to incorporate a degree of skeletal analysis into his examination of weapons burials in the Anglo-Saxon period in Britain. Weapons burials have long been used to make inferences regarding status, economic power, social stratification and the distribution of wealth within cemetery populations. Härke tested the weapons = warriors assumption using archaeological, historical and skeletal sources of information, and found no correlations between 'warrior specific' criteria (e.g. inclusion in periods of unrest, adult age, osteological build, presence of fractures and so on) and the insertion of weapons in graves. Härke concluded that "the fact that weapon burial in this period was a Germanic rite make[s] it probable that the men buried with weapons in Anglo-Saxon cemeteries were predominately or exclusively of Germanic stock, whereas the group of men buried without weapons in the same cemeteries included a sizable Celtic (Romano-British) element" (*ibid.*: 40). While there was no correlation between the factors mentioned above, and the inclusion of weapons in graves, Härke did find that those individuals with weapons were, on average, between 2 and 5 centimetres taller than those individuals without weapons. This, he suggests is due to genetic rather than nutritional differences within the cemetery population, on the basis that there was no difference between the groups in the incidence of enamel hypoplasia (an indicator of nutritional stress in childhood). In addition to these correlational studies, Härke conducted a frequency analysis of a number of epigenetic traits in groups with and without weapons. He found that in two of the five cemeteries studied, a 'clear pattern' emerged, "individuals buried with weapons have some traits which do not appear among individuals without weapons, and/or vice versa. [...] In other words, the two groups belonged to different descent groups (families in the modern sense)" (*ibid.*: 41).

While Härke's analyses have been commended, in that he questions the assumptions made by archaeologists in the interpretation of grave goods in general, and weapons in particular, and attempts to involve osteological evidence in his analysis, Lucy (2000) and Tyrrell (2000), have criticised Härke's study firstly for his reliance on traditional views of ancestry and ethnicity, and secondly for his 'unscientific' treatment of the epigenetic evidence. Tyrrell argues that the analyses of stature and of non-metric traits are flawed, and suggests that the six epigenetic traits used by Härke are neither well chosen, nor numerous enough to fulfil scientific expectations, further noting that the 'dental anomaly' is not even identified in Härke's publication (2000: 150-1). Additionally, Tyrrell maintains that the method used (frequency) to analyse the epigenetic traits is scientifically ineffectual, suggesting that in order to compute the relative distance between groups a non-Euclidian distance measure must be used (*ibid.*: 151). Tyrrell goes on to state that environmental effects on such polymorphic traits are such that "the same individual who expresses a trait in one environment may not express it under different developmental environments [therefore] comparing individuals within a population is meaningless in terms of determining genetic relationship" (*ibid.*: 152).

In *Corpus Saxonum* Tyrrell presents the results of his 'comprehensive study' of one of the cemeteries (Berinsfield) used in Härke's studies (it is unfortunate that Tyrrell has failed to publish this study in full, and that acquisition of further information is hampered by the fact that his PhD thesis may not be accessed at the time of writing). Tyrrell also split his sample into those with and without grave inclusions – comprising both male and female adults in both groups. 35 cranial traits were examined for each individual, which were then analysed using the Mean Measure of Divergence test, which measures the relative dissimilarity of two groups. Tyrrell's analysis showed no difference between the two groups, a result contrasting with Härke's analysis.

While Tyrrell strongly states his criticisms of Härke's research, a number of omissions and contradictions are apparent in his own paper. Three main points may be made in this regard. Firstly, whilst noting the importance of biological research in terms of the construction of identity, he concludes his research by noting that "the actual presence of 'Germanic' or continental genes is likely to have been totally irrelevant" (*ibid.*: 154), a rather odd statement considering his earlier assertion regarding the importance of considering biological ancestry in the construction of identity (and see section 2.10). Secondly, Tyrrell criticises Härke fundamentally for his use of non-metric traits (*ibid.*: 152), stating that "comparing individuals within a population is meaningless in terms of determining genetic relationship, especially when one considers that even tiny fluctuations in the environment can alter the expression of a trait, so potentially even identical twins may vary in their trait expression", and for failing to identify one of these traits. Despite this, Tyrrell details the results of his own non-metric trait research without identifying any of the traits used. Thirdly, having also criticised Härke's comparative analysis of stature, Tyrrell makes no further reference to stature, and fails to discuss or justify this criticism.

Non-metric dental traits have also been used to examine population relationships in Romano-British / Anglo-Saxon England by Lloyd-Jones, for his PhD at Glasgow University (1997, 1999). 13 traits (chosen for their level of genetic control and independence from each other, lack of sexual dimorphism and ease of observation) were examined for a total of 304 individuals from 7 cemeteries in the south and east of England, and analysed using the Mean Measure of Divergence (MMD). Lloyd-Jones found that most of the standardised MMD scores were statistically significant, although two of the neighbouring sites were indistinguishable from one another. "In general each site tends to have greater biological similarity with its neighbour than with sites of greater geographic distance even though it is separated from the neighbour by time and cultural material" (1997: 27). One particular site, however (Lechlade), has consistently higher scores from all other sites, particularly in comparison to its geographically closest neighbours. Through the use of multidimensional scaling, however, it becomes apparent that although the cluster representing Lechlade intersects with the other groups, much of its spread is away from those other groups, resulting in the highly divergent MMD score. Lloyd-Jones concludes that "The overlap implies a common ancestry with the other groups, while the divergence shows that the period of isolation from those groups was long enough to make the population of Lechlade very different from its neighbours to the east. This would support the theory that Lechlade is an indigenous population that had been isolated from its neighbours for political, or historical reasons" (*ibid.*: 29).

Lloyd-Jones concludes that in Suffolk and Oxfordshire, neighbouring Romano-British and Anglo-Saxon sites are indistinguishable, while in Hampshire a statistically significant difference is more likely due to geographical, not biological (in terms of ancestry), distance. Finally, he suggests that the results support the theory that a small number of incomers initiated the replacement of the indigenous Romano-British culture with a new Anglo-Saxon culture, and notes that despite the small site sample of his research, such results would be unlikely to occur by chance, if the Romano-British / Anglo-Saxon transition had been caused by a series of invasions from the continent.

2.5 Archaeogenetic research

Within the last decade, an entirely new discipline has emerged from the marriage of genetics to archaeology and population history; a discipline which is so new that its name has yet to be decided, although it has been described variously as *historic genomics* (Distante 2004: 275) and, as here, *archaeogenetics* (Renfrew 2001: 4830). Within this discipline, genetic analysis of DNA polymorphisms is applied to historical problems, including the study of ethnic groupings, population history and migration.

In contrast to other areas of historical and archaeological research, archaeogenetics has wholeheartedly embraced the possibility of migration as an explanatory tool, and, with relation to the present research, archaeogenetic methods have been applied to questions of population history focussing on the Iron Age, the Anglo-Saxon period and the Viking period in Europe (although research has been concentrated in the last two of these three periods).

In this subsection the evidence relating to the present research is reviewed. While this review presents work done in a broadly historically chronological manner, because some of the work done necessarily focuses on more than one possible migration period, there are occasions where, for example, evidence regarding Celtic and Viking migrations is presented simultaneously.

Relatively little archaeogenetic research has been done so far that focuses on the question of Iron Age movements in Europe (see section 2.2.1 for an overview of this period). McEvoy *et al.* (2004), however, have compared the linguistic, historical and archaeological evidence for an Iron Age (Celtic) expansion westwards from a central European 'homeland' with European mitochondrial DNA (mtDNA) and Y chromosome data. Previous archaeogenetic research had suggested an early (Palaeolithic) shared ancestry across Atlantic Europe, relatively undisturbed by Neolithic and presumably Celtic population movements. Conversely, previous work on mtDNA suggested that at least one of the transitions in Britain had involved female immigration, indicated by a greater mtDNA than Y chromosome link with central Europe (*ibid.*: 694, see also Wilson *et al.* 2001 below).

McEvoy *et al.* analysed both old and new mtDNA datasets in comparison with Y chromosome and autosomal markers, and found that shared genetic ancestry on the Atlantic Façade of Europe may date back as far as the end of the last Ice Age. While they agree with Weale *et al.* (see below) that some heterogeneity is apparent on the Y chromosome, and that long-term gene flow could not be ruled out as the cause of the aforementioned general homogeneity, they argue against a relatively recent (i.e. Iron Age or Anglo-Saxon) origin for this, at least partially on the basis of the lack – in their view – of archaeological evidence in support of that theory for the Anglo-Saxon period, and genetic evidence for general homogeneity across Europe for the Iron Age.

McEvoy *et al.*'s research to some extent supports that of Wilson *et al.* (2001), who also explored Y chromosome, mtDNA and X chromosome variation in Britain with regard to the possibilities of migrations occurring in the Neolithic, Iron Age and post-Roman periods. Wilson *et al.* found that while there was little Y chromosome evidence to support a mass migration involving males in either the Neolithic or Iron Age periods, mtDNA and X chromosome variation suggested that one of these periods could have seen substantial female movement into the British Isles. Wilson *et al.* also note that later immigration from Scandinavia does appear to have had a significant impact on the male genetic profile of the British Isles, originating in either the Anglo-Saxon or Viking periods. McEvoy *et al.* would, as has been noted above however, question Wilson *et al.*'s interpretation of their findings on, in my opinion, a rather anti-migrationist reading of the archaeological evidence.

A recent genetic study by Weale *et al.* (2002) has also suggested that there may have been a substantial Anglo-Saxon contribution to the modern English gene pool – i.e. a large-scale population movement or immigration in the early Anglo-

Saxon period. This study is the most comprehensive so far to focus specifically on the Anglo-Saxon period in Britain, taking into account a number of different origins for immigrants from the Anglo-Saxon and Viking periods, for which reason this review contains some considerable detail regarding samples and conclusions.

Weale *et al.* attempted to test alternative migratory models using samples from living individuals in seven towns along an east-west transect of Central England and North Wales, in order to evaluate evidence of local genetic transitions, or male population migration (*ibid.*: 1009). These data were compared with samples from Friesland (thought to be one of the geographical sources for Anglo-Saxon invasion) and Norway (a source of Viking invaders) in order to evaluate evidence regarding continental immigration.

The population simulation model used allowed two processes to be modelled; continuous background gene flow and a single migratory event from one population to another, also accounting for variation in time and scale of movement. From this, a range of predicted differences between two populations (English and Frisian) were obtained. Predicted differences were then compared with those observed in the modern population data to enable evaluation of the alternative migratory models. (Thomas 2007 pers. comm.)

The results of genetic distance and population differentiation analyses showed that there were no significant within-England clinal patterns. In contrast, the two North Wales towns were found to differ significantly from each other as well as from the Central English towns. No significant differences were found between the Friesland and the Central England towns, whilst comparisons between Central England towns and Norway were (with just one exception possibly explicable by small sample size) all significant. North Wales towns were statistically different from both the Friesland and Norway samples. As Weale *et al.* suggest, "Taken together, these results suggest considerable male-line commonality between Central England and Friesland" (*ibid.*: 1017). The lack of similarities between the Norway and Central England samples fail to provide any evidence of a substantial Norwegian Viking contribution to the Central English gene pool (*ibid.*).

Weale *et al.* state that their results "indicate the presence of a strong genetic barrier between Central England and North Wales and the virtual absence of a barrier between Central England and Friesland" (*ibid.*: 1018). They conclude that the most likely explanation for this 'barrier' is that "the Anglo-Saxon cultural transition in

Central England coincided with a mass immigration event from the continent. Such an event would simultaneously explain both the high Central English-Frisian affinity and the low Central English-North Welsh affinity" (*ibid.*). They note further that within the given parameters of the study, "an Anglo-Saxon immigration event affecting 50% - 100% of the Central English male gene pool is required [however] our data do not allow us to distinguish an event that simply added to the indigenous Central English male gene pool from one where indigenous males were displaced elsewhere or where indigenous males were reduced in number" (*ibid.*).

Although Weale *et al*'s results cannot prove that an Anglo-Saxon migration occurred, they note that a background migration rate of 0.3% would be required to effect the same results, a rate which is described as "an extremely high rate even by modern standards and [which] would have to have been maintained continuously over thousands of years" (*ibid.*). Additionally, they note that the results could have been caused by a mass migration event outside the Anglo-Saxon period, and that during the Roman period in Britain small numbers of Frisian mercenaries were recruited, some stationed well into the north of England. However, they argue, it would be extremely odd to suggest that such recruitment-related movement was effectively a mass migration, whilst denying the post-Roman Anglo-Saxon migration, as some archaeologists are inclined to do (*ibid.*: 1019).

Weale *et al.*'s research has been supported and extended by that of Capelli *et al.* (2003), who, in their study of Y chromosome variation in the British Isles, found that while there is indeed evidence to support the notion of a mass migration in the Anglo-Saxon and/or Viking periods in England, the picture is also rather more complex in terms of regional variability than was apparent on the basis of Weale *et al.*'s study. Norwegians were genetically particularly influential in northern areas (i.e. Orkney, Shetland and the Western Isles – a finding which has been consistently supported by a substantial body of historical, archaeological, biological anthropological and archaeogenetic research (e.g. Fellows-Jensen 2000, Renfrew 2001, Wilson *et al.* 2001). Both mainland England and Scotland showed evidence of German / Danish influence; the greatest being in York and Norfolk, fitting well with the historical data while southern England generally seemed to have had much less input from these sources.

With particular relevance for the present research, they also found that while Norwegian samples were significantly different from other north European samples, there was no such difference between their Danish and north German samples (and by extension from Weale *et al.*'s research, Frisians). These findings support one of the assumptions made in this research that, in addition to including Danish skeletal material on the basis that modern-day Denmark historically represents the homeland of the Angles, it is reasonable to view Danish samples as biologically representative of an 'Anglo-Saxon' population in general, while populations containing substantial numbers of migrants with a more northern origin (e.g. Norwegian and Swedish Vikings) should be distinct.

Unfortunately Weale *et al.* and Capelli *et al.*'s research also demonstrates that were successive migrations to have taken place in both the Anglo-Saxon and Viking periods, both with origins at least partly in Denmark, genetic research, and by extension other biological anthropological research that uses phenotypic characteristics as a proxy for genetic data, would quite possibly be unable to distinguish the two.

Finally, for the Anglo-Saxon period, and in contrast to the research mentioned above, Töpf *et al.* (2006) investigated the role of women in the population history of 4th-11th century Britain using mtDNA from the skeletal remains of individuals living during this period (all previous research has focussed on genetic samples from living populations), in comparison with modern samples from England, Europe and the Middle East.

Töpf *et al.* examined mtDNA from one Romano-British cemetery and four Anglo-Saxon cemeteries, finding that the late Saxon site (Norwich, 9th-11th centuries AD) had a closer genetic distance to northern populations (Scotland, Estonia, Norway, Finland and the Western Isles), while the early Saxon site (presumably Norton East Mill, Cleveland - this is unclear in the paper) is closer to more southern European samples (Germany, Spain and the Near East).

This research avoids one of the main problems involved with the research discussed above; its inability to easily distinguish between population movement in different periods, as a consequence of using samples from living individuals. In the discussion of results presented in this paper, Töpf *et al.* do not consider the archaeological, historical or indeed, potentially, the genetic distinction of the Romano-British sample at Leicester (in its context as an urban late Roman cemetery, with all that implies about the genetic makeup of its population – see section 2.2.2), which detracts from the usefulness of this study in the context of the present research. The sample sizes used, following extraction and authentication of the DNA sequences (2006: 154), are also rather small, particularly for the Romano-British sample, for which data for only 6 individuals could be used, and the early Anglo-Saxon sites for which data from no more than 12 individuals were available.

As mentioned previously, one of the most-studied periods in the history of the British Isles is the Viking period, particularly with reference to differences between mainland England, Scotland, Ireland and the Northern and Western Isles. In archaeogenetics much research in this field has focussed on ascertaining the geographic and temporal origin and subsequent spread of the HFE-C282Y (also known as Cys282Tyr) haemochromatosis mutation in Europe. This mutation is relatively common in northern Europe, with around one in eight people being heterozygous and one in 200 homozygous for C282Y, although relatively few individuals who are homozygous accumulate enough iron for the disorder to become clinically diagnosed (Distante *et al.* 2004: 270).

Hereditary haemochromatosis is a disease which, despite having long-term negative consequences for the health of sufferers, may also be associated with selectively beneficial phenotypic characteristics in both homozygous and heterozygous individuals. These include increased intestinal iron absorption, which may have been of benefit to women of childbearing age, and protection against type I insulin-dependent diabetes mellitus, a disease which in the past may have limited reproductive potential by leading to premature death, (Milman & Pedersen 2003) as well as possible resistance to historical pandemics caused, for example, by plague, cholera or typhoid fever (Distante *et al.* 2004). These selectively positive characteristics may explain why this mutation, thought to have had a unique origin in Europe, has spread so widely throughout the modern population (Milman & Pedersen 2003, Distante *et al.* 2004).

Various geographic and temporal origins have been suggested for this mutation; from a Celtic (i.e. Iron Age) origin and spread from central Europe, to a Scandinavian origin and spread with the Vikings. Milman and Pedersen note that analysis of this topic is complicated by the fact that at the present time it is impossible to date the origin of this mutation with any degree of accuracy. According to their calculations, depending on whether a mean generation time of 20, 25 or 30 years is assumed, the date of origin would be ~600-800 AD, 250-500 AD or 100 BC

– 200 AD respectively, thus potentially supporting any of an Iron Age, Anglo-Saxon or Viking origin! (Milman & Pedersen 2003).

Distante *et al.* (2004) recently reviewed the evidence for an origin in the Neolithic, Celtic, Anglo-Saxon and Viking periods. They criticised previous calculations of the date of origin of the mutation, and concluded that although the evidence for both Celtic and Viking origins seems substantial, in their view the mutation is most likely to have had an earlier origin, before 4000 BC.

Further complicating this research, and archaeogenetic research in general, is the influence of various interpretations of the archaeological and historical evidence, alongside changing fashions in the popularity of migration models in studies of population history. Since the date of the mutation cannot be pinned down, the likely origin and spread of the mutation must be analysed in terms of its current geographical distribution, and in conjunction with analyses of other heritable conditions (Distante *et al.* 2004). As has already been discussed, this process is open to considerable subjectivity on the part of researchers.

It must also be remembered that there is a difference between the 'origin' of a characteristic and the 'spread' of the same, although the two are clearly theoretically and practically linked. Additionally, I would note that analysts of the origin/spread of the C282Y mutation must rely on others' interpretation of the other evidence (and by extension, prevailing fashions) in order to interpret their own research. Distante *et al.*, for instance, seem happy to accept the reality of Anglo-Saxon / Viking mass migrations, on the basis of genetic, archaeological and historical evidence, whilst rejecting the possibility of a Celtic migration on archaeological grounds.

At the present time, and on the basis of the geographical distribution of this mutation, it seems equally possible that C282Y could have originated and spread during the Pre-Neolithic, Neolithic or post-Roman periods, and reasonably unlikely that a central European/Celtic origin is accurate. Of course, this conclusion does not take into account the possibility of long-term British-continental movement from areas other than central Europe, not limited to the Anglo-Saxon and Viking periods – a key failing, in my opinion, of much of the research reviewed above, and a subject that will be discussed further in the light of the results from the current research.

To sum up this review of the relevant archaeogenetic research done to date, and with reference to the present study, it seems unlikely that a significant Celtic (Iron Age) migration from a central European origin took place. The general homogeneity of European populations as demonstrated by data reflecting both male and female population history suggests to some researchers that few significant cultural changes in the British Isles have been accompanied by mass migration, prior to the Anglo-Saxon and Viking period, for which (in contrast to the bulk of the research and interpretations discussed in other sections of this review) there is strong evidence for large-scale population movement between northern Europe and parts of the British Isles. Whilst to an extent tying in well with some more recent historical and archaeological interpretations, this conclusion has disturbed some researchers because of the huge number of migrants some estimates suggest.

A recent study by Thomas *et al.* (2006) has made some progress toward resolving the massive disparity between genetic and archaeological estimates of the size of Anglo-Saxon migration.

Thomas *et al.* note that even relatively conservative genetic estimates indicate an Anglo-Saxon Y chromosome ancestry of 50% or more in the British Isles, which would require (on the basis of a Romano-British population at the end of the Roman period of between 2 and 3.7 million – much greater than has previously been estimated) a male migration numbering over 500 000 in the early Anglo-Saxon period. Although the archaeological evidence is now seen by some as supporting the notion of a large-scale migration from the continent, no researchers have suggested that the numbers involved approach this figure. Thomas *et al.* suggest that an 'apartheid-like' social system limiting intermarriage between Anglo-Saxon and Briton, along with legal systems favouring the former (for both of which textual, archaeological and skeletal evidence exist), could be responsible for an Anglo-Saxon reproductive advantage. If this were indeed the case, from a starting point of no more than 10% immigrants, the proportion of Anglo-Saxon Y chromosomes could easily reach 50% in less than 15 generations. (15 generations is considered to be the upper generational limit for this increase as, after this time, legal changes suggest that intermarriage was no longer prohibited, and there was no difference in the legal status of Anglo-Saxons and Britons. 2006: 2653)

The question which remains is of the differences between males and females which is apparent from research using different genetic systems – particularly that which fails to demonstrate a comparable intrusion of women in this period, and a lack of modern homogeneity between the sexes (which should eventually occur due to intermarriage). Thomas *et al.* have suggested that this may be explicable if the immigrant Y chromosome replacement of indigenous Y chromosomes was exacerbated by any of a number of factors, all of which have reasonably well-studied precedents (*ibid.*: 2655). These factors include the likelihood of Anglo-Saxon / native offspring assuming the identity of the father, rather than the mother, further reducing the effective intermarriage rate; 'forced' extramarital matings being more likely to occur between Anglo-Saxon men and native women than vice versa; and finally a sex-based strategy of parental investment favouring sons over daughters.

Thomas *et al.* have provided the first piece of archaeogenetic research which goes a long way towards resolving the discrepancies between archaeological models (even those which emphasise the role of migration) and the genetic evidence. It is to be hoped that those (e.g. Higham 1992, Lucy 1998, 2000, Tyrrell 2000) who favour models of acculturation and deny even the *relevance* of any significant migration, will take this research on board, and revisit both the archaeological, historical and biological evidence, and their own theoretical stance, in its light.

To close this section, I would reiterate the point I made earlier, that the difference between an early origin of shared genetic ancestry, and the effects of long-term, continuous gene flow within Europe, may not be immediately recognisable in this type of research (which focuses on genetic data from living populations), and that relying on the changing fashions of archaeological interpretation compounds this problem. More prosaically, as Renfrew (2001: 4830) points out, if similar haplotypes exist anyway at both the origin and destination of a proposed migration, a substantial movement of people could take place that would remain archaeogenetically invisible. It is noted that the same caveats must also apply to the present research.

2.6 Isotope analysis

A second recent approach to the problem of Anglo-Saxon migration has been made in the field of dental enamel isotope analysis. Isotope analysis (particularly of carbon and nitrogen) of bone collagen has been widely used to investigate archaeological questions relating to palaeodiets, and the relationships between diet, social structures, status and health in past populations (see e.g. Privat *et al.* 2002 with relation to the Anglo-Saxon period, and Jay & Richards 2006 with relation to diet at Iron Age Wetwang Slack). More recently, isotope analysis of dental material has been applied specifically to questions relating to population history and intra- and extra- regional migration (see e.g. Price *et al.* 2004 regarding the Bell Beaker period in Europe, and Montgomery *et al.* 2000 with relation to Neolithic migration).

Analysis of dental enamel isotopes in the context of population history research is based on the fact that, as with other bones of the body, dental material 'traps' information about an individual in terms of the ratios of various isotopes which derive from the natural and anthropogenic environment. Unlike bones, however, the human dentition does not remodel during an individual's life, and the dentition therefore contains information about an individual's *childhood* environment. (Hence bone collagen which remodels approximately every 15 years is used to examine the period prior to death, whereas dental material is used to identify differences within or between populations in terms of childhood environment.) For this reason, isotope ratios (most commonly strontium, lead and oxygen) within an individual's dentition can be examined in relation to the environment in which they died and were buried, and in some cases can indicate which individuals within a cemetery population were born locally, and which were not – i.e. it has the potential to identify first generation immigrants within a population.

With regard to the present research, the core piece of work has been done by Montgomery *et al.* (2005), who used lead and strontium isotope analyses to investigate variation in the childhood origins of 32 individuals from the early Anglo-Saxon cemetery at West Heslerton, East Yorkshire. A small number of earlier and later individuals from the same area were included for comparison.

Montgomery *et al.* found that, while the lead isotope analysis resulted in a picture of a single, homogenous population, the strontium isotope analysis showed bimodality, indicative of the presence of two distinct (i.e. local and non-local) groups among the adult population. Adding weight to this interpretation is the fact that when plotted against each other, Anglian adults and Anglian juveniles do not overlap, the juveniles overlapping instead with the plots for prehistoric and 'local' groups. These findings suggest that within the adult population, at least two groups can be identified, of local and non-local origin, spanning both early and later phases of the use of the cemetery, whereas the juveniles are not similarly divided, and appear to have lived and died in the same location. Interestingly, the distribution of local and non-local individuals does not correlate with any of the traditional archaeological indicators of immigration, such as grave goods, household groupings or sex.

Having discovered evidence for a non-local component at West Heslerton, Montgomery *et al.* proceeded to attempt to identify the origin of the non-local group. Unfortunately (and this is indicative of one of the major problems with this type of research at the present time), comparative skeletal data are lacking, and geological similarities between East Yorkshire and some regions of continental Europe meant that they could not distinguish between a continental origin and an origin in some other region of Britain. With regard to this problem, Montgomery *et al.* note that while high strontium ratios are seen in Norway, Sweden and in some of the individuals from West Heslerton, the presence of the highest strontium ratios in the Neolithic/Early Bronze Age and Iron Age individuals (for whom the possibility of a Scandinavian origin is discounted) means that local variation within the UK must be seen as a viable explanation for the origin of the non-local adult group.

As mentioned in the introduction to this subsection, Jay and Richards (2006) have carried out work investigating Iron Age diet in relation to social factors at Wetwang Slack, East Yorkshire, using carbon and nitrogen isotopes in bone collagen. Although their main focus was on factors not related to migration and population history, they do note that – with perhaps two exceptions – there is little evidence to indicate that there were any differences in origin between individuals buried throughout the duration of this cemetery's use. This interpretation is based on the population as a whole appearing homogenous in terms of diet through both early and later phases of the cemetery. They also point out, however, that the sample used (*n*=62 of over 450 burials covering a time-span of between two and four hundred years) may have simply missed any immigrant individuals.

There is also a rather intriguing trend observable "in the overall data from individuals with high nitrogen and more negative carbon values, down to those with lower nitrogen values and less negative [carbon values]" (2006: 657). When a trend line of data points is plotted for all adults, the male sub-sample, even before age is taken into account, appears different from the female sub-sample, and when age is considered show an increasing separation which is significantly correlated with increasing age. Females show no such correlation. As with the analysis of the population as a whole, this trend does not appear to be related to social or temporal factors, and the authors of this work cannot, at the present time, explain this finding.

In conclusion, although little work has been done in this field specifically in relation to the Iron Age to Viking periods in Britain, that which has been done demonstrates that this approach does have some utility. The results of the study at West Heslerton are particularly interesting in the context of the present research, however, the problems encountered by Montgomery *et al.* in trying to identify the geographical origin of the non-local group aptly reveal the limitations of applying isotopic analysis to questions of population history – for the present time at least.

2.7 Summary of biological research

The research reviewed in sections 2.4 to 2.6 of this chapter presents a rather mixed picture of biological continuity and change between the Iron Age and later Anglo-Saxon / Viking periods in Britain.

Although research done has been unequally focussed on the periods with which the present work is concerned, it is clear that for each period, research done by different individuals, from diverse disciplines and across various geographical regions has resulted in radically different conclusions being drawn, with regard to questions of continuity or change.

Some recent genetic research (Wilson *et al.* 2001, Weale *et al.* 2002, Capelli *et al.* 2003) provides the most compelling evidence yet, for a substantial population movement from northern Europe to Britain, at some point – possibly during the Iron Age to Anglo-Saxon periods. Although such research cannot pin down the timing of this change, or its nature, precisely at the present time, Weale *et al.*'s results strongly support an Anglo-Saxon date. Relatively fewer archaeogeneticists argue against some form of Scandinavian / British movement (but see McEvoy *et al.* 2004).

This is in contrast to some research done in biological anthropology (Tattersall 1968, Lloyd-Jones 1997, Tyrrell 2000), however the majority of recent and not-so-recent research done outside of the fields of archaeogenetics and isotope analysis has tentatively indicated that population change was occurring in Britain throughout the periods in question (e.g. Morant 1926, Brothwell & Krzanowski 1974, Härke 1990), and regional and temporal differences alluded to by some researchers (Härke 1990, Capelli *et al.* 2003, Töpf *et al.* 2006) may explain the contradictory findings arrived at by researchers studying different, limited, geographical regions and temporal periods. Recent research in the field of isotope analysis demonstrates considerable potential, however at the present time results regarding the origin of population movement in the Anglo-Saxon period are inconclusive (Montgomery *et al.* 2005).

However, the theoretical and methodological differences between research done in different disciplines, and over time, make direct comparisons between the findings of such research difficult. Much research done in biological anthropology has avoided explicitly addressing the question of population change and migration. Additionally, as will have become clear from the review, it has been extremely limited in quantity and (with the exception of work done in archaeogenetics) has largely failed to compare British samples with continental 'source' samples, again contributing to difficulties of direct comparison. Two of the major reasons for the lack of such research are discussed next, in sections 2.8 and 2.9.

2.8 Craniofacial plasticity and heritability

Since Boas' publication of *Changes in the Bodily Form of Descendants of Immigrants* (1912) many researchers have been dissuaded from using anthropometric and craniometric measurements as phenotypic expressions of genetic relationships. Boas' findings regarding the relationship of cranial form to environmental influences have been cited as irrefutable evidence of the magnitude of importance of cranial plasticity in humans, and as an insurmountable impediment to the success of biodistance studies which rely on cranial or anthropometric measurement data.

Within the last decade, however, a variety of reassessments and critiques of Boas' study have been published. Boas' data has been used by Konigsberg & Ousley (1995) to test the assumption that a phenotypic variance-covariance matrix (P) (specifically based on metric traits) is proportional to the additive genetic variance-covariance matrix (G). Crucially for the present study, they found that G is indeed proportional to P, and therefore even when h=<1 (where h=heritability of traits) phenotypic distances may be used as proxies for genetic distances. Sparks (2001) replicated Boas' original study, using modern multivariate statistical analyses, and found that cranial traits display a high heritability, the differences between ethnic groups far outweighing differences between parents and offspring (2001: 60), and that phenotypic data consequently provides a good proxy for genetic data (*ibid.*: 66). Relethford (2004b) has come to a similar conclusion; whilst conceding that developmental plasticity and environmental adaptation can and does occur upon migration, and may in some circumstances confound interpretation, the *relationship* between Boas' ethnic groups is not necessarily altered, and craniometric data may therefore reasonably be used in the study of population history.

While many researchers are content to use the phenotypic variance of the human cranium as a proxy for genetic data, there is no doubt that the phenotype is affected by environmental as well as heritable factors (e.g. Kohn 1991, y'Edynak & İşcan 1993, Larsen 1997), and factors including climate, diet, prematurity birth and artificial deformation are all thought to influence skull shape (Brodie 1994). For example, cranial index has been found to covary with climate (both humidity and temperature appearing important), and the rate of cranial change associated with climate may be relatively fast, perhaps even inter-generational (*ibid.*: 51-54).

Much research has been done with regard to assessing the heritability of the regions of the human cranium; Brown, for example (1973 in Kohn 1991), found that lines, angles and chords of the cranial vault were more similar within than between families, despite those spanning several bones being less heritable. Kohn states "studies consistently find a high degree of inheritance in craniofacial dimensions. That is, genetic variation appears to contribute significantly to observed variation in craniofacial morphology" (Kohn 1991: 267-8). Kohn also suggests that there may be reason to suspect that the dimensions of the neurocranium have a higher heritability than do the dimensions of the facial skeleton, due to the former's relatively early growth phases, and the latter's influence from environmental factors (*ibid.*: 270). While Kohn found no difference in the heritability of neurocranial and facial traits via an examination of anthropometric data (*ibid.*), other researchers have come to different conclusions. y'Edynak & İşcan (1993) note Endo's (1966) research, and state that "the face receives most of the stresses [from mastication], while the vault, with the exception of the glabella and superciliary arches receives little" (*ibid.*: 15). Endo thus proposed that the stresses of mastication are capable of significantly modifying the form and structure of the facial skeleton (Endo 1966 in y'Edynak & İşcan 1993: 16). Factors related to diet (specifically nutritional stress) have also been linked to skull base height to the point where this has been proposed as an indicator of growth stress in childhood (Angel 1982). In a study of Belgian adults Vercauteren (1990 in y'Edynak & İşcan 1993: 23) found statistically significant differences between age groups for 3 measurements (cranial breadth, bizygomatic breadth and bigonial breadth), while Tanner found that neurocranial and craniofacial dimensions can be expected to increase throughout life, albeit with no more than a 2-4% change after age 20 (1988 in y'Edynak & İşcan 1993: 23).

More recently, Jantz and Jantz (2000) found evidence for secular change in craniofacial morphology between the mid 19^{th} century and the 1970s, both in the cranial vault and the facial skeleton. They note, however, that such changes in the vault must take place in childhood. González-José *et al.* (2005) have also explored the evidence for the extent of environmental and adaptive influences on craniofacial structures, using a 'functional-cranial approach' whereby the cranium is divided for analysis into structural-functional units. They found that while differences in economic strategy have a significant impact on cranial structures (particularly, as would be expected in terms of dietary differences, in the masticatory and alveolar regions), whole craniofacial variation remains greater and representative of historical relationships between populations.

It is only very recently that narrow sense (i.e. on the basis of additive genetic variance as opposed to that due to dominance or interaction effects) heritability estimates for individual craniometric dimensions have been investigated using pedigreed skeletal samples (Carson 2006 in press). This is important not only because population-genetic analyses require that an estimate of heritability is provided for the traits used, but also in terms of what it means for the *a priori* selection of metric dimensions in future studies of this type. In the past, calculations of the heritability of traits have been based on anthropometric data from living individuals, or have been calculated on the basis of invalid assumptions, and the most common heritability estimate used (through necessity) in statistical analyses of metric traits has been either h^2=1 or, as in the present study and many others, h^2=.55, on the basis that it represents an *average* heritability for a suite of traits (*ibid.*: 2).

However, given the knowledge that different traits and/or regions of the crania respond differently to environmental (i.e. non-genetic) influences, this generalisation is now quite reasonably deemed by Carson to be unsatisfactory, and indeed her research shows that while cranial measurements do have higher heritabilities in general than those of the facial skeleton, and that lengths have higher heritabilities than breadths, considerable variation exists between both individual measurements and different regions of the skull. While Carson does not advocate "the calculation of a mean heritability value" (*ibid.*: 10), she does note that some popular programs such as RMET leave the user with no other choice.

In summary, although the state of our knowledge regarding cranial form, heritability and environmental influence, and the post adolescent ontogeny of cranial form is rather limited, and the evidence difficult to interpret, more recent work is beginning to redress this. In this study, it is not anticipated that significant environmental differences will have any real impact on the groups studied, as they all originate from broadly similar latitudes. However, in order to attempt to control for factors such as sex and demographic variation, only adults are used in the present study, and where possible analyses are conducted by sex.

2.9 Anti-migrationism and biological research

The scant number of studies reviewed above is indicative of a long-standing reluctance, in British academic circles, to address issues of biodistance in archaeological problems. There are many reasons for this neglect, but two major and related factors appear to be at work: firstly, a reluctance to investigate biological identity, at a time when the importance of cultural constructions of identity has become paramount, and secondly changing 'fashions' with regard to the popularity or unpopularity of models of migration and/or invasion. (A detailed exploration of these factors is beyond the scope of this thesis, but see for example Adams *et al.* 1978, Anthony 1990, 1992, Chapman 1992, Chapman & Hamerow (eds) 1997.)

From intense popularity in the late 19th and early 20th centuries, anthropometric studies of archaeological populations in the pursuit of knowledge about population history have gone almost completely out of favour. Simon Mays suggests that this phenomenon may be "linked with the general decline in interest in population history witnessed in the last few decades in British archaeology. The ultimate causes of this decline are complex and likely embedded in the cultural and political milieu in which we work" (2000: 277). He notes that a theoretical reorientation in the 1960s prompted the demise of theories involving the use of migration or invasion as an explanation for cultural change, in favour of theories emphasising the "continuity of populations and indigenous cultural development" (*ibid.*: 277-8).

Chapman and Hamerow examined this phenomenon in some detail, and concluded that the rejection of migration models in archaeology reflected two main problems. Firstly, the lack of fit between the archaeological evidence and models of migration was interpreted as reflecting failure of the models themselves (1997: 4). Secondly, weaknesses which were at the time being identified in models used to explore the "conception of cultures" were blamed on the migration models which had for so long been used to explain cultural construction (*ibid.*). Essentially, Chapman and Hamerow suggest that migration models fell out of favour because of misconceptions and misunderstandings surrounding how models of migration, and the archaeological evidence *should* fit. Compounding the effects of these perceptions was the post-war decline of colonialism, Britain's insularity, and the 'temperaments' of individual but influential archaeologists (Chapman 1997: 13). In addition to all these is the development of academic reflectivity – or 'critical biography', whereby academics – particularly in the social sciences – must attempt to stand back and acknowledge (if not critically assess) the impact of their own subjective perspective on their work, as well as that of social, political and economic influences on their discipline as a whole (*ibid.*: 11).

As with all 'fashions', attitudes have recently come full circle, and evidence from the literature suggests that models of migration and invasion are once again rising back into favour. (Indeed this resurgence was predicted (Chapman 1997: 18) due to recent national and international factors not unrelated to those which caused it to go out of fashion in the first place.) 'Migration' periods are now beginning to be examined in a much more objective manner, and in the context not just of migration theory from archaeology, but also from the large body of research which has been done in other fields (e.g. Burmeister 2000).

Despite the recent rise of interest in migrations, and an increasing focus on the construction of ethnicity (e.g. Tyrrell 2000), there has been no concomitant rise in the use of craniometry, although research in other fields within the biological sciences is becoming more commonplace. Mays notes that "This reflects the rather jaundiced view of craniometry held by many archaeologists whose training is not in osteology. The value of craniometric work for investigating ancient migrations is denigrated, and it appears to be seen as a rather old-fashioned and politically questionable pursuit" (2000: 278).

Despite this increasing popularity within some disciplines, Mays (2000, 1997) and Larsen (1997) have both observed that preference is still given to the pursuit of knowledge about the diets and health, as opposed to the biological composition / origin, of archaeological populations. Mays suggests that this phenomenon is due to the large number of researchers from the 1960s who came to the study of osteoarchaeology from a medical background, leading to an increased interest in paleopathology, but also to a neglect of normal human variation (1997: 601). Mays goes on to suggest that researchers today might begin to remedy this neglect, and to "progress towards a more population-based approach, in which the osteological findings are combined with other archaeological data in order to produce a more complete picture of the human past" (*ibid.*: 604).

On a similar topic, Heinrich Härke (1998: 19) suggests that the attitude of British scholars toward the issue of migrations in general, and the use of skeletal data in particular, is influenced more by factors in the present, than by the archaeological past itself.

> The British reception has been characterised by disbelief at the suggested scale of the immigration, a reaction perfectly in line with current antimigrationist tendencies in British archaeology. Some reactions have been outright hostile, although it has to be said that a good deal of this hostility was directed against my analysis of skeletal in addition to archaeological and historical evidence. This kind of approach to group differentiation has been viewed with extreme scepticism since the racist misuse of skeletal data by Nazi archaeologists and anthropologists.
> German reactions have been an inverted mirror image of the British reaction: there has been disbelief at the implied number of surviving natives. [...This] is probably a fair reflection of the widely held view that post-Roman migrations led to large-scale population replacement in western Europe.

Such differences in perspective, suggests Härke, are largely attributable to the political and national histories of the two nations, and the ensuing historical relationship between archaeology and politics. This, he proposes, created a predominantly 'insular' outlook in British archaeology in contrast to German perspectives which, possibly for reasons pertaining to geographical location and concepts of 'ethnic citizenship', are more favourably inclined toward the idea of large-scale migrations (*ibid.*: 20-21). Härke's own experiences illustrate the impact that national and historical differences in perspective have on the research which is done, and the way the results of such research are viewed by the wider community.

2.10 Summary and conclusions

From the previous sections, it is evident that amid historical, archaeological and anthropological research into the origin of the Anglo-Saxon period in Britain, theorists from various disciplines have failed to come to any agreement about the mechanism by which this period developed out of the preceding Romano-British period. There is certainly a preference, at the present time in archaeology, for explanations which do not emphasise the role of mass migration/invasion, and which instead allow for rapid acculturation by indigenous populations in response to a small-scale elite take over of political control. Shifts in the attitude of researchers to models of change involving migration have, unfortunately, led some to conclude that the pursuit of knowledge about the biological component in this process is irrelevant (Lucy 1998), or unlikely to provide any answers at the current time (Higham 1992). However as Tyrrell rightly notes, "The lack of a biological perspective in archaeological and historical discourses on identity in effect denies the study or existence of a fundamental constituent of corporeal identity: that which is the sum of the interplay between genome, environment and body idiom" (2000: 318).

In recent years, researchers from within the fields of biological anthropology, archaeogenetics, and isotope analysis have once more begun to address this question as, despite what some archaeologists or historians may suggest, such questions *are* still important, and will remain so as long as they remain unanswered. Despite the small number of studies which have so far been done, it is clear that results are conflicting, with the bulk of recent (albeit scanty) biological anthropological research suggesting biological continuity in this period. These conclusions stand in stark contrast to the majority of research from archaeogenetics which suggests a substantial continental biological contribution to the Anglo-Saxon gene pool. Thomas *et al.*'s 'apartheid' theory (2006), and an appreciation of regional variation, may go some way toward reconciling these apparently irreconcilable conclusions. As yet, results from recent applications of isotope analysis to problems of population change and composition are inconclusive, although the divide in the sample from West Heslerton has the potential to lead to interesting results.

In sum, then, the question of a continental biological contribution in this period remains, despite the assertions of some archaeologists, unanswered, and ripe for further study. It has been noted that the differences in conclusions drawn by members of different disciplines may owe considerably to differences in personal perspective, and in scope and method of research.

Research into the Romano-British / Anglo-Saxon transition is increasingly being done in an academic atmosphere which welcomes multidisciplinary and holistic research methods. Although unpopular in recent years in Britain, craniometry has been widely used overseas to provide a perspective on biological (genetic) change and population movement in many parts of the world. For these reasons, the present research applies traditional and modern statistical analyses to craniometric data, in order to address questions regarding relationships both within Britain, and between Britain and continental populations, from the Iron Age to the Anglo-Saxon period. Hypotheses, and the materials and methods used to test them are the subject of the next chapter.

CHAPTER 3

MATERIALS AND METHODS

3.1 Introduction

The aim of this research is to provide a perspective on population change or continuity between the Iron Age, Romano-British and Anglo-Saxon periods in Britain, through an analysis of cranial morphology over time. Craniometric data on up to 37 variables have been collected from 1464 individuals from a number of sites in Britain and from continental Europe. This chapter describes the research hypotheses, methodology and materials used.

In section 3.2 the research hypotheses are described. In section 3.3 the samples used are described, and information about their geographical, historical and archaeological background, and their relevance to this research, is detailed. In section 3.4 the data collection and processing procedures used are explained, and in section 3.5 the statistical methods used to analyse these data are described. Finally, section 3.6 presents a summary of the chapter, along with consideration of the limitations of both the data and methods employed here.

3.2 Hypotheses

In order to address the research problem set out in section 1.1, and taking into consideration work that has been done in the fields of archaeology, historical research, biological anthropology, archaeogenetics and isotope analysis, which were discussed in chapter 2, specific research hypotheses have been formulated which link directly with the research question and analyses described in Chapter 1.

More detail regarding the statistical methods and analyses used are given in the current chapter.

The hypotheses are presented below in an order which allows the research question to be explored in a logical manner, and which also broadly corresponds to the order in which results are presented in Chapter 4.

3.2.1 Hypothesis 1

There are observable, measurable, differences in craniofacial morphology between the Iron Age, Romano-British and Anglo-Saxon periods in Britain.

Hypothesis 1 is intended to test whether there are statistically significant differences between samples, on the basis of univariate measures (craniofacial indices). Descriptive statistics give an overview of the craniofacial morphology of each major sub-sample, *t*-tests are used to test within-sample, between-sex, differences and analyses of variance (ANOVA) are used to test for differences between samples.

3.2.2 Hypotheses 2a, b and c

Hypothesis 2a

Samples will cluster according to their geographic proximity – i.e. British samples through time will be closer to other British samples than to Danish samples.

Hypothesis 2b

There is evidence for changes in British-Danish relationships, as indicated by minimum genetic distance (d^2), through time.

Hypothesis 2c

If there are differences in British-Danish relationships through time, greater similarities will be seen in the Anglo-Saxon period, compared to the Iron Age and Romano-British periods.

The hypotheses in group '2' are all intended to allow for a systematic analysis of the biodistances derived from the R matrix, with regard to the research problem. Hypothesis 2a relates to the expectation that, if acculturation models of change in the Anglo-Saxon period (and indeed in the Iron Age) are correct, British samples will be more similar to each other than they are to Danish samples, and there will be a clear British-Danish distinction, based on a model of geographical isolation, and a general lack of significant gene flow between the two. In contrast, hypothesis 2b proposes that if 2a is rejected, period-specific differences in British-Danish relationships will be observed. Hypothesis 2c proposes that, if 2a is rejected, and 2b accepted, a model of migration-based change between the Romano-British and Anglo-Saxon periods might be supported if greater similarities are observed between Britain and Denmark in the Anglo-Saxon period than in preceding periods.

3.2.3 Hypotheses 3a and b

Hypothesis 3a

Both within Britain, and between Britain and Denmark, biological relationships indicated by the minimum genetic distance (d^2) matrix can be explained by an isolation by distance (geographic continuity) model.

Hypothesis 3b

Both within Britain, and/or between Britain and Denmark, samples which are more similar temporally will be more similar biologically.

Hypotheses 3a and 3b are intended to test the association between the biodistance matrix (d^2) and matrices of geographic and temporal distance between samples. The geographic distance matrix represents a model of isolation by distance (or geographic continuity), and is tested by hypothesis 3a. The temporal distance matrix represents an alternative model of isolation by distance in time (or temporal continuity), and is tested by hypothesis 3b. Essentially, hypothesis 3a proposes that samples which are closer geographically will be more similar biologically, and 3b proposes that samples which are closer in time will be closer biologically.

3.2.4 Null hypothesis 4

There are no differences in genetic within-group variation between the Iron Age, Romano-British and Anglo-Saxon periods in Britain.

Although the data and samples available for this study do not readily lend themselves to analysis via the Relethford-Blangero method (see Chapter 3, section 3.4), null hypothesis 4 is intended to allow differences between samples in terms of intra-sample variability (and therefore extra-regional gene flow) to be assessed. The null hypothesis states that no differences are expected between samples.

3.3 Sites & samples

3.3.1 Samples: geography & chronology

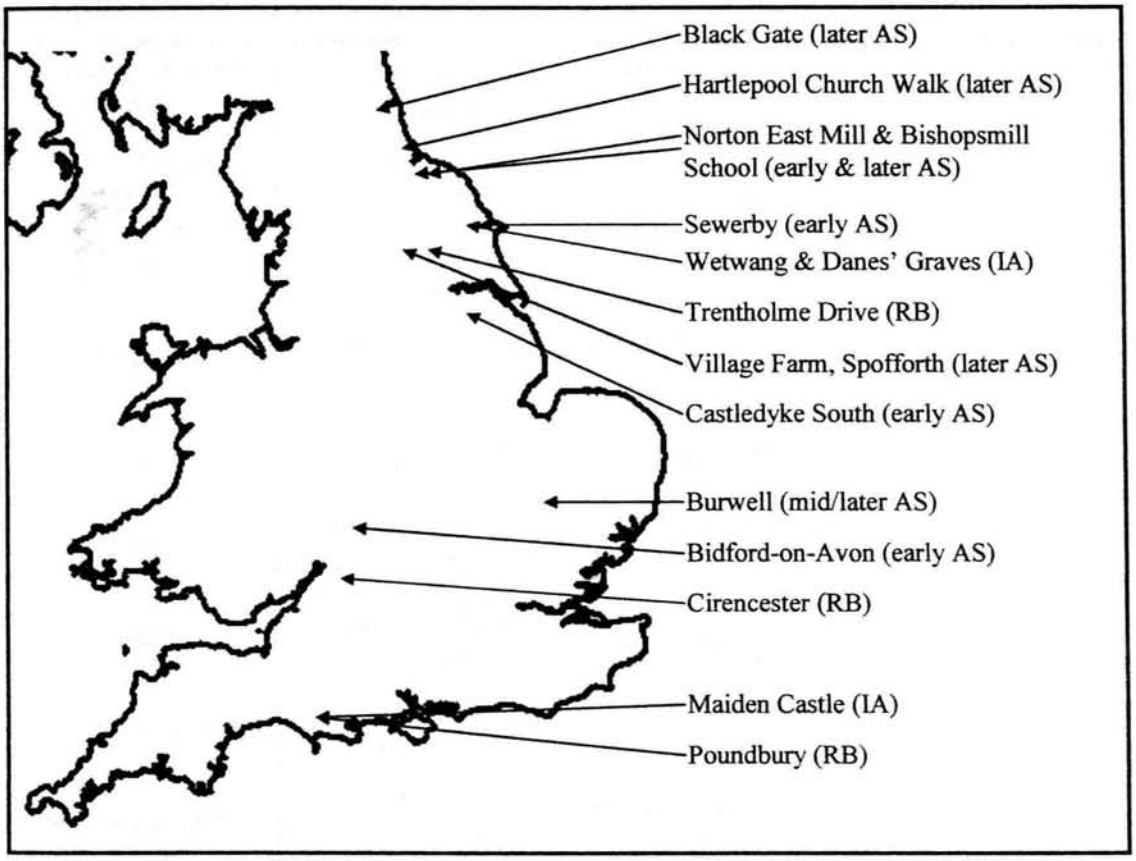
Samples used in this study represent a broad range of geographically and temporally differentiated populations, and vary considerably in size. These samples range from the Iron Age to the late Anglo-Saxon period, and are distributed from Tyneside in the north of England to Dorset in the south, and from Warwickshire in the west to Norfolk in the east (figure 3.1). Continental samples comprise a Danish dataset which includes samples from pre-Roman to Viking periods, and a sample of medieval individuals from Maastricht, The Netherlands.

In selecting samples for use, the aim was to represent English populations both geographically and temporally through the periods in question. Unfortunately the major limiting factor was the level of preservation of the samples, particularly from the Anglo-Saxon period. Skeletal material from this period seems particularly subject to post-deposition factors which result in poor preservation. Many of the well known early Anglo-Saxon cemeteries from the north-east of England, such as Norton East Mill, Castledyke South and Sewerby yielded only a few cases suitable for inclusion in this research; however the recent discovery of later Anglo-Saxon cemeteries, at Village Farm, Spofforth and Norton Bishopsmill School, has contributed a quantity of new, previously unstudied, data to this analysis.

Very few large Iron Age cemeteries are known from England, however Romano-British cemeteries, particularly those associated with Roman towns, are much more common, and skeletal material is often relatively well preserved.

Figure 3.1 provides a map locating all British samples, with the exception of Morant's geographically pooled sample. Table 3.1 provides an overview of individual samples used in this study, and summarises basic information for each.

Figure 3.1 Sample site locations



Note that Morant's London Museums sample is not identified on this map since it is a geographically pooled sample, comprising data mainly from southern and central England, but ranging as far north as Lincolnshire.

Similarly, Danish samples have not been located on a map, as they are also geographically pooled, and comprise individuals from sites covering the whole of modern-day Denmark.

Table 3.1 Summary of Samples

Site Name	Period	Dates	*n* male	*n* female
Wetwang / Garton Slack	Iron Age (Yorkshire)	5th century BC to 1st century AD	146	205
Danes' Graves Driffield	Iron Age (Yorkshire)	Arras – similar date to Wetwang?	15	7
Maiden Castle	Iron Age (Dorset)	?1st Century AD	30	27
Trentholme Drive	Romano-British (Yorkshire)	2nd to 4th Centuries AD	137	42
Poundbury	Romano-British (Dorset)	4th Century AD	28	21
Cirencester	Romano-British (Gloucestershire)	4th-5th Centuries AD	45	21
Sewerby	Early AS (East Yorkshire)	5th/6th to 7th Centuries AD	7	3
Castledyke South	Early AS (Lincolnshire)	5th to 7th Centuries AD	4	3
Norton East Mill	Early AS (Cleveland)	6th to 7th Centuries AD	14	12
Bidford-on-Avon	Early AS (Warwickshire)	?6th - 7th Centuries AD	32	17
Morant's London Museums	Anglo-Saxon (England)	?5th to 10th Centuries AD	67	60
Burwell	?Mid-AS (Cambs)	?7th century AD	46	23
Norton Bishopsmill School	Later AS (Cleveland)	7th to 9th Centuries AD	8	10
Village Farm Spofforth	Later AS (Yorkshire)	8th to ?11th Centuries AD	30	18
Black Gate, The Castle	Later AS (Newcastle)	?8th Century AD	43	12
Hartlepool Church Walk	Later AS (Cleveland)	8th Century AD	20	7
Danish Iron Age	Pre-Roman – Viking Ages (Denmark)	500 BC to 1050 AD	149	104
Maastricht St Servaas	Early Medieval (The Netherlands)	?350 A.D to ?950 AD	23	28

3.3.2 Sample acquisition

Some data included in this study were collected personally by the author, whose techniques are discussed in section 3.4. In order to collect these data, access to the skeletal material was negotiated, and all data collection took place at the relevant repository. Material from Spofforth Anglo-Saxon cemetery was examined at the offices of Northern Archaeological Associates in Barnard Castle, that from Norton East Mill was examined at the offices of Tees Archaeology in Hartlepool, and material from Castledyke South was examined at the North Lincolnshire Museum in Scunthorpe. Material from Sewerby was examined at Sewerby Hall Museum, although the data used in this study were collected by Don Brothwell, and sourced from Sewerby Hall archives.

Data for the majority of samples, however, were gathered from published and unpublished reports and archives. This method of data collection was used in cases where the material was inaccessible, or in order to ensure the maximum data were obtained, as many skeletal samples had been reburied, split up, or had significantly physically deteriorated since their initial assessment and analysis by an osteoarchaeologist. Data sourced in this way comprise that from Wetwang and Garton Slack (paper archive made available by Hull Museums), Trentholme Drive, York (Wenham 1968), the Danish Iron Age (Sellevold *et al.* 1984), Morant's Anglo-Saxon data (Morant 1926), Bidford-on-Avon (Brash *et al.* 1935), Burwell (Layard & Young 1935), Maiden Castle (Goodman & Morant 1940) and Hartlepool Church Walk (M. Knight, unpublished MSc thesis, date unknown).

Finally, large amounts of data were made available by colleagues. Generally, these data had only been summarised in published reports, and the raw data were generously made available upon request. In the case of the sample from St Servaas church, Maastricht, the data forms part of an on-going project, and I am especially indebted to Raphael Panhuysen for its provision. Data from the Poundbury Romano-British cemetery, Dorset, were derived from the CRANID database (collected by Rob Kruszynski), and provided by Professor Richard Wright. Data from Norton East Mill and Black Gate Newcastle were provided by Ms M. Marlow, and the Norton Bishopsmill School data were made available by Ms J. Higgins.

3.3.3 Background to sites and samples

Wetwang / Garton Slack, East Yorkshire ~ Iron Age

The Iron Age cemetery at Wetwang/Garton Slack (henceforth referred to simply as 'Wetwang'), East Yorkshire (Dent 1984), is the largest of two pre-Roman cemeteries from the north-east of England to be included in this study.

Wetwang and Garton Slacks, so far as the cemetery and associated Iron Age settlement are concerned, represent the same archaeological site, and are distinguished in the present day only by dint of a parish boundary. The cemetery is thought to have been in use for up to six centuries, between the 5th century BC and the 1st century AD, although the majority of burials may date from the last 2-4 centuries of use (Jay 2006). Wetwang represents one of the largest Iron Age cemeteries in Britain, with 446 inhumations discovered, although further burials may have been lost to medieval ploughing and modern activity. Out of 362 inhumations where burial position was determinable, 285 individuals were buried in a crouched position, and 75 flexed. There was evidence for coffins or wood lined cists in some graves, and 96 burials were accompanied by grave goods. Skeletal preservation was very good, and 351 adults have been included in the present research.

Wetwang is considered to be representative of the Iron Age in East Yorkshire, and is one of a number of Arras Culture cemeteries in the area. The 'Arras Culture' is defined by four-sided ditch enclosures, inhumations positioned on the side in a crouched or flexed position, artefacts in the European La Tène tradition, and the occasional inclusion of a two-wheeled vehicle.

Danes' Graves, Driffield ~ Iron Age

This sample of Iron Age barrow inhumations (Wright 1903), for which precise dates are unknown, derive from a site just north of Driffield in the Yorkshire Wolds, which lies only a few miles north-east of Wetwang. The name 'Danes' Graves' is a local one of long-standing tradition, but is in fact a misnomer, as the graves are not, in fact, thought to be those of Danes, rather they are thought to date to some time in the (later?) British Iron Age. The graves were oval in form, and the individuals within buried in a very tightly flexed position. Grave goods were found in some instances, and include faunal remains, ornaments, pottery and, in one grave (and typical of an Arras Culture site), the remains of a chariot. No weapons were found in the graves.

Of the hundreds of burials at Danes' Graves, only seven females and fifteen males – are available for analysis here.

Maiden Castle, Dorset ~ Iron Age

The Iron Age / Romano-British sample from Maiden Castle (slightly south-west of the present town of Dorchester), Dorset (Goodman & Morant 1940) was excavated under Dr R. E. M. Wheeler between 1934 and 1937. 104 individuals were represented in the sample recovered, of which 83 were sufficiently well preserved to be worthy of inclusion in Goodman and Morant's paper. The individuals reported on were allocated to periods ranging from the Neolithic (four individuals) to the Saxon period (one individual), however most (seventy-eight) are classed as late Iron Age / Romano-British. Included within this latter category are thirty-one individuals from the so-called 'Belgic War Cemetery' – a cemetery which, according to Goodman and Morant, was the final resting place of the Belgic defenders of Maiden Castle against Roman invaders in 43 AD. The evidence has, however, been reviewed by Niall Sharples (1991), who refutes this interpretation, suggesting that neither the nature of the burials, nor the 'evidence' for the sacking of the fort are entirely consistent with the notion of a hastily assembled war cemetery.

Goodman and Morant's own study found that there were no statistically significant differences between the Belgic War Cemetery series and the rest of the individuals of Iron Age or Romano-British date pooled together. Interestingly, they also found that when pooled together the Maiden Castle series as a whole was indistinguishable from an Anglo-Saxon series (see also Morant 1926).

Trentholme Drive, York, Yorkshire ~ Romano-British

The Romano-British cemetery of Trentholme Drive, York (Wenham 1968), provides the largest comparative sample immediately preceding the Anglo-Saxon period in Yorkshire, and dates from 140 AD to the end of the fourth century. Around 340 inhumations have been found at this site, although the cemetery is known to have extended further than the excavated area – this unexcavated area is now overlain by buildings and roads. Skeletal preservation at this site was comparatively very good – the bones even of very young children surviving – and the sample available for use in this study (*n*=179) reflects this. There is a high male to female ratio, both in the sample used here and in the overall cemetery sample, of around 4:1, a ratio which is not uncommon in cemeteries of this period.

Although this cemetery provides an excellent comparative sample, it must be noted that York, as a garrison town, would have been home to individuals from a potentially wide variety of geographical origins. It may be, for example, that the population represented in this sample resulted at least in part from the marriage of soldiers – some perhaps from overseas – and local Romano-British women. It is also an urban area – a fundamental division is inherent between the urban settlements and cemeteries of the Romano-British period and the more rurally focussed early Anglo-Saxon period, as discussed in Chapter 2 – and the impact of this difference will be noted and explored in the within- and between- group analyses. Care must therefore be taken in comparing this to the other samples utilised in this study.

Poundbury, Dorchester, Dorset ~ Romano-British

The Romano-British sample from Poundbury in the south of England consists of cranial data from 49 individuals which are derived from the CRANID database, and thus represents a sub-sample selected for its completeness relative to the measurements required for CRANID.

Most of the individuals within this sample were buried within the main late Roman cemetery at Poundbury (Farwell & Molleson 1993) which lies on the north-western edge of the present township of Dorchester, along with a small number from the eastern peripheral burial group, and from late Roman burials on site C. In total, the remains of over 1400 individuals were recovered from the area. Burials from the main cemetery were, on the whole, single inhumations in wooden coffins, positioned supine and extended, and orientated with their heads to the west. Grave goods were not common in this cemetery, which is thought to have served both urban and rural populations. The original report indicates that female and male samples appear relatively homogenous, and the sexes are represented equally within this apparently civilian cemetery, suggesting it served "an indigenous British population which lived and died in the area" (*ibid.*: 170).

The dating of this cemetery has relied on the small number of grave goods found, which suggest a date for the main cemetery of the first to third quarters of the 4th century AD.

Bath Gate, Cirencester, Gloucestershire ~ Romano-British

The Romano-British cemetery at Cirencester (McWhirr *et al.* 1982), lying either side of the Fosse Way, was discovered during the development of land south-west of Cirencester in the late 1960s and excavated between 1969 and 1976. Over 450 individual skeletons were excavated, however in most cases the condition of the bone was poor, and often completely fragmented. The skeletal material was examined by Calvin Wells and was divided for the sake of convenience into sub-samples from north and south of the Fosse Way. Due to differences in preservation, comments here refer to the southern sample. Of the 454 burials, 330 were placed in a supine position, 33 prone, and 10 on the left or right side. 77 were indeterminate and there were 3 cremations. The majority (n=181) were orientated south-north with north-south orientations being the next most common (n=104).

Of the 293 adult burials recovered south of the Fosse Way, only 66 (including 45 males and 21 females) were well enough preserved to allow some cranial measurements to be taken without requiring craniofacial reconstruction. The inequity in the ratio of males to females does not just reflect sex-related differential preservation; as at Trentholme Drive, many more men than women (207 to 93) were buried in the Bath Gate cemetery. Wells suggests that the most likely reason for this phenomenon is that like York, Cirencester may have been largely occupied by retired legionaries and Roman officials, who lacked female partners (*ibid.*: 135). However Viner and Leech, in the same volume, seem to doubt this explanation, stating "The [age] range, for both males and females, is representative of a normal, civilian population, unless as Dr. Wells has suggested the males are retired legionaries, material and archaeological evidence for which is not evident from the excavations" (*ibid.*: 109). Unfortunately when the standard eight variable multivariate dataset is considered in this study, the number of females from Cirencester is reduced to only two, and so in analyses where sexes are pooled males dominate over females, and where they are considered separately the female sub-sample has been omitted. The descriptive analyses in section 4.2, however, allow some comparison of male and female craniofacial features to be made.

From the original 1982 report, it appears the period of time in which this cemetery was in use is rather difficult to determine. The report on coins found associated with burials suggests most coins (and probably therefore burials) date to 310-360 AD, however the latest coin dating to Honorius (395-406 AD) suggests that use of the cemetery extended into the 5th century AD (1982: 105) An intriguing suggestion has been made (Wacher cited in McWhirr 1993: 48) that following the decline of the Roman city, the inhabitants may have moved into the town's amphitheatre, thus potentially extending the date of the cemetery into the late 5th or even early 6th century – overlapping the start of the Anglo-Saxon period. This, and the relatively close proximity of Cirencester to Bidford-on-Avon (see below), make this sample particularly interesting in the context of this study.

Sewerby, East Yorkshire ~ Early Anglo-Saxon

The pagan Anglo-Saxon cemetery at Sewerby, near Bridlington, East Yorkshire (Hirst 1985), was excavated in 1959 and 1974. Around 50 graves were excavated, representing an unknown proportion of the whole cemetery. Material from the 1959 excavation was assessed by Don Brothwell, whose measurements are used in this study. This and the material from the 1974 excavation were examined personally, but no further useful data were collected. Graves were dated to between the late 5th or early 6th and the 7th centuries, and were generally orientated east-west or west-east, although a considerable number were orientated north-south. The majority of individuals excavated were buried in a supine, extended position, while around a quarter were buried on one side, with legs semi-flexed. Prone burials accounted for 9% of the total, and crouched burials for 3%. Individuals were commonly buried with grave goods, including dress fasteners, beads, belt fittings and appendages, weapons and vessels. Skeletal preservation was very variable at Sewerby, thus only seven males and three females could be included in this study, within the pooled north-east early Anglo-Saxon sample.

Castledyke South, Lincolnshire ~ Early Anglo-Saxon

The pagan Anglian cemetery at Castledyke South, Lincolnshire (Drinkall & Foreman 1998), lies 250 metres west of St Peter's Church, Barton-on-Humber. It was excavated between 1982 and 1990, and yielded over 227 burials. The true extent of the cemetery remains unknown, however, and there may have been more than 400 individuals inhumed here between the late 5th and late 7th centuries AD.

The nature of the burials within this cemetery was varied, with some laid out in rows, and others in various clusters, many with an exceptional range of grave goods. Orientation was similarly variable, but later skeletons were found orientated east-west, with the head at the west end of the grave. It has been suggested that the later tendency toward an east-west orientation, and ordered rows of graves reflects the influences of Christianisation on the community. The overall impression of the population is of a well ordered, relatively prosperous, healthy community.

Unfortunately the poor preservation of the skeletons from this cemetery, along with the fact that a number of the better examples have been removed from the archive, means that only a small sample (*n*=7, data collected personally) were suitable for inclusion in analyses using raw data. This sample is therefore included in the pooled north-east Anglo-Saxon sample.

Norton East Mill, Cleveland ~ Early Anglo-Saxon

Initially discovered in 1982, the pagan Anglian cemetery at Norton East Mill (Sherlock & Welch 1992) has proved to be exceptional in the Tyne-Tees region of the north of England, both for its scale, and for its proximity to the later cemetery at Norton Bishopsmill School.

Norton East Mill spanned the period 550 to 610 AD, and encompassed an extremely variable mixture of burial types, in terms of the inclusion – or otherwise – and number of grave goods, and the deposition and orientation of the grave cuts and skeletons (there were, for example, 32 crouched, 46 extended and 7 prone burials). With only three exceptions, graves were aligned within 40° of north-south within the cemetery; those which were not were aligned east-west, and include two of the prone burials. Graves appear to be divided into two groups with different alignments, and within these there appear to be some which are arranged in plots or groupings.

The analysis provided in the CBA report suggests that, from grave and grave-goods evidence, the population represented in the cemetery appears to be a farming community, rather than elite or noble Anglo-Saxons. Such an analysis has clear implications for hypotheses of mechanisms of change in the early Anglo-Saxon period. Social analysis also shows that women are relatively better equipped in terms of wealth and grave goods than are the men of the cemetery.

Comments made in this publication show how traditionalist frames of thought affected the study of Anglo-Saxon cemeteries, even in the early 1990s. "We could only hope to answer the questions as to whether Anglian settlers took over and integrated with a thriving hamlet, or instead occupied run-down or deserted farmland" (*ibid.*: 104). This quote reveals that the author does not question the presence of 'biologically Anglo-Saxon Angles', only how and under what circumstances 'they' got there. This cemetery sample provided the initial inspiration for this research, which will contribute to the debate about the extent to which (if at all) 'Anglian settlers' contributed biologically to this, and the wider Anglo-Saxon, population. Unfortunately, however, as with so many of the north-eastern early Anglo-Saxon samples in this study, poor preservation has severely reduced the number of individuals available for inclusion in the final dataset. This sample therefore comprises part of the pooled north-east early Anglo-Saxon sample.

Bidford-on-Avon, Warwickshire ~ Early Anglo-Saxon

The early Anglo-Saxon cemetery at Bidford-on-Avon (Brash *et al.* 1935) in Warwickshire was first discovered in 1921, during road construction. The human remains and associated archaeological material were subsequently excavated in 1922 and 1923, and were assigned by the excavators (via methods unknown, but presumably by a typological method of dating) to the first part of the 6^{th} century AD. A mixture of cremation urns and inhumations were recovered (numbering approximately 151 and 222 respectively), of which ~51 were adult remains in what Brash *et al.* considered a fair state of preservation for further analysis.

The duration of use of the cemetery is not known, but it is considered to be representative of a community, as young, adult and older individuals are all represented. Individuals appear to have been buried invariably in an extended, supine position, with the head in the majority of cases at the south end of the grave cut. Grave goods found included spears, shields and knives with the apparently male burials, and brooches, beads, pots and knives with the females. In what is thought to be the later part of the cemetery an inclination toward an east-west alignment is seen, along with an absence of grave goods. Craniometric data for 32 males and 17 females are included in the present study.

Morant London Museums, England ~ Anglo-Saxon

This large Anglo-Saxon sample was derived from Morant (1926), and was made up primarily of skulls curated at that time in the British Museum (Natural History), the Museum of the Royal College of Surgeons and the London Museum.

This sample was compiled by Morant in response to the lack of any such substantial Anglo-Saxon samples at that time, and was used to provide a statistical analysis of pre- and early- historic English populations (see Chapter 2, section 2.4.1 for a discussion of Morant's contribution). Morant divided the sample into four geographically delimited groups: West Saxons (*n*=25) from Wiltshire, Berkshire, Oxfordshire, Gloucestershire, Buckinghamshire, Dorsetshire and Somersetshire; South Saxons (*n*=26) from the London district, Sussex and Essex; Angles (*n*=46) from Lincolnshire, Cambridgeshire, Yorkshire, Norfolk, Nottinghamshire and Northamptonshire; and Jutes (*n*=30) from Kent. As will be evident from the earlier discussion of the historical sources pertinent to this research, these divisions correspond with those devised by Bede in his chronicling of the Anglo-Saxon invasion and settlement of England. It should also be noted that most crania derive from the south and east of England, and the only significant more northerly sub-sample is from Sleaford, Lincolnshire. There is only one skull from Yorkshire, and none from any more northerly regions.

As a whole, this sample consists of skeletons from sites which, according to Morant, can be dated between the fifth and early tenth centuries AD, thus combining the 'early' and 'later' Anglo-Saxon groupings used in the present study. It does appear, however, that the majority of individuals included in Morant's sample date from the earlier portion of the 'Anglo-Saxon' period, as reference is made to the paucity of remains from later Anglo-Saxon cemeteries (due to a lack of archaeological interest because of the lack of grave-goods in this later period). Morant confidently states "It should be remembered that hardly any of the Anglo-Saxons with which we are dealing were interred later than the 6th century" (1926: 78). In this study, this sample has been tentatively considered to represent the early/mid Anglo-Saxon period.

Burwell, Cambridgeshire ~ ?Early-Mid Anglo-Saxon

The Anglo-Saxon cemetery at Burwell, north-east of Cambridge (Layard & Young 1935) was discovered in 1884, and between 1926 and 1929 around 125 inhumations were excavated. In general, individuals were buried with the head toward the west, and with few grave goods. The cemetery has been dated to the 7th century AD (although this date was probably based on typological analysis of the grave goods found, and the 'Christianised' nature of the majority of the burials), thus bordering the early-later Anglo-Saxon periods. Of the 125 inhumations excavated, 69 were well enough preserved to allow craniometric measurements to be taken. 46 males and 23 females are included in this study.

Norton Bishopsmill School, Cleveland ~ Later Anglo-Saxon

The later Anglo-Saxon cemetery at Bishopsmill School, Norton, Stockton-on-Tees (http://www.teesarchaeology.com/projects/bishopsmill_norton/index.html) was excavated by Tees Archaeology in 2003, prior to the extension of the school. 83 graves containing 107 individuals were found, the majority of which had been buried on an east-west orientation. The alignment of the graves and the lack of grave goods is strongly suggestive of a Christian population.

Despite the relatively large cemetery size, the usefulness of this sample is unfortunately limited in the present study, due to poor preservation of the remains. This is the result of a number of factors including medieval ploughing, modern agriculture and the construction of the school in the 1970s, along with the effects of the acidic soil and high water table.

Nevertheless, the sample represents a useful contribution to the present study, due to its close proximity to the Norton East Mill early Anglo-Saxon cemetery which immediately predates Norton Bishopsmill School. There is also a fascinating link between this and other later Anglo-Saxon cemeteries in the region, in that a number of unusual chest fittings were found at this cemetery, the like of which are rare, and have so far only been discovered at Ripon, York and Spofforth (NAA, pers. comm.). These factors make this sample – one which has not been studied beyond its initial osteoarchaeological assessment – worth including in this study.

Village Farm Spofforth, Yorkshire ~ Later Anglo-Saxon

This later Anglo-Saxon cemetery was discovered during construction work at a housing development site in Spofforth, in the Harrogate district of North Yorkshire, and excavated by Northern Archaeological Associates (NAA) in 2001. A total of 127 recognisable individuals were recovered from 117 recognisable graves, along with 53 disarticulated skulls (NAA, pers. comm.). It is certain, however, that this cemetery has not been excavated in its entirety, as the site was truncated by Village Farm itself, and further graves undoubtedly lie outside the limits of the development.

Currently, dates assigned to the cemetery rely on artefactual material – specifically chest fittings – found within some of the grave fills. The use of chest fittings as funerary items is considered to date from the mid-Anglo-Saxon period. Some fills contained post-conquest material; this is thought to have been intrusive, however the possibility of there being post-conquest burials present cannot be ruled out at this time. A substantial amount of disarticulated charnel was also recovered from this site, and is thought to represent some of the earlier interments. The cemetery appears to have originated in the 8th century and may have continued in use as late as the 12th or 13th centuries. It therefore potentially spans the mid/later Anglo-Saxon period, the Viking incursions and the Norman Conquest. As at Bishopsmill School, Norton, particular types of chest fittings were found. These are paralleled at the early to mid- Anglo-Saxon cemetery at Ailcy Hill, Ripon. (Unfortunately skeletons from the latter were too poorly preserved to be of use in this study.)

On the whole, individuals were buried with the head to the west end of the grave, and the great majority were buried in a supine extended position. The nature of the burials suggests the population were both Christian and laymen – there is no evidence of pagan or clerical burials within the area.

This sample holds great importance in both regional and national contexts, and is a valuable addition to the present research. There are very few Anglo-Saxon cemeteries in the immediate vicinity, and those which are known tend to be extremely poorly preserved. It has not been studied previously, apart from a partial post-excavation assessment, and thus represents a new and original contribution to the study of the Anglo-Saxon population of northern England.

Preservation at Village Farm, Spofforth was varied, but enough individuals were well enough preserved to allow the crania of 30 males and 18 females to be included in at least some elements of this study. This sample also forms part of the pooled north-east later Anglo-Saxon sample.

Black Gate, The Castle, Newcastle ~ Later Anglo-Saxon

Very little is known about this sample, since to the best of my knowledge, no report on it has ever been published.

From the 8th century, the area of the Pons Aeilus – a Roman fort – was used as a Christian Anglo-Saxon cemetery, probably part of a small monastic settlement on the site of the Roman fortress (no excavation report has been published for this cemetery; details from http://www.museums.ncl.ac.uk/keep/keep_history.htm). William Curthose, son of William the Conqueror, built a wooden castle on the site of

Pons Aeilus as an outpost against the Scots; this castle became known as (the) New Castle upon Tyne. In 1250 a stone barbican was added to protect the north gate, which is now known as the Black Gate. The Anglo-Saxon cemetery takes its name from this barbican, and the sample forms part of the pooled north-east later Anglo-Saxon sample.

Hartlepool Church Walk, Teesside ~ Later Anglo-Saxon

This sample was excavated in two phases during 1972 and 1976 (Knight, unpublished MSc thesis, date unknown; http://www.teesarchaeology.com/projects/saxon_monastery/index.html). Church Walk is located just to the south of the medieval church of St Hilda, and radiocarbon dating has assigned the cemetery to the 8th century, in the later Anglo-Saxon period. The burials at this site included men, women and children, buried with their heads to the west, 31 of which are included in the present study.

The cemetery may be associated with the monastery at Hartlepool, which is thought to have met its demise either at the hands of Viking raiders (although there is little evidence to support this assertion) in the 9th century, or through abandonment due to the political troubles occurring in the late 8th century.

This sample forms part of the pooled north-east later Anglo-Saxon sample.

Danish Iron Age, Denmark

This sample represents all the skeletal remains found within the present borders of Denmark, which could be dated securely to the 'Iron Age Period'. This period is much broader than that of the same name in Britain, and ranges from the pre-Roman period to the end of the Viking period – approximately 500 BC to 1050 AD. Dating of the material was based on associations between skeletons and grave goods, along with selective C14 analyses.

The material presented in *Iron Age Man in Denmark* (Sellevold *et al*. 1984) has been subdivided by the authors into six archaeologically defined periods: the pre-Roman period (ca. 500 BC-ca. 0), the early Roman period (ca. 0-ca. 160/170 AD), the late Roman period (ca. 160/170 AD-ca. 400 AD), the Migration period (ca. 400 AD-ca. 550/575 AD), the late Germanic period (ca. 550/575 AD-ca. 800 AD) and the Viking Period (ca. 800 AD-ca. 1050 AD). The most interesting of these in the context of the present research are the Migration and late Germanic periods, however skeletons from this period represent only 0.9% and 2% of the total material presented respectively. This is apparently due largely to the preference, during these periods for cremation, rather than inhumation. As in Britain, soil conditions also had considerable impact on the preservation of skeletal remains, which was particularly poor in mid- and west Jutland, and variable within and between all the regions of Denmark. Geographical and chronological representitiveness is therefore clearly limited by the cultural and environmental factors discussed above.

Despite problems with poor preservation, and sub-sample sizes, this sample remains the major comparative group used in this research, and – in terms of comparison with the Anglo-Saxon groups – the focus is on the late Roman and Viking periods, as the samples most closely related temporally to the early and later Anglo-Saxon period settlers in Britain. Additionally, the early and late Roman samples may reasonably be considered as temporally comparable to the late Iron Age and Romano-British period samples from Britain.

Maastricht St Servaas, The Netherlands

This sample represents the second comparative sample from the continent, and falls within the Romano-British, and Anglo-Saxon time periods used in this study. Data have been provided by Raphael Panhuysen (pers. comm. 2003), who is conducting an ongoing project using this material. This is part of the St. Servaas project, which aims to bring data from all excavations around the church into one large database and publication. The samples are stored in Amsterdam and Maastricht.

These burials are not associated by culture, but are placed into chronological order on the basis of their stratigraphy and other contextual information (Panhuysen, pers. comm.) Then they are categorised by historical period. The Maastricht Servaas sample consists of burials dated from circa 350 AD to 1800 AD. The largest sub samples are individuals dated to the late Roman period, the Merovingian and Carolingian period. All burials come from a large cemetery situated in and around the St Servatius church (excavated in 1954 and from 1981-1989) and a smaller cemetery in close vicinity (excavated 1969-1970). The total number of individuals for the period between 350 AD and 950 AD is circa 560, and data from 52 individuals have so far been made available. This dataset currently consists of only three variables; cranial length, breadth and height, and is thus considered here only in the descriptive and univariate analyses.

3.4 Data collection & processing

3.4.1 Instruments and data collection

Standard osteological instruments were used in the collection of craniometric data; a set of spreading scale callipers, a set of Mitutoyo digital sliding callipers and a narrow metal measuring tape. Measurements taken with the digital callipers were read to 0.01 of a millimetre, while those taken with the spreading callipers and the tape were measured to the nearest 0.5mm.

Data collected personally were recorded on specifically designed data recording sheets. These recorded the individual skeleton code, the craniometric data and my assessment of the individual's sex and age (see sections 3.4.5 and 3.4.6), along with any additional information regarding the individual.

Data gathered from archives and published reports were transferred directly to an Excel database. Data acquired in electronic database form required reprocessing only in terms of standardisation, error checking and so on. These processes are explained in section 3.4.4.

3.4.2 Craniometric variables

Many thousands of craniometric measurements have been devised by the craniologists and osteologists of the past, covering in immense detail all areas of the cranial vault and base, facial skeleton and mandible. The main criterion used for selection was that techniques used and data gained should concur as far as possible with the standard measurements used by other researchers in the field. Secondly, measurements should allow the amount of useful data and number of samples available to the study to be maximised.

Although there is evidence that both craniofacial and cranial vault measurements may be regarded to an extent as reflecting biological affiliation (see Chapter 2, section 2.8), in this study issues of preservation impact significantly on those measurements which could most usefully be employed. It has been suggested in a number of previous studies that measurements of the cranial vault are useful in morphological population comparisons. Brothwell and Krzanowski addressed the issues of preservation and morphological analysis, finding that an analysis based on commonly available vault measurements allowed a highly satisfactory separation of chronologically and, to an extent, geographically defined archaeological populations in Britain. These measurements, including both whole vault and individual bone dimensions are, they state, "reasonably likely to record variation in different regions of the cranial vault" (1974: 250).

For these reasons, the measurements described below (tables 3.2 and 3.3,), include a relatively large number of commonly used vault measurements and a relatively smaller number of measurements of the facial and mandibular skeleton. Of these, relatively few were ultimately employed in the statistical analyses, however they have all been described here for the benefit of future researchers who may wish to use this dataset (Appendix 4). Most measurement definitions have been taken from Brothwell (1981), as these are commonly used by other researchers, and correspond most frequently with those given in other texts. There are a few exceptions however. Definitions for maxillo-alveolar length (MAL), breadth (MAB) and height of the ascending ramus of mandible (ARH) are given by Bass (1995), as descriptions of these measurements are not given by Brothwell. The same applies to the definitions given for the upper facial breadth (FMB) and biorbital breadth (EKB) measurements, which are described by Buikstra and Ubelaker (1994).

3.4.3 Variable codes

The variable codes used in this study (tables 3.4 and 3.5) have been adapted from the system used by Howells (1989). Each variable has been allocated a three letter code which is, to an extent, descriptive of its meaning. This system has been used for a number of reasons. The codes used by Howells will be familiar to a number of researchers, and have been used in the CRANID worldwide craniometric database. Where measurements used in this study did not have a code (i.e. were not used by Howells), one was devised which fit into the overall rationale of the Howells codes. These codes were preferred over other systems (e.g. Biometric, Martin) as they are more descriptive than numerical codes, are shorter than 'word-based codes' and are acceptable to SPSS as no symbols are used.

As the data used in this study were derived from a number of disparate sources, using a variety of coding systems, it was important that variables be standardised to ensure comparability of data. All sources of data and coding were checked for equivalence of technique, and where techniques were the same, the datasets were recoded using the codes described in tables 3.2 and 3.3. The only variables which differed in technique were those where prosthion was used instead of alveolare, and these have been given separate codes accordingly.

Table 3.2 Cranial vault and base measurements

Code	Definition
GOL	Maximum cranial length from glabella to opsithocranion
XCB	Maximum cranial breadth from euryon to euryon
BBH	Maximum cranial height from basion to bregma
WFB	Minimum frontal breadth from frontotemporale to frontotemporale
BNL	Basi-nasal length from basion to nasion
BAL (BPL)	Basi-alveolar length from basion to alveolare (or prosthion)
FRC	Frontal chord from nasion to bregma
PAC	Parietal chord from bregma to lambda
OCC	Occipital chord from lambda to opsithion
FOL	Foraminal length from basion to opsithion
FOB	Foraminal breadth between lateral borders of the foramen magnum
ASB	Biasterionic breadth from asterion to asterion
FRA	Frontal arc from nasion to bregma
PAA	Parietal arc from bregma to lambda
OCA	Occipital arc from lambda to opsithion
TBA	Transverse biporial arc from porion through bregma to porion

Table 3.3 Facial and mandibular measurements

Code	Definition
MFH	Total facial height from nasion to gnathion
NAH (NPH)	Upper facial height from nasion to alveolare (or prosthion)
ZYB	Bizygomatic breadth – greatest breadth between zygomatic arches
NLH	Nasal height from nasion to nasospinale
NLB	Nasal breadth from alare to alare, perpendicular to height
OBB	Orbital breadth from dacryon to ectoconchion
OBH	Orbital height – maximum perpendicular to breadth, bisecting orbit
MAL	Maxillo-alveolar length from prosthion to alveolon
MAB	Maxillo-alveolar breadth from ectomolare to ectomolare
IPL	Internal palate length from orale to staphylion
IPB	Internal palate breadth from endomolare to endomolare
ZMB	Bimaxillary breadth from zygomaxillare to zygomaxillare
WNB	Minimum breadth of nasal bones along maxillo-nasal sutures
DKB	Bi-dacryonic chord from dacryon to dacryon
FMB	Upper facial breadth between external points on fronto-malar suture
EKB	Biorbital breadth from ectoconchion to ectoconchion
BCB	Bicondylar breadth from lateral condylion to lateral condylion
BGB	Bigonial breadth from gonion to gonion
ARH	Height of ascending ramus from top of condyle to gonion
WRB	Minimum ramus breadth measured perpendicular to height
SYH	Height of mandibular symphysis from gnathion to infradentale
MTB	Foramen mentalia breadth from mentale to mentale

Table 3.4 Cranial vault and base measurement codes

Measurement Description	Current	Howells	Biometric
Maximum cranial length	GOL	GOL	L
Maximum cranial breadth	XCB	XCB	B
Maximum cranial height	BBH	BBH	H’
Minimum frontal breadth	WFB	-	B’
Basi-nasal length	BNL	BNL	LB
Basi-alveolar length	BAL (BPL)	(BPL)	GL
Frontal chord	FRC	FRC	S’1
Parietal chord	PAC	PAC	S’2
Occipital chord	OCC	OCC	S’3
Foraminal length	FOL	FOL	FL
Foraminal breadth	FOB	-	FB
Biasterionic breadth	ASB	ASB	BiastB
Frontal arc	FRA	-	S1
Parietal arc	PAA	-	S2
Occipital arc	OCA	-	S3
Transverse biporial arc	TBA	-	BQ’

Table 3.5 Facial and mandibular measurement codes

Measurement Description	Current	Howells	Biometric
Total facial height	MFH	-	-
Upper facial height	NAH (NPH)	(NPH)	G’H
Bizygomatic breadth	ZYB	ZYB	J
Nasal height	NLH	NLH	N’H
Nasal breadth	NLB	NLB	NB
Orbital breadth	OBB	OBB	O’1
Orbital height	OBH	OBH	O2
Maxillo-alveolar length	MAL	MAL	-
Maxillo-alveolar breadth	MAB	MAB	-
Internal palate length	IPL	-	G’1
Internal palate breadth	IPB	-	G2
Bimaxillary breadth	ZMB	ZMB	GB
Simiotic chord	WNB	WNB	SC
Bi-dacryonic chord	DKB	DKB	DC
Upper facial breadth	FMB	FMB	-
Biorbital breadth	EKB	EKB	-
Bicondylar breadth	BCB	-	W1
Bigonial breadth	BGB	-	GoGo
Height of ascending ramus	ARH	-	-
Minimum ramus breadth	WRB	-	RB’
Height of mandibular symphysis	SYH	-	H1
Foramen mentalia breadth	MTB	-	ZZ

3.4.4 Preparation of data for analysis

Having been collected and transferred to an Excel database, data were then prepared for analysis via a number of processes.

Measurement variables in datasets that were not collected personally were checked for equivalence of technique and recoded as described in section 3.4.3. Those using slightly different techniques for the same measurement (e.g. upper facial height) were identified and recoded as described above (e.g. NAH/NPH). Where variables were measured in very different ways (e.g. Morant's palatal lengths) they were removed altogether from the dataset. A number of sources included variables which had not been chosen for inclusion in this study at all, and these too were deleted from the working dataset.

Following the standardisation of variables, the data were then 'trimmed' in order to remove juvenile individuals and those who could not be, or had not been, sexed. The age range for juveniles was somewhat arbitrarily set at 0-17 years, on the basis that after this point the individual could be reasonably considered mature in terms of cranio-morphological growth. However, it is recognised, firstly, that individuals do not all mature at the same rate, and therefore (depending on the techniques used) an individual estimated at 18 years may or may not have completed their growth. It is considered, however, that equivalence of ageing techniques can reasonably be assumed to be such that an individual reported to be 18 or older may be considered an adult for the purposes of this research. Secondly it is recognised (see Chapter 2, section 2.8) that an individual's cranial morphology has the potential to change constantly throughout the lifetime; bone responding plastically to the stresses of mastication and muscle use, and also potentially degeneratively to nutritional and pathological factors, as well as to factors relating to the ageing process. However, after the age of 20 a relatively small 2-4 % change in cephalic and facial dimensions is anticipated (Tanner 1988 in İşcan & Helmer 1993).

Finally, the data were checked for errors arising from faults occurring either at the data input stage, or from typographical or printing errors in published sources. A number of techniques were used to achieve this end. The data were visually checked for mistakes, and were transferred to SPSS, where univariate 'Descriptives' and 'Frequencies' analyses were used to indicate the presence of 'unnatural outliers' in the dataset. However, none of these techniques can identify cases where measurements were misread (e.g. from hand-written skeletal data sheets), reported or inputted incorrectly, but within the 'normal' range for any particular variable. Further sources of potential error in the data are considered in section 3.4.7.

3.4.5 Sex assessment

Where data were gathered personally, it was necessary also to arrive at sex and age estimates for all individuals for which craniometric data were collected. Techniques for age estimation are discussed in section 3.3.6. Accurate sex assessment is vital in a study of this nature, in order that male and female variation can be considered separately. It is also important that males and females can be identified and separated for analysis. This allows the effects of sexual dimorphism (in size) to be removed, and allows analyses of pooled sex samples to be conducted.

Where individuals were considered to be developmentally mature, sex was assessed following traditional methods (e.g. Bass 1995, Brickley & McKinley 2004, Brothwell 1981, Krogman 1962, White 2000), focussing on the pelvis, skull and overall robusticity of the skeleton. In all cases, pelvic features were weighted most heavily, although variability in the completeness and preservation levels of individual skeletons frequently required that alternative criteria were used. Pelvic features are favoured in terms of providing sexing information due to their functional adaptation for parturition and locomotion. Relatively, the female pelvic inlet, greater sciatic notch and sub-pubic angle are wider compared to the male. The female pubic ramus is longer and narrower than the male, and the presence of a pre-auricular sulcus and ventral arc are indicative of a female individual.

In the skull, male features are generally larger and more robust; supraorbital ridges and temporal and nuchal lines are more prominent, mastoid processes, palate and teeth tend to be larger, the orbital border is blunt rather than sharp, and the frontal and parietal bones display less bossing. The mandible is more robust in male individuals, with a square rather than pointed chin and greater gonial flaring.

Postcranially males again tend more toward greater size and robusticity, with more prominent muscle attachment markings and relatively larger joint surfaces.

Due to the amount of variation within and between populations, the process of attributing biological sex to an individual is always more accurate when this population-level variation is taken into account, and where possible (i.e. where sample numbers allowed), individual features were assessed for size, robusticity and so on, relative to others within the sample.

3.4.6 Age assessment

Although analyses based on age as a variable have not been conducted in this study, it is important to have accurate age estimates for those individuals included in the data in order that sub-adults could be removed from the craniometric analyses. The age of an individual also has an impact on the expression of sexually dimorphic features, and thus aids in the provision of sex estimates for individual skeletons.

Two major processes are considered when assessing an individual skeleton for age; developmental processes are those of the growth and maturation of the individual bones and dentition, whereas degenerative processes include joint and bone degeneration and dental attrition.

Age estimation is easier and more accurate for younger individuals (in contrast to sexing, which is more accurate for adults), as a definite chronological sequence of bone growth and development may be observed. To this end, the stage of epiphysial union of bones are observed and compared against charts, thus allowing an age range to be attributed. The stage of dental eruption is similarly observed and compared against developmental charts to provide an age-range estimate.

Although developmental processes allow reasonably narrow age ranges to be allocated, it is important to remember that genetic and environmental factors can influence the rate of an individual's development, and the age provided must be considered a biological, not chronological, estimate.

For older individuals who have completed the developmental processes, degenerative factors are used to provide an age estimate. This is inevitably less accurate than using developmental processes, as the degeneration of bony features is influenced much more by environmental (physical, occupational, pathological) factors, and age ranges tend to be wider than for younger individuals. For these individuals, dental attrition is observed and compared against a chart in order to obtain an age range (Brothwell 1981). The pubic symphysis is similarly used (White 2000), and the degenerative processes visible in joint surfaces are observed. As with sexing, the accuracy of age estimates is improved by considering each individual in terms of the overall population variation for the factors described above.

3.4.7 Sources of error

In a study of this nature, there are invariably a number of potential means of introducing error into the data. Below I consider the possible sources of such error, and explain what measures have been taken to attempt to limit their impact.

Measuring techniques and inter- and intra- observer error. Where data were collected personally, internal (intra-observer) error was countered using a number of methods. Craniometric data were collected from the Norton East Mill sample using the techniques described above, and were then compared with data collected by Ms M. Marlow during the sample's assessment for publication. It was found that the two sets of measurements contained only slight differences, with no measurements varying by more than 1mm (mean difference ~ 1.5%), and no systematic discrepancies evident. Data collected which remain unstudied by any other osteologists were continuously checked via repeated measures of randomly selected crania, and again very little variation was evident between measurements, with a mean difference between measurements of less than 0.5mm (~ 1%).

Due to the large amount of data obtained through means other than personally collecting data, there was little that could be done to assess variation (error) between observers. Data collected by Ms Marlow and myself appear free of any systematic variation, but it is impossible to verify the methods used by other researchers, other than by checking the stated techniques used (i.e. definitions of landmarks, with the assumption being implicit that the same landmark definitions are used by all observers, and measurements) as has been described in sections 3.4.2 and 3.4.3. Despite the precautions noted above, it is likely that inter-observer error exists in the dataset, and indeed research conducted by Utermohle & Zeruga (1982) which found both statistically significant intra-observer variation, and "rampant and serious interobserver error" (1982: 307) suggests that this problem should be taken into consideration in all studies such as this.

Calibration of instruments used. Again, it is impossible to confirm that the instruments used in collecting the data obtained from third parties were correctly calibrated, and indeed absolutely equivalent to my own. However, a single set of instruments was used throughout, and were constantly checked and calibrated during the data collection period.

Cranial ambiguities and deformation. As with other areas of the skeleton, the skull is subject to considerable variation arising from genetic variation, and from in-vivo and post-mortem changes to the bones of the skull. The main factors of this type impacting on the accuracy of craniometric measurements are the presence of wormian bones (extra ossicles – small, irregularly shaped bones) at suture lines, particularly at lambda and asterion, in-vivo and post-mortem deformation (e.g. skew, usually along the long axis of the skull), and post-mortem degradation of the cortical bone of the skull (e.g. chemical or mechanical abrasion of the outer bone surface, especially on the vault of the skull). Pathological conditions can also affect the size and shape of the skull, and its surface morphology, but these are obvious in most cases, are always worthy of note in skeletal reports and are thus easy to eliminate from the study. In samples for which data were collected personally, it was possible to monitor the presence of these factors during the data collection process, and to eliminate those individuals which showed evidence of post-mortem modification from the sample. In samples acquired from elsewhere, it is to be hoped that the researcher had made similar observations, and in most cases, these peculiarities had been noted somewhere in the dataset, and could thus be eliminated at the data preparation stage.

The most problematic of the features noted above (in terms of this research) is the presence of wormian bones. In most cases, these are not a hindrance to the collection of data, but when they occur at lambda or asterion, a judgement must be made by the individual collecting the data about the location of the landmark in question. Generally this is not too difficult, as quite often the natural 'path' of the suture (edge of bone) in question is clearly visible, and the landmark may be logically visually located with relative ease. In some cases, however, this is not possible (due to the nature of the bone itself, or of the suture or ossicles) and the location of the landmark is less obvious. In serious cases the measurement would not be taken, in order to preserve the validity of the dataset as a whole. Alternatively, two measurements would be taken – one above and one below the ossicles – again, in these cases, the measurement was removed from the working dataset entirely. As mentioned above, it is not possible to account for the data collected by other researchers, but it is assumed that sufficient experience would ensure a certain degree of consistency and logic in most situations. This remains, however, one of the least controllable sources of error.

3.5 Statistical treatment of the data

3.5.1 Introduction

The penultimate subsection of this methodology chapter describes the descriptive and analytical statistics employed in this study, and indicates how these analyses relate to the hypotheses presented in section 3.2. Section 3.5.2 outlines the methodological assumptions necessary in the analysis of the data. Section 3.5.3 covers the descriptive element of this research. Section 3.5.4 describes the univariate analyses undertaken between females and males within, and between, groups; section 3.5.5 introduces the multivariate analyses of variance; section 3.5.6 describes the R matrix analyses; and sections 3.5.7 and 3.5.8 describe the Mantel matrix correlation and Relethford-Blangero analyses.

3.5.2 Assumptions

A number of theoretical and methodological assumptions are implicit in the analysis of populations in this study. Theoretical assumptions will be discussed within the relevant sections below, where they pertain to specific statistical analyses. Methodologically, it is assumed that:

- Estimates of sex have been carried out correctly among all the samples.
- The individuals within each sample are representative of the populations they are thought to represent.

Of these considerations, the former is probably the least problematic, in that sex estimates are, on the whole, likely to have been made across samples with a reasonable degree of accuracy. In a number of cases, sex assessments made by other researchers have been cross-checked with assessments made personally, and in these situations there has been a high degree of concordance. More troublesome are cases where samples have been drawn together from a number of varied sources, such as is the case with Morant's London Museums data, where sub-samples are likely to have been examined by a number of different researchers. However, as was noted in section 3.4.5, the data were examined for cases of dubious sex, and these cases were removed prior to any analysis taking place.

The second methodological assumption concerns the representitiveness of the samples in question as regards the *populations* these samples are supposed to represent. For the purposes of this study it is assumed that individuals buried within cemeteries are individuals who lived within that geographical area, although as has been previously noted, it is not possible to identify cases where individuals living elsewhere in life have returned to a particular location for burial. It is also assumed, perhaps more problematically, that the individuals recovered from each cemetery, and the individuals that ultimately make it into the analyses here, have not been subject to any systematic pre- or post-mortem taphonomic bias or sampling bias.

It is also assumed that the date ranges attributed to the various cemetery samples, or combined samples, are correct. In a number of cases, absolute methods of dating, for example C14 analysis, have been used to attribute dates. In other cases, however, dating has been based on relative or typological evidence utilising archaeological features or material cultural artefacts. The methods that have been used to attribute dates, where this information is known, have been noted in the descriptions of samples given in section 3.3.3.

3.5.3 Descriptive statistics

The following cranial and facial indices have been calculated (as described in Bass 1995), where the raw data allow, to provide descriptive measures of shape.

Note that in interpreting these analyses in terms of categories, I have accounted for and corrected the error in Bass' orbital index categories (1995: 82).

Table 3.6 Formulae for craniofacial indices used in this study

Index	Formula
Cranial Index	= XCB * 100 / GOL
Cranial Length / Height Index	= BBH * 100 / GOL
Cranial Breadth / Height Index	= BBH * 100 / XCB
Fronto-Parietal Index	= WFB * 100 / XCB
Total Facial Index	= MFH * 100 / ZYB
Upper Facial Index	= NAH [or NPH] * 100 / ZYB
Nasal Index	= NLB * 100 / NLH
Orbital Index	= OBH * 100 / OBB
Maxilloalveolar Index	= MAB * 100 / MAL
Palatal Index	= IPB * 100 / IPL

It was not considered that a similar analysis of raw variables would add significantly to this research. Descriptive analyses (produced in SPSS 11.0 for Windows) for each of the samples used in this study have been provided, which, for each craniofacial index, include the number of individuals with available data for each variable, the central tendency (mean), minimum and maximum values (range) and standard deviation (measure of dispersion/variation of the data around the mean). These statistics are provided for all the major sample groups, and for site-specific samples where appropriate, and are presented by sex.

3.5.4 Univariate analyses

The analyses described below allow hypothesis 1, and observations resulting from the descriptive analyses, to be statistically tested. They also allow samples to be examined with regard to their suitability for pooling in subsequent analyses.

Independent samples *t*-tests were used to compare within-sample, between-sex means for all craniofacial indices where possible. This statistic was computed using SPSS 11.0 for Windows, employing Levene's test for equality of variance, and using a significance level of $p<0.05$. This test has been chosen on the basis that biological metrical variables generally conform to the assumption of normality of distribution required by parametric tests, although very small sample sizes in some cases may violate this assumption. The results of the *t*-tests are presented alongside the descriptive analyses for each sample.

Additionally, one-way analyses of variance (ANOVA) in SPSS 11.0 for Windows were used, solely with craniofacial indices, in order to explore differences among samples. The one-way ANOVA is a means by which the presence of statistically significant differences among groups may be established, without incurring the greatly increased risk of type I errors (i.e. with subsequent comparisons, increasing the probability of obtaining a significant result due to chance alone) that would result from conducting multiple *t*-tests between pairs of samples. While the *post hoc* tests used with ANOVA necessarily conduct multiple pairwise comparisons, a variety of different tests are available in SPSS which, using various methods and having different levels of liberalness or conservativeness associated with them, reduce the likelihood of type I errors occurring. In the present research, both relatively liberal and relatively conservative *post-hoc* tests (LSD, Tukey's HSD and Games-Howell as appropriate) have been employed.

3.5.5 Multivariate analyses: MANOVA

Multivariate analyses of variance have been utilised in order to assess whether there are statistically identifiable differences among the samples used in this study, and were carried out on both minimally and maximally pooled sample sets.

These have been conducted using SPSS 11.0 for Windows, using the general linear model procedure, and were conducted on the basis of the eight z-score transformed (sex-standardised) raw variables ultimately used in the RMET analyses.

Box's M (test of equality of covariance matrices) and Pillai's Trace statistics were used. Pillai's trace is considered more robust than Wilks' Lambda in cases where the assumption of equality of covariance matrices is violated. Between-subjects effects tests in MANOVA work in the same way as repeated one-way analyses of variance, and these are used to examine the significance of differences in individual variables among groups.

3.5.6 Multivariate analyses: RMET and R matrix analyses

Core multivariate analyses used to test hypotheses 2a to 4 were performed using RMET 5.0 for Windows, a quantitative genetics software package provided by Dr J. Relethford (2003, available at http://konig.la.utk.edu/relethsoft.html), designed to test minimum genetic differentiation among samples.

RMET has been used to provide analyses of quantitative data from a number of sources, including craniometrics and anthropometrics (e.g. González-José *et al.* 2001a, 2005, Nystrom 2006 in press, Relethford *et al.* 1997, Sardi *et al.* 2005, Schillaci & Stojanowski 2003, 2005, Stefan & Chapman 2003, Stojanowski 2005), skin colour (e.g. Relethford 2002), and dermatoglyphics (e.g. Relethford & Blangero 1990, Weisensee & Siváková 2003), and to investigate topics including population history, population variation, genetic flow and drift, and the heritability of phenetic traits, on both regional and global levels of analysis.

RMET performs a number of analyses, based in this case on raw (or sex-standardised) craniometric data, which allow the assessment of inter- and intra-population relationships and variation. Analyses produced include:

- An R matrix, and related d^2 matrix
- Estimates of F_{ST}
- A Relethford-Blangero analysis
- A plot of the first two principal coordinates for the R matrix

3.5.6.1 Processes

RMET requires that data are entered in ASCII format, whereby rows in the data file are cases, and columns are variables. There must be no missing data, and the variables in the data file must be space-delimited. Preceding the data in the source data file are a title line (giving a description of the data), a parameter line (indicating the number of populations and number of variables in the dataset), population lines (one for each population, including a population label, the population code used in the input data, and the estimate of the census population size which is used for weighting), and finally variable lines giving variable labels. If, as in this case, the population census size cannot be estimated, a value of 1 is used for all populations. The inclusion of these pre-data lines enables RMET to allow the user to select different combinations of populations and variables to be used in the analysis. RMET also allows the user to enter an average heritability (default is 1), correct for sampling bias (due to small sample sizes) if required, and to compute R and d^2 matrices after scaling by population size (in order to control for genetic drift). RMET allows the user to determine which analyses are performed, how results are displayed on screen, and gives a choice of formats for saving the output. Output is usually saved in ASCII (.txt) format, but some output may also be saved in formats more suitable for inputting to other programs (e.g. list or matrix, comma or space delimited or in NT-SYS format).

For the purposes of this study data passed through a number of steps in order to create data input files that RMET could use. In order to improve sample sizes, for many multivariate analyses, males and females were pooled. Additionally, some analyses required that male and female groups be included for comparison in the same analysis. For these reasons, the effect of size differences between males and females was removed (using the 'descriptives' function in SPSS) by separating males and females, then for each sex transforming variable data into z-scores (also known as standardised scores), whereby **z =(x-mean)/sd** when **x** = variable measurement, **mean** = whole (sex specific) dataset mean for that variable and **sd** = standard deviation. It should be noted that whilst absolute size differences between males and females could be corrected for using this method, any overall difference in *shape* would remain, potentially biasing the results of pooled sex analyses in which female and male samples were unequal in favour of the numerically dominant sex. Male and female datasets were then recombined into a working dataset (containing both raw data and z-scores for each case), and the z-scores rather than the raw data were used for all subsequent analyses using RMET. RMET also automatically transforms inputted data to z-scores for the whole dataset, in order to remove the effect of size differences between larger and smaller variables (e.g. cranial length vs. nasal length), so that all variables have a mean of 0 and a standard deviation of 1.

In order to produce the d^2 matrix, the error-checked, standardised data were combined in a single SPSS database, where individual cases were allocated a grouping variable which was recoded as required to allow individual cases to be regrouped appropriately for each specific analysis (e.g. as single site samples, temporally pooled samples, and so on).

For any particular combination of populations and variables, in order to exclude cases with missing data, the 'select cases' function in SPSS was used to select cases where each raw variable in turn was greater than 0 (if **x>0**, i.e. was not missing data). Unselected cases were deleted from the dataset. This was achieved using a dataset comprising both the raw data and the z-scores, so that cases could be selected on the basis of a raw measurement greater than 0, and the corresponding z-scores for each individual case/variable remaining selected for analysis.

Following the exclusion of cases with missing data, variables (which for each case included the population code and desired variable columns) were selected and copied and pasted into WordPad. Once in WordPad, title, parameter and variable lines were added as described above, and then the contents of the file were copied and pasted into a Notepad (.txt) file which could be opened using RMET. This route, while rather circuitous, allows a master database to be created using SPSS whilst also allowing a space-delimited file acceptable to RMET to be the end result.

For all RMET analyses default settings were used for all options, except for average heritability which was set at h=.55 rather than the default of h=1 (see e.g. Hemphill 1998, Relethford 2004 and section 2.8). Correction for sampling bias was requested, but scaled R and d^2 matrices were not requested (as population size could not be estimated in this study).

3.5.6.2 Minimum genetic distance (d^2)

The major aim of this study is to investigate archaeological population relationships within Britain and between Britain and Denmark over time. Accordingly, one of the most important elements of the statistical analyses is the production of measures of biological distance between samples. Analyses of the distance matrices, and plots derived thereof (see section 3.5.6.3), relate specifically to hypotheses 2a-c.

The R matrix is a variance-covariance matrix that estimates genetic distances from phenotypic (in this case, sex-standardised craniometric) data (see Relethford 1996, Relethford *et al.* 1990, 1997, and section 2.8 for a discussion of the relationship between genetic and phenotypic distances). From the R matrix RMET produces a related minimum genetic distance (d^2) matrix whereby $\boldsymbol{d_{ij}^2 = r_{ii} + r_{jj} - 2r_{ij}}$ (Relethford *et al.* 1997: 462). This matrix can (on the user's request) be corrected for sample bias by substituting bias corrected r_{ii} and r_{jj} values into that formula. If a negative distance results, it is truncated to 0 (*ibid.*: 463). Standard errors for the matrices are provided.

Throughout this thesis, the notation 'd^2' is used with a small-case 'd', to distinguish this distance from the commonly used Mahalanobis distance (D^2).

In the present research the Relethford-Blangero and F_{ST} analyses produced directly by RMET are based on the R matrix, whilst the d^2 matrix is the basis for interpretation of genetic distance (i.e. via hierarchical cluster analysis and principal coordinates analysis) and the Mantel matrix correlation analyses.

3.5.6.3 Principal coordinates and cluster analyses

Although RMET reports and plots the first two principal coordinates for the biased R matrix, in order to obtain hierarchical cluster analysis dendrograms (where the relative distance between pairs of samples is reflected in the form of a dendrogram) and principal coordinates (PCO) plots for the first and second and second and third eigenvectors, a different programme is used (PAST 1.37, a freely available statistical analysis package made available by Øyvind Hammer and D.A.T. Harper at http://folk.uio.no/ohammer/past).

Having run an analysis in RMET, the d^2 matrix is saved as a space delimited symmetrical matrix in a .txt file. The .txt file can be opened using PAST, and the principal coordinates and hierarchical cluster analyses performed. In the cluster analysis the 'paired group' (also known as UPGMA) algorithm is used, and the similarity measure set to 'user distance' (Hammer *et al.* 2001). In the PCO analyses 'user distance' is also selected, and the default transformation exponent of C=2 is used.

3.5.7 Matrix correlation analyses: Mantel 3.1

Mantel matrix correlation analyses are used to test the association between biodistance and temporal, geographic and cultural distance (hypotheses 3a and 3b).

When comparing distance matrices derived from different sets of data (e.g. biodistance with geographical or temporal distance) a standard probability test for correlations cannot be used, as a fundamental assumption of such methods is violated (the pairwise elements of such matrices are not mutually independent – if one element is changed, the others will change also).

Within the last two decades a test of matrix correspondence originally developed by Mantel (1967), which avoids this violation, has gained popularity, particularly in ecology, biology and anthropology (Smouse & Long 1992). The Mantel matrix correlation permutation test is non-parametric, therefore avoiding the complications usually associated with parametric tests, and tests the hypothesis that the observed correlation coefficient between two matrices (r_{XY}) is significantly different from zero. This is achieved by permuting the rows and columns of one matrix while the other is held constant. With each permutation, a new r_{XY} is calculated, and the number of permutations yielding an r_{XY} at least as large as the observed r_{XY} provides a test of the null hypothesis. If the null hypothesis is correct (i.e. there is no relationship between matrix X and matrix Y) then it will not matter which X goes with which Y. If the p value is low (i.e. only a small proportion of permutations resulted in a r_{XY} larger that originally observed), usually $p<0.05$, the null hypothesis is rejected, and the observed relationship between matrices may be taken to be significant. In practice, although a one-tailed (unidirectional) test is most commonly used, a two-tailed test is also available in Mantel 3.1, and may be required in circumstances where either a negative or a positive r_{XY} may be expected (*ibid.*).

For a small matrix all possible permutations are calculated, while for a larger matrix (where the number of populations is greater than eight) a random sub-sample of permutations is chosen. In Mantel 3.1 the default number of random permutations is 999, but can be set as high as 9999.

Matrix correlation methods have been widely used to investigate problems relating to population history, and in recent years have successfully been used in conjunction with RMET analyses or other measures of biological / genetic distance. The bulk of anthropological / genetic work which has been done, and particularly some of the earliest uses of this method, almost invariably focussed on global human variation, notably with respect to models concerning the emergence of modern humans, contemporary human variation and isolation by distance (e.g. Eller 1999, Sokal *et al.* 1997, Waddle 1994). In more recent times research has been done which focuses more narrowly on inter- and intra- regional population history, particularly with regard to questions concerning the nature of prehistoric settlement in the Americas (e.g. González-José *et al.* 2001a, 2001b, 2002, Scherer 2004, Schillaci & Stojanowski 2005, Tatarek & Sciulli 2000), and also in the Iberian peninsula (Lalueza Fox *et al.* 1996) and Asia (Hemphill 1998).

The software package Mantel 3.1, which is also provided by Dr J. Relethford (available at http://konig.la.utk.edu/relethsoft.html), is used here to test the association between various factors (e.g. geographic or temporal distance between the populations under study) relative to the d^2 biological distance matrix produced by RMET. This is achieved by the construction of a matrix representing the distances (in terms of separation in time, in space, or by group membership) between populations, and correlating this against the biological distance matrix.

One of the key benefits of this method is that comparative matrices need not be limited to those deriving from continuous distance measures; for example, matrices indicating linguistic or cultural affiliation can be similarly used, and 'design matrices' may also be constructed to represent explanatory models or hypotheses.

3.5.7.1 Process

Like RMET, Mantel 3.1 requires a source data file that is in ASCII format, containing space-delimited data whereby rows in the data file are cases (pair-wise comparisons), and columns are matrices in list form. A title line, parameter line and variable lines must be entered in this file which indicate the number of unique comparisons in each matrix, the number of matrices in the file, and labels identifying each matrix. As with RMET, these parameter and information lines allow the user to select a number of different comparisons from one dataset.

In order to create a file for use with Mantel 3.1, an RMET analysis is first performed using the population and variables under study. The d^2 matrix is copied and pasted into Excel, and the comparative matrix or matrices entered in adjacent columns. The matrices are then copied and pasted back into Notepad, where title, parameter and variable lines are added to create the source file for Mantel 3.1.

3.5.7.2 Matrix construction

This subsection sets out the rationale for, methods used and processes involved in constructing matrices for comparisons with the biological distance matrix produced by RMET. Copies of the actual matrices used are included in Appendix 1. In addition to geographical and temporal distance matrices, which are standard in studies of this nature, an additional 'design matrix' was also used. As noted previously, one of the benefits of the Mantel matrix correlation method is that it allows for considerable creative freedom in terms of designing potentially explanatory matrices which do not need to be based on continuous, linear, quantitative measurements (see for example Smouse & Long, 1992). Matrices representing migratory models or group membership are relatively commonly used (e.g. to ascertain the correlation between linguistic affiliation and biological distance). In this study a 'cultural distance' matrix is used, and is described below along with details regarding the temporal and geographic matrices.

Biodistance – the d^2 matrix (see section 3.5.6.2) produced by RMET is copied and pasted directly from the on-screen RMET output into Excel. Excel's text-to-columns function is used to format the imported data. Comparative matrices are then entered directly into adjacent columns in Excel as appropriate.

Geographical distance – In order to test the association between genetic distance and geographical distance, matrices were constructed to represent approximate linear distances in kilometres between samples. This was achieved by first measuring the distance between locations on a map (Bartholomew *et al.* 1972) using a plastic rule. The scale on the UK map used was 40 mm = 120 km, so measurements in mm were multiplied by three to give an approximate distance between the two points in km. A rather arbitrary measurement of 820 km was entered as the distance between sites in the north of England and Denmark, and 880 km between sites in the mid/south of England and Denmark. It is recognised that these distances will be neither particularly accurate nor realistic in terms of representing actual 'travelling distances' between points, as they do not take into consideration likely routes across land or sea (and that travel via the latter may have been considerably easier than via the former), or avoidance of obstacles. However, for the purpose of the tests carried out here, they are considered to be acceptable in a relative sense. For highly geographically pooled samples (e.g. UK Anglo-Saxons) a distance of 850 km was set from Britain to Denmark.

Temporal distance – In order to test the association between genetic distance and temporal separation, matrices were constructed to represent distances in time between samples. These were constructed on the basis of the difference (in number of years) between the dates for pairs of sites. As most cemetery sites were in use for a century or more, the mid-point of the date range for each sample was worked out, and the difference between these mid-points calculated, so all temporal distances were positive. The same principle applied to the calculation of dates for pooled samples, although in some cases known facts about the composition of individual samples were instrumental in biasing dates in an earlier or later direction.

Cultural distance – In order to test the association between genetic distance and cultural affiliation, matrices were constructed to represent varying degrees of cultural similarity or difference between samples. 'Cultural distance' matrices were designed in order to escape the bounds of geographical and temporal distance, whilst still allowing both to play a part, and to allow comparison of the observed biodistance between samples in terms of their hypothetical continental links. Although rather complicated to describe in words, this is essentially a 'group membership matrix', whereby samples that are culturally the same = 0 (i.e. the same) and those which are unrelated = 1 (i.e. different). Samples which are related but not the same and not extremely different = 0.5.

Practically, what this means is that, for example, a pair of UK early Anglo-Saxon samples would = 0, while an early Anglo-Saxon and Romano-British pair would = 1.

A 0.5 value was also used in order to allow hypothetical continental links to be proposed, and cultural similarity / difference to be taken into account. For example an early and late Anglo-Saxon pair would = 0.5, as would an Anglo-Saxon and Danish pair. However Romano-British samples would always = 1 when paired with anything other than other Romano-British (culturally and temporally similar = 0) samples. As well as modelling links between samples, this matrix also allows differences to be enumerated (e.g. when comparing 'single site samples', Maiden

Castle and Wetwang = 0.5, since cultural differences between these sites have been noted).

3.5.8 F_{ST} and Relethford-Blangero analyses

The R matrix upon which the RMET software bases analyses is a matrix in which pairs of populations that are closer phenotypically (and by extension genetically) have positive values, and those which are less close have negative values. A property which makes the R matrix particularly useful is that the "diagonal elements (r_{ii}) provide the genetic distance of each population to the group centroid, and the weighted average diagonal is equal to Wright's F_{ST}, a measure of average genetic differentiation relative to the contemporary gene pool" (Relethford 1996: 32).

RMET therefore produces estimates of F_{ST} (i.e. genetic differentiation among populations) and also conducts a Relethford-Blangero analysis; a multivariate extension to quantitative traits of the Harpending-Ward model which was originally designed for use with allele frequencies (Relethford & Blangero 1990). Essentially, the Relethford-Blangero analysis allows one to investigate levels of extra-regional gene flow by comparing the *observed* within-group variation of each population within a region with that which is *expected* on the basis of its distance from the regional group centroid. Upon analysis, a positive residual is indicative of greater variation within, and therefore a greater than average level of gene flow into, a population, and *vice versa* (Relethford & Blangero 1990, Relethford *et al.* 1997). Gene flow indicated by a positive residual may have its origin outside the region under analysis, or alternatively in a population within the same region, but which was not included in the Relethford-Blangero analysis. Similarly a negative residual does not imply that no gene flow was occurring; only that it did not originate from an extra-regional (or extra-sample) source (Relethford & Blangero 1990).

Although Relethford-Blangero analyses have been employed in this study, some theoretical and methodological limitations mean these analyses could not be exploited to their full potential. One of the fundamental assumptions of the Relethford-Blangero method is that all individuals within all populations involved in any one analysis form a 'potential mating network', which in effect means that populations that are very distant in a temporal sense should not be compared. To put this into context, it means that one should not, for example, analyse Anglo-Saxon samples alongside Iron Age samples, as this would clearly violate the mating potential assumption. Additionally, while it is sometimes necessary to pool samples both geographically and, to a more limited extent temporally, one cannot easily compare pooled with un-pooled samples, as this would have patent (and also unpredictable) implications for a comparison of within-group variation. In the context of the current research this means that in practice, the samples which do not violate these assumptions are limited (as a result of the small size of some of the individual site samples following exclusion of individuals with missing data) within each time period to those which are not geographically pooled.

The extent to which this analysis has been used in the present research is therefore extremely limited. Its use, to this limited degree, provides an additional novel dimension to this analysis of pre- and early historic population relationships in Britain, and allows null hypothesis 4 to be tested.

3.6 Summary, and limitations of data and methods

Within this chapter, details of the samples used, data collected, and the descriptive, univariate and multivariate methods used to analyse these data have been presented, and the processes involved in conducting these analyses described.

The major limitations of this research revolve around issues of poor skeletal preservation and consequently small sample sizes (which necessitate the pooling of sexes and sub-samples) and representitiveness. These issues, and variation in the measurements available for each sample, mean the biodistance analyses have been based on a relatively small (n=8) number of variables.

The accuracy of dates attributed to individual sites and pooled samples limits the accuracy with which matrix comparisons can be assessed. Most regrettably, the lack of 'coherent samples' (i.e. well preserved samples of good size, from single, well dated sites) means that some of the most useful and interesting analyses available (particularly the Relethford-Blangero analysis) cannot be exploited to their full potential.

It is hoped, nevertheless, that the results of the present study will encourage future workers to take up this method, and that studies of British population history will benefit as a result. The limitations identified, what needs to be done to address them, and the potential demonstrated by this work are issues that will be returned to in the final chapter of this thesis.

CHAPTER 4

RESULTS

4.1 Introduction

In this chapter, the results of analyses conducted are presented. In section 4.2 to 4.5 the descriptive statistics and between-sex *t*-tests for all samples, ANOVA and MANOVA results are presented. In sections 4.6 to 4.8 the biodistance, matrix correlation and Relethford-Blangero results are presented.

4.2 Descriptive analyses

In this sub-section descriptive statistics are given in tabulated form for the ten cranial indices described in Chapter 3, section 3.5.3. Descriptive statistics comprising minimum, maximum, mean and standard deviation are given for males and females separately, along with the number of individuals used in the calculation of each of these, and allow an initial description of the morphological nature of the samples to be provided. All indices are described where possible, however for the majority of samples one or more index was not able to be calculated due to small sample size, poor skeletal preservation, the specific measurements not being available, or having been measured using different specifications than those employed in the present study (see tables 3.2 and 3.3 in Chapter 3). Following the tabulated descriptions for each sample, a brief description of the mean for each index is given in the text, along with the results of *t*-tests comparing females and males, ANOVA results (where possible) for pooled samples and any notes regarding the sample with relation to subsequent analyses.

As categories (see Bass 1995) are used within the text to describe craniofacial shape, where an index is close to the next category (within one unit), the shape has been described giving first the category into which the index falls, followed by a hyphen and then the category to which it is close (e.g. a cranial index falling into the mesocephalic category but being toward the dolichocephalic end of this category would be described as medium-long headed).

Descriptive statistics for north-east England datasets are given for pooled samples, as they will be used in subsequent analyses. Individual descriptive data are also presented for Spofforth, Norton Bishopsmill School, Hartlepool Church Walk and Black Gate, Newcastle in Appendix 2, however, since these sites represent new and/or unpublished material and thus warrant individual description.

4.2.1 Wetwang

Table 4.1 Wetwang: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	166	61.31	83.62	73.64	3.813
CLH index	139	64.86	78.53	72.51	2.994
CBH index	140	83.78	123.33	98.31	5.851
FP index	152	61.68	81.14	71.01	3.485
TF index	0				
UF index	67	45.13	77.71	55.42	4.888
N index	72	34.33	59.08	47.01	4.477
O index	89	68.61	98.58	83.52	6.102
MA index	0				
P index	71	60.00	105.45	80.85	8.259
Valid N (listwise)	0				

Table 4.2 Wetwang: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	117	63.27	83.24	73.46	3.752
CLH index	102	63.45	78.57	72.95	2.889
CBH index	102	86.58	113.60	99.37	5.667
FP index	111	62.95	84.03	70.96	3.518
TF index	0				
UF index	61	44.71	64.74	54.07	3.466
N index	75	32.94	55.23	45.50	4.164
O index	79	68.05	103.79	82.00	6.751
MA index	0				
P index	69	64.78	100.26	81.54	8.085
Valid N (listwise)	0				

Iron Age females from Wetwang are long headed, with medium height skulls relative to length, and high-medium skulls relative to breadth. The forehead is broad relative to the maximum cranial breadth, and the upper face is narrow-average. The nasal aperture is narrow-average and the orbit average-wide. The palate is average-narrow.

Wetwang males are long headed, with medium height skulls relative to length, and high skulls relative to breadth. The forehead is broad-medium relative to the maximum cranial breadth, and the upper face is average-narrow. The nasal aperture is very narrow and the orbit is wide-average. The palate is average.

Females and males are very similar in craniofacial morphology, with the sole statistically significant difference between the sexes being in the nasal index (p=.036).

The standard deviations for each index within the female and male groups are also remarkably similar, suggesting little difference between the sexes in terms of morphological variability.

4.2.2 Danes' Graves

Table 4.3 Danes' Graves: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	7	72.22	80.25	75.60	3.119
CLH index	2	67.60	72.88	70.24	3.736
CBH index	2	85.82	99.23	92.52	9.486
FP index	6	63.12	73.08	69.54	4.084
TF index	0				
UF index	3	51.22	55.00	53.29	1.915
N index	6	40.00	54.17	47.32	4.764
O index	6	76.32	89.47	84.92	4.666
MA index	0				
P index	0				
Valid N (listwise)	0				

Table 4.4 Danes' Graves: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	15	67.89	78.57	73.27	3.465
CLH index	6	69.19	77.84	73.99	3.356
CBH index	6	95.52	102.92	99.27	2.755
FP index	14	64.34	73.76	69.91	3.197
TF index	0				
UF index	4	51.13	59.66	55.37	4.526
N index	8	42.11	52.17	46.96	3.485
O index	7	79.55	86.05	82.97	2.498
MA index	0				
P index	0				
Valid N (listwise)	0				

Although sample sizes for some of the indices calculated are very small, the description of craniofacial indices is as follows. Iron Age females from Danes' Graves are medium-long headed, with medium-low skulls relative to both length and breadth. The forehead is medium-broad and the upper face is average. The nasal aperture is narrow-average and the orbit is average.

Danes' Graves males are long headed, with medium height skulls relative to length and high skulls relative to breadth. The forehead is medium-broad and the upper face is narrow-average. The nasal aperture is narrow and the orbit is wide-average.

Although there are differences between females and males in their mean cranial indices, there are no statistically significant differences, possibly due to the relatively small sample sizes involved. The small sample sizes also preclude any comparison of female and male morphological variability.

4.2.3 Maiden Castle

Table 4.5 Maiden Castle: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	23	71.62	86.98	75.86	3.478
CLH index	23	68.75	78.70	73.78	2.692
CBH index	20	89.68	103.32	98.07	3.835
FP index	23	59.18	73.43	68.78	3.707
TF index	0				
UF index	9	49.80	60.32	54.21	3.846
N index	14	41.18	61.64	48.71	5.366
O index	14	72.32	82.59	77.76	3.366
MA index	0				
P index	8	78.18	96.32	88.08	6.550
Valid N (listwise)	0				

Table 4.6 Maiden Castle: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	23	67.00	80.34	74.64	2.968
CLH index	20	69.25	79.10	72.93	2.492
CBH index	20	89.51	104.44	97.00	4.308
FP index	24	64.30	78.22	69.49	3.395
TF index	0				
UF index	11	47.35	57.99	53.77	3.776
N index	13	41.42	58.00	49.37	4.972
O index	15	69.73	86.03	77.21	5.114
MA index	0				
P index	12	80.63	97.19	88.71	4.782
Valid N (listwise)	0				

Late Iron Age females from Maiden Castle are medium-long headed, with medium height skulls relative to length and high-medium skulls relative to breadth. The forehead is medium relative to the maximum cranial breadth, and the upper face is average-narrow. The nasal aperture is average-narrow, and the orbit wide. The palate is broad.

Males are long-medium headed with medium height skulls relative to length, and medium-high skulls relative to breadth. The forehead is medium-broad relative to the maximum breadth of the skull, and the upper face is average. The nasal aperture is average and the orbit wide. The palate is broad.

Taken as a single sample, there are no statistically significant differences between females and males in any of the craniofacial indices calculated.

This sample is rather unusual in that some researchers have proposed that it is composed of two distinct sub-samples; the main late Iron Age and Romano-British sample (*n*=33) and a sample composed of individuals from within the so-called Belgic War cemetery (*n*=24). The original investigators of this material (Goodman & Morant 1940) found that there were no statistically significant differences between these two sub-samples. An ANOVA conducted by the present author employing both liberal (LSD) and conservative (Tukey's HSD) *post hoc* tests, with males and females pooled, confirms that there are no statistically significant differences between the Iron Age and Belgic War cemetery samples in any of the craniofacial indices.

However, both *post-hoc* tests indicate that the Romano-British sub-sample is significantly or almost significantly different, in having a lower skull relative to skull length, from both Iron Age (LSD *p*=.02; Tukey's *p*=.052) and Belgic War cemetery (LSD *p*=.008; Tukey's *p*=.02) samples.

Despite the statistical differences between these samples, the small sample size of the Romano-British sub-group overall (*n*=8) and for the statistically different index (*n*=5), and the lack of any further significant differences between any of the samples for any other indices, justifies pooling all the sub-samples into one major 'Maiden Castle' sample for all subsequent analyses.

4.2.4 Trentholme Drive

Table 4.7 Trentholme Drive: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	42	69.23	82.22	75.74	2.477
CLH index	33	64.86	76.92	71.14	2.780
CBH index	33	82.58	101.45	94.41	4.177
FP index	37	59.72	73.88	69.56	3.105
TF index	16	82.03	98.31	91.91	4.559
UF index	21	50.78	61.86	56.52	2.743
N index	21	42.31	58.33	48.19	4.345
O index	22	76.74	100.00	87.68	6.600
MA index	0				
P index	0				
Valid N (listwise	0				

Table 4.8 Trentholme Drive: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	136	68.00	87.91	76.62	3.658
CLH index	104	62.94	79.12	71.67	3.546
CBH index	104	78.71	108.82	93.53	4.993
FP index	115	62.16	76.92	69.46	3.231
TF index	37	79.58	101.67	89.03	5.043
UF index	51	43.88	60.94	54.53	3.290
N index	49	38.46	59.65	47.47	4.731
O index	55	70.45	97.37	83.83	5.376
MA index	0				
P index	0				
Valid N (listwise	0				

Trentholme Drive females are medium-long headed, with medium height skulls relative to both length and breadth. The forehead is medium-broad relative to the maximum cranial breadth, and the face is narrow both including and excluding the mandible and teeth. The nasal aperture is average-narrow, and the orbital index is average.

Trentholme Drive males are medium headed, with medium height skulls relative to both length and breadth. The forehead is medium-broad, and the face both including and excluding the mandible and teeth is average-narrow. The nasal aperture is narrow-average, and the orbital index is average-wide.

Although the mean cranial indices for males and females appear reasonably similar, there are significant differences in the upper facial index (p=.017) and the orbital index (p=.01). The difference in the total facial index approaches significance (p=.055).

From the standard deviations of the craniofacial indices for females and males, there appears to be more variation within the male sub-sample compared to the female, across most indices. This difference is very slight, however, and the differences in sample size preclude any further analysis of this difference in terms of the composition of females and males from Romano-British York.

4.2.5 Poundbury

Table 4.9 Poundbury: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	21	72.93	82.39	77.01	2.866
CLH index	21	64.13	75.14	69.71	3.150
CBH index	21	80.27	97.06	90.61	4.785
FP index	0				
TF index	0				
UF index	0				
N index	21	43.30	56.25	50.06	4.117
O index	21	78.23	105.41	86.62	6.812
MA index	0				
P index	0				
Valid N (listwise)	0				

Table 4.10 Poundbury: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	28	70.41	85.00	77.40	2.974
CLH index	28	63.30	76.34	72.03	2.684
CBH index	28	82.07	102.17	93.16	4.560
FP index	0				
TF index	0				
UF index	0				
N index	28	42.31	57.43	48.23	4.286
O index	28	73.81	100.00	83.71	6.132
MA index	0				
P index	0				
Valid N (listwise)	0				

The number of indices which could be calculated for this sample is restricted compared to others by the availability of a limited amount of data.

Romano-British females from Poundbury are medium headed, with low-medium skulls relative to length, and low skulls relative to breadth. The nasal aperture and orbit are both average.

Males are medium headed, with medium height skulls relative to both length and breadth. The nasal aperture is average-narrow and the orbit average-wide.

There is a statistically significant difference between females and males in the cranial length-height index (p=.008).

As with Trentholme Drive, the standard deviations of the craniofacial indices indicate that male variability is rather greater overall than female variability, however due to relatively small sample sizes it would be unwise to attempt further analysis of this variability here.

4.2.6 Cirencester

Table 4.11 Cirencester: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	18	70.82	83.80	76.7658	3.11611
CLH index	16	66.03	74.35	69.5340	2.85098
CBH index	18	80.80	98.03	89.9619	4.84306
FP index	20	62.87	80.10	69.0901	3.53590
TF index	0				
UF index	4	52.99	59.42	56.5469	2.73517
N index	8	42.62	53.04	47.4410	3.12567
O index	5	70.39	80.69	76.0601	4.32400
MA index	0				
P index	3	83.59	90.85	87.1148	3.63097
Valid N (listwise)	0				

Table 4.12 Cirencester: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	40	69.55	82.41	75.5087	2.95765
CLH index	32	64.30	77.37	70.4718	3.29350
CBH index	32	82.58	103.70	93.4208	5.26166
FP index	40	62.31	75.21	68.7193	3.01040
TF index	0				
UF index	14	40.73	56.83	53.3942	4.05550
N index	21	38.73	52.14	46.5559	3.72487
O index	28	67.15	92.31	80.4712	5.23234
MA index	0				
P index	10	76.47	101.70	87.1912	8.07505
Valid N (listwise)	0				

Romano-British females from Cirencester are medium headed, with low-medium skulls relative to length and low skulls relative to breadth. The forehead is medium-broad relative to the maximum breadth of the skull, and the upper face is narrow. The nasal aperture is narrow-average and the orbit wide. The palate is broad.

Males are medium headed with medium-low skulls relative to length and medium skulls relative to breadth. The forehead is medium relative to the maximum breadth of the skull, and the upper face is average. The nasal aperture is narrow and the orbit wide. The palate is broad.

The sole statistically significant difference between females and males is in cranial breadth-height index (*p*=.026).

There are no particularly notable differences in female and male variation, although the standard deviation of the indices is generally higher for males than females, particularly with regard to facial indices. However, the small size of the (particularly female) samples involved in calculating some of the indices means that this difference does not warrant further discussion here.

4.2.7 Bidford-on-Avon

Table 4.13 Bidford-on-Avon: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	11	68.39	76.88	73.82	2.823
CLH index	8	66.75	76.86	71.98	3.967
CBH index	7	89.16	103.86	96.39	5.891
FP index	11	66.91	79.77	70.78	3.636
TF index	0				
UF index	4	50.21	53.33	51.74	1.290
N index	9	44.00	54.02	48.81	3.585
O index	10	74.94	89.74	85.75	4.427
MA index	0				
P index	0				
Valid N (listwise)	0				

Table 4.14 Bidford-on-Avon: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	19	69.54	77.78	73.49	2.748
CLH index	11	69.63	76.19	71.67	1.827
CBH index	11	91.50	101.48	97.97	2.877
FP index	17	63.64	77.66	69.22	4.004
TF index	0				
UF index	12	47.06	57.46	51.62	3.074
N index	19	40.37	58.64	46.85	4.757
O index	20	72.64	97.37	83.95	6.375
MA index	0				
P index	0				
Valid N (listwise)	0				

Early Anglo-Saxon females from Bidford-on-Avon are long headed, with medium height skulls relative to both length and breadth. The forehead is broad-medium relative to the maximum breadth of the skull, and the upper face is average in breadth. The nasal aperture is average-narrow and the orbit is average.

Males are long headed with medium height skulls relative to length and medium-high skulls relative to breadth. The forehead is medium-broad relative to the maximum breadth of the skull, and the upper face is average in breadth. The nasal aperture is narrow, and the orbit average-wide.

There are no statistically significant differences between females and males in any of the craniofacial indices calculated for this sample, although the female sub-sample is rather small, and so any differences which exist may be unlikely to achieve statistical significance.

In general, the standard deviation for female cranial indices is larger than the male and the standard deviation for male facial indices is greater, indicating greater variation respectively. However, as has already been noted, small sample sizes mean that analysis of female / male variation is problematic.

4.2.8 North-east early Anglo-Saxons

Table 4.15 North-east early Anglo-Saxon: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	13	68.51	81.56	74.18	3.399
CLH index	3	69.15	75.00	72.24	2.940
CBH index	3	94.89	103.85	98.44	4.759
FP index	11	63.70	73.69	69.12	3.096
TF index	0				
UF index	3	53.33	58.56	56.35	2.707
N index	5	47.83	53.19	50.21	1.917
O index	5	74.37	82.05	78.23	3.366
MA index	1	122.61	122.61	122.61	.
P index	4	74.47	92.79	80.50	8.383
Valid N (listwise)	0				

Table 4.16 North-east early Anglo-Saxon: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	8	67.72	79.89	73.06	3.845
CLH index	5	67.51	77.84	72.79	4.816
CBH index	3	93.66	101.48	98.14	4.031
FP index	8	66.42	72.26	69.46	1.814
TF index	0				
UF index	1	49.26	49.26	49.26	.
N index	2	47.06	48.10	47.58	.740
O index	4	75.00	85.49	80.93	4.685
MA index	3	105.10	117.99	113.47	7.255
P index	3	71.89	82.36	78.31	5.623
Valid N (listwise)	0				

This 'north-east early Anglo-Saxon' sample is a pooled sample comprising individuals from Sewerby, Castledyke South and Norton East Mill. Despite being pooled, the number of individuals involved in the calculation of some indices is very small. Nevertheless, north-east early Anglo-Saxon females are long headed, with medium height skulls relative to length, and high-medium skulls relative to breadth. The forehead is medium-broad relative to the maximum breadth of the skull, and the upper face is narrow. The nasal aperture is average, and the orbit wide. The palate is average-narrow in breadth.

Males are long headed with medium height skulls relative to length, and high-medium skulls relative to breadth. The forehead is medium-broad relative to the maximum breadth of the skull, and the upper face is broad (although this index is based on only one skull). The nasal aperture is narrow-average and the orbit wide. The maxillo-alveolar region is average relative to its length, and the palate is narrow.

There are no statistically significant differences between females and males for any of the craniofacial indices calculated. Due to the nature of the composition of this sample, and of the small sample sizes involved, no further analysis of female / male variation is justified, and no ANOVA has been carried out to assess differences between the sub-samples from which this sample is composed.

4.2.9 Morant's London Museums sample

Table 4.17 Morant's London Museums: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	41	66.49	82.66	74.20	3.377
CLH index	20	67.59	76.88	71.83	2.457
CBH index	20	87.82	104.20	96.64	3.326
FP index	38	61.47	77.31	70.17	3.648
TF index	0				
UF index	16	46.19	63.03	52.08	5.130
N index	18	44.04	58.01	50.95	4.357
O index	23	70.82	87.06	79.26	4.585
MA index	0				
P index	0				
Valid N (listwise)	0				

Table 4.18 Morant's London Museums: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	41	65.68	86.25	74.00	3.877
CLH index	21	65.72	76.80	71.60	2.858
CBH index	21	89.19	103.94	96.13	4.930
FP index	41	60.00	76.67	68.78	3.202
TF index	0				
UF index	9	47.19	58.25	54.54	3.467
N index	20	41.76	51.73	47.53	2.879
O index	16	75.18	85.68	79.38	3.410
MA index	0				
P index	0				
Valid N (listwise)	0				

Females in Morant's London Museums Anglo-Saxon sample are long-medium headed, with medium height skulls relative to both length and breadth. The forehead is broad-medium relative to the maximum breadth of the skull and the upper face is average in breadth. The nasal aperture is average and the orbit is wide.

Males are long-medium headed, with medium height skulls relative to both length and breadth. The forehead is medium in breadth relative to the maximum breadth of the skull and the upper face is average-narrow. The nasal aperture is narrow-average and the orbit is wide.

Taken as a whole, there is a statistically significant difference between females and males in the nasal index (*p*=.009). In terms of female/male variability, females appear more variable than males, on the basis of some of the standard deviations of their craniofacial (particularly facial) indices, however, the samples for both sexes are relatively small, and bearing in mind the composite nature of this sample, this difference probably does not warrant further discussion here.

This is a composite sample composed (probably – see Chapter 3, section 3.3.3) of early Anglo-Saxons from a large number of sites throughout England. In the original study in which these data were published together (Morant 1926) the series was divided geographically and the sub-samples found to be relatively homogeneous. An ANOVA conducted by the present author confirms that there are no statistically significant differences between these geographically and sex pooled groups (at *p*<.05). There are also no statistically significant differences between these groups when considered by sex, although in this analysis the sample sizes of some sub-groups become very small.

It is therefore considered justifiable to include this sample as a pooled UK sample of Anglo-Saxons in the present work.

4.2.10 Burwell

Table 4.19 Burwell: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	20	69.71	83.82	75.81	3.997
CLH index	12	64.85	76.88	70.61	3.780
CBH index	12	87.41	102.62	92.47	4.756
FP index	16	63.76	73.96	68.74	3.346
TF index	0				
UF index	5	46.88	56.20	51.37	4.107
N index	11	42.59	56.25	48.55	4.528
O index	9	77.50	89.87	82.42	4.438
MA index	0				
P index	0				
Valid N (listwise)	0				

Table 4.20 Burwell: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	45	68.69	82.35	74.84	3.255
CLH index	40	66.16	80.11	71.61	3.149
CBH index	40	86.01	103.76	95.54	4.814
FP index	43	60.06	72.18	67.20	2.732
TF index	0				
UF index	21	42.42	60.77	51.52	4.487
N index	33	39.47	59.09	48.70	3.832
O index	32	69.77	86.25	78.51	3.909
MA index	0				
P index	0				
Valid N (listwise)	0				

Later Anglo-Saxon females from Burwell are medium-long headed with medium-low skulls relative to both length and breadth. The forehead is medium in breadth relative to the maximum cranial breadth, and the upper face is average in breadth. The nasal aperture is average-narrow and the orbit wide-average.

Males are long-medium headed with medium height skulls relative to both length and breadth. The forehead is medium in breadth relative to the maximum breadth of the skull, and the upper face is average in breadth. The nasal aperture is average-narrow and the orbit wide.

The difference between the female and male orbital index is statistically significant (*p*=.014), while the difference in the cranial breadth-height index approaches statistical significance (*p*=.058). Females appear to be slightly more variable than males, based on the standard deviations of their craniofacial indices overall), however the female sub-sample is substantially smaller than the male sub-sample, and so further investigation of that difference is not warranted here.

4.2.11 North-east later Anglo-Saxons

Table 4.21 North-east later Anglo-Saxon: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	20	67.90	85.51	75.10	4.096
CLH index	11	65.78	76.80	72.10	3.629
CBH index	11	88.32	103.91	96.44	5.257
FP index	18	63.04	77.24	69.60	3.900
TF index	3	86.16	93.22	90.35	3.712
UF index	8	47.06	58.62	53.45	3.491
N index	17	44.87	59.21	50.45	4.399
O index	16	76.16	92.79	84.41	6.074
MA index	16	100.00	130.43	116.26	9.358
P index	17	58.02	117.07	80.99	12.294
Valid N (listwise)	2				

Table 4.22 North-east later Anglo-Saxon: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	40	67.84	85.16	74.35	4.136
CLH index	29	61.93	80.22	71.02	3.906
CBH index	24	83.56	111.85	95.56	6.960
FP index	36	63.06	76.59	69.84	3.361
TF index	8	82.93	94.62	89.15	3.690
UF index	11	50.14	57.25	54.08	2.281
N index	24	38.18	59.18	48.17	4.308
O index	24	71.43	100.00	83.09	7.125
MA index	19	99.03	125.93	113.87	6.869
P index	25	59.32	97.47	76.32	10.496
Valid N (listwise)	4				

This pooled 'north-east later Anglo-Saxon' sample comprises individuals from Village Farm Spofforth, Norton Bishopsmill School, Hartlepool Church Walk and Black Gate Newcastle. (The Norton Bishopsmill School sample has been excluded from the ANOVA below due to its very small size, which meant it was not included in the pooled north-east later Anglo-Saxon sample used in subsequent multivariate analyses.)

Females are medium-long headed with medium height skulls relative to both length and breadth. The forehead is medium-broad relative to the maximum cranial breadth, and the face including the mandible and teeth is narrow-average, while the upper face is average. The nasal aperture is average, and the orbit is average. The maxillo-alveolar region is broad relative to length, and the palate is average-narrow.

Males are long-medium headed with medium height skulls relative to both length and breadth. The forehead is medium-broad relative to the maximum cranial breadth, and the face both including and excluding the mandible and teeth is average-narrow. The nasal aperture is average-narrow and the orbit average-wide. The maxillo-alveolar region is average in breadth, and the palate narrow.

There are no statistically significant differences between females and males for any of the craniofacial indices calculated, and standard deviations are not considered further due to the composite nature of this sample.

An ANOVA employing both liberal (LSD) and conservative (Tukey's HSD) *post hoc* tests, with females and males pooled, indicates that there are statistically significant differences between the sub-samples from which this sample is composed. *Post hoc* tests reveal a significant difference in cranial breadth-height index between Black Gate and Hartlepool Church Walk (LSD p=.049), and an almost significant difference between Hartlepool Church Walk and Spofforth (LSD p=.055). The more conservative Tukey's HSD tests, however, do not indicate that these differences are significantly significant. There are also significant differences between Black Gate and both Hartlepool Church Walk and Spofforth in the orbital index (LSD p=.000 and p=.001 respectively). This difference is confirmed by Tukey's HSD tests (p=.001 and p=.004 respectively). Lastly there are significant differences between Hartlepool Church Walk and both Black Gate and Spofforth in the palatal index (LSD p=.003 and p=.001 respectively). This difference is confirmed by Tukey's HSD tests (p=.007 and p=.002 respectively).

Although ANOVA indicates significant differences between these groups, because of small sample sizes resulting from the use of a multivariate dataset in analyses to come, it has been necessary to pool these samples together.

4.2.12 Danish early Roman

Table 4.23 Danish early Roman: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	19	69.19	79.65	72.97	2.960
CLH index	13	67.21	77.84	73.57	2.853
CBH index	13	93.06	108.00	99.95	4.674
FP index	18	63.43	77.34	70.75	3.467
TF index	5	83.87	98.36	90.91	5.635
UF index	9	50.00	57.63	52.89	2.463
N index	6	42.55	60.00	48.93	6.483
O index	13	72.50	100.00	83.79	7.518
MA index	0				
P index	4	75.56	88.89	83.68	6.374
Valid N (listwise)	0				

Table 4.24 Danish early Roman: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	48	63.73	78.49	71.09	3.593
CLH index	23	65.79	79.07	70.90	3.741
CBH index	21	88.28	110.69	99.74	5.760
FP index	43	63.97	77.21	70.86	3.301
TF index	8	83.46	98.39	91.89	4.523
UF index	13	48.84	60.48	55.60	3.576
N index	17	40.00	57.14	47.92	5.392
O index	22	73.81	90.48	81.90	4.687
MA index	0				
P index	20	72.92	100.00	86.92	7.095
Valid N (listwise)	0				

Danish early Roman females are long headed, with medium height skulls relative to length and high skulls relative to breadth. The forehead is broad-medium relative to the maximum breadth of the skull, and the face is narrow-average including the mandible and teeth and average excluding them. The nasal aperture is average-narrow and the orbit average-wide. The palate is average in breadth.

Males are long headed, with medium-low skulls relative to length and high skulls relative to breadth. The forehead is broad-medium relative to the maximum breadth of the skull, and the face is narrow including the mandible and teeth, and narrow-average excluding them. The nasal aperture is narrow-average and the orbit is wide. The palate is broad.

There are significant differences between females and males in the cranial index (*p*=.048) and the cranial length height index (*p*=.032).

From the standard deviations, males appear more variable overall in their cranial indices, while females appear more variable in their facial indices. However, because this is a country-wide pooled sample, this difference does not warrant further discussion here.

4.2.13 Danish late Roman

Table 4.25 Danish late Roman: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	20	63.16	78.09	71.21	3.950
CLH index	14	67.72	79.65	72.34	3.472
CBH index	14	93.98	110.85	100.79	4.379
FP index	19	65.41	78.33	71.03	2.986
TF index	10	82.17	100.00	91.79	5.448
UF index	11	50.39	62.07	55.54	3.514
N index	15	41.51	58.00	47.76	4.085
O index	18	76.19	97.30	86.70	5.815
MA index	0				
P index	12	73.81	94.87	85.57	7.067
Valid N (listwise)	0				

Table 4.26 Danish late Roman: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	33	62.78	86.21	72.00	4.773
CLH index	19	67.03	78.38	71.59	3.325
CBH index	18	87.94	108.15	99.38	6.686
FP index	33	58.67	77.14	69.50	4.073
TF index	14	77.24	117.39	90.15	10.391
UF index	18	47.29	69.57	54.22	5.189
N index	18	41.67	58.14	48.02	4.226
O index	23	71.11	94.87	81.06	6.474
MA index	0				
P index	11	81.63	93.62	87.81	4.239
Valid N (listwise)	0				

Danish late Roman females are long headed, with medium height skulls relative to length, and high skulls relative to breadth. The forehead is broad relative to the maximum cranial breadth, and the face including the mandible and teeth is narrow, while the face excluding the mandible and teeth is narrow-average. The nasal aperture is narrow-average and the orbit average. The palate is broad-average.

Males are long headed with medium height skulls relative to length, and high skulls relative to breadth. The forehead is medium-broad relative to the maximum cranial breadth and the face including the mandible and teeth is narrow-average, while the face excluding the mandible and teeth is average-narrow. The nasal aperture is average-narrow, and the orbit is wide. The palate is broad.

The sole significant difference between females and males is in the orbital index (p=.006).

Although males appear much more variable in their craniofacial indices overall, because this is a country-wide pooled sample, this difference does not warrant further discussion here.

4.2.14 Danish Viking

Table 4.27 Danish Viking: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	26	67.93	82.29	74.67	3.432
CLH index	26	57.51	74.60	70.30	3.899
CBH index	24	82.88	104.80	95.57	5.603
FP index	24	61.11	77.37	69.41	4.135
TF index	2	85.47	89.76	87.62	3.036
UF index	4	53.85	56.52	54.68	1.242
N index	19	41.67	55.32	49.42	3.343
O index	22	72.50	95.24	82.21	5.864
MA index	0				
P index	14	78.95	107.32	89.63	7.434
Valid N (listwise)	0				

Table 4.28 Danish Viking: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	17	68.39	79.79	74.08	2.976
CLH index	13	65.83	76.11	71.32	3.246
CBH index	13	84.46	108.33	94.81	6.244
FP index	17	59.72	72.79	67.60	3.559
TF index	6	76.92	96.67	87.78	7.531
UF index	7	49.65	58.33	53.41	2.925
N index	10	38.46	52.94	45.80	4.201
O index	12	67.44	87.50	80.17	5.536
MA index	0				
P index	10	71.43	100.00	84.38	8.828
Valid N (listwise)	0				

Danish Viking females are long-medium headed, with medium-low skulls relative to length, and medium height skulls relative to breadth. The forehead is medium-broad in relation to maximum breadth of the skull and the face including the mandible and teeth is average, while the face excluding the mandible and teeth is average-narrow. The nasal aperture is average and the orbit is average-wide. The palate is broad.

Males are long headed, with medium height skulls relative to both length and breadth. The forehead is medium in breadth relative to the maximum breadth of the skull, and the face both including and excluding the mandible and teeth is average in breadth. The nasal aperture is narrow and the orbit is wide. The palate is average-broad.

The sole significant difference between females and males is in the nasal index (p=.017).

There are no patterns of difference in female and male variability evident from the standard deviations of the indices calculated, and, as with the previous two samples, because this is a country-wide pooled sample, any difference would not warrant further discussion here.

4.2.15 Maastricht

Table 4.29 Maastricht: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	18	70.68	79.67	75.47	2.289
CLH index	16	60.10	79.07	70.23	4.942
CBH index	14	82.86	107.41	92.61	7.503
FP index	0				
TF index	0				
UF index	0				
N index	0				
O index	0				
MA index	0				
P index	0				
Valid N (listwise)	0				

Table 4.30 Maastricht: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	17	68.23	81.25	74.47	3.294
CLH index	14	62.37	74.46	68.89	3.538
CBH index	13	77.56	100.76	92.08	6.553
FP index	0				
TF index	0				
UF index	0				
N index	0				
O index	0				
MA index	0				
P index	0				
Valid N (listwise)	0				

Only three cranial indices could be calculated for this sample, due to the limitations of the data available.

Maastricht females are medium-long headed, with medium-low skulls relative to both length and breadth.

Males are long headed with low-medium skulls relative to length, and medium-low skulls relative to breadth.

There are no statistically significant differences between females and males for the indices calculated, and the standard deviations of the indices calculated do not indicate any patterns of greater or lesser female or male variability.

4.2.16 Descriptive analyses: summary

Some broad temporal trends are evident from the descriptive analyses presented above. These are most apparent for the cranial rather than cranio-facial indices. For the cranial index, Iron Age, early Anglo-Saxon and Danish samples are all long-headed, although the Danish early and late Roman samples have particularly long heads. Romano-British samples are all medium-headed, and later Anglo-Saxon females have medium-long skulls, whilst later Anglo-Saxon males have long-medium skulls.

While all samples have remarkably similar cranial length-height indices in that all are medium with the exception of females from Poundbury and Cirencester which are low-medium, differences are apparent in the cranial *breadth*-height indices between periods. With the exception of Danes' Graves females (which have a very small sample size), all Iron Age samples have high or high-medium skulls relative to breadth, and all Danish samples also have high skulls. Romano-British samples have mainly medium height skulls, except females from Poundbury and Cirencester which have low skulls. All Anglo-Saxon skulls fall into the 'medium' category, except early Anglo-Saxons from Bidford-on-Avon, which have high-medium skulls.

Relatively few statistically significant differences are seen between females and males of the same sample indicating that, overall, males and females of the same sample have similar craniofacial morphology, although the sample sizes for separate sexes were often very small, and thus differences which did exist may not have been statistically significant.

Within-sample analyses of variance (employed where sample sizes permitted) indicated that there were relatively few significant differences between sub-samples of samples which had already been pooled. The exception was the north-east later Anglo-Saxon sample, however because of the small sub-sample sizes, there is no option but to use this as a pooled sample.

The results of these analyses suggest that some differences are evident which appear to link samples by temporal period. They also suggest that pooling by sex and by period in order to improve sample sizes in the multivariate analyses is justified, at least on the basis of the craniofacial indices calculated here. In the next section, analyses of variance are conducted to investigate whether differences between samples are statistically significant. If so, patterns of difference noted here may be found to be supported statistically, and new patterns revealed.

4.3 ANOVA

In this subsection the results of the one-way analyses of variance (ANOVA) are presented for each of the craniofacial indices calculated. Although not all indices could be calculated for all samples, and not all indices provide meaningful insights, all possible analyses have been presented here for the sake of completeness.

ANOVA can assist in confirming the observations made on the basis of descriptive analyses in the previous section, and can also identify statistically significant differences between samples in both craniofacial shape and variance which were not previously noted. They are used in this instance to give an indication of which samples differ significantly in their mean cranial indices, both within and between time periods, which allows hypothesis 1 to be tested, and which also has implications for justifying the pooling of samples for the multivariate analyses presented in section 4.4 onward. In order to improve sample sizes for these tests, female and male sub-samples are pooled. Preceding the results of these analyses, in each subsection, charts are presented which provide a visual comparison of each cranial index for all samples together, in roughly chronological order.

For each ANOVA the result of Levene's test for homogeneity of variance has been presented first, followed by the ANOVA test statistic and p value. In instances where Levene's test has indicated that there are statistically unequal variances between groups, Welch's robust test of equality of means has also been used. The nature of the sample (number of samples included) has been summarised, noting any samples which had particularly small sample sizes, as these factors have relevance for interpretation of the *post-hoc* tests. A summary of the descriptive statistics and *post hoc* multiple comparisons tests are then presented, in order to ascertain specifically which samples differ significantly for the index under consideration. Where equal variances can be assumed, the results of both liberal (LSD) and conservative (Tukey's HSD) *post hoc* tests are presented. Where variances are unequal, Games-Howell tests have been used.

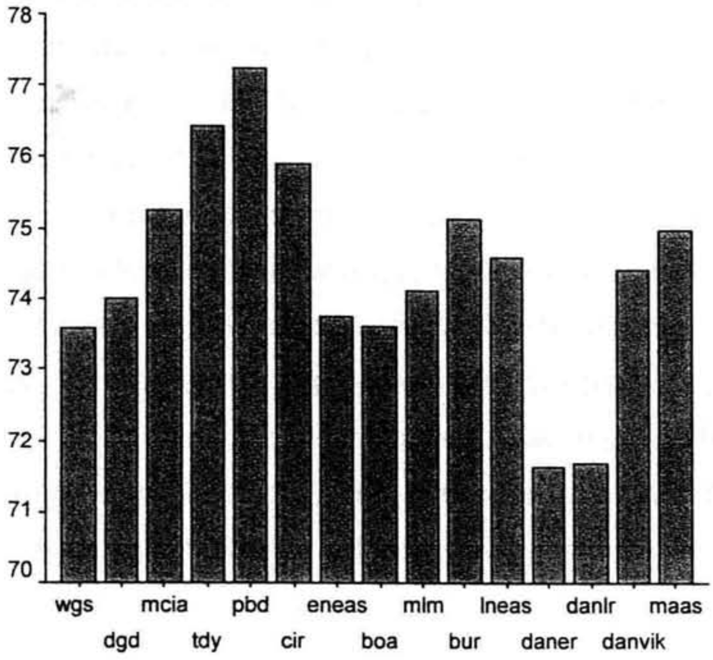
The abbreviations used in charts are detailed in table 4.31 below:

Table 4.31 Key to abbreviations used

Code	Sample	Period
wgs	Wetwang	IA
dgd	Danes' Graves	IA
mcia	Maiden Castle	IA
tdy	Trentholme Drive	RB
pbd	Poundbury	RB
cir	Cirencester	RB
eneas	Early north-east Anglo-Saxon	Early AS
boa	Bidford-on-Avon	Early AS
mlm	Morant's London Museums	Early/mid- AS
bur	Burwell	Mid- AS
lneas	Later north-east Anglo-Saxon	Later AS
daner	Danish early Roman	ER
danlr	Danish late Roman	LR
danvik	Danish Viking	Viking
maas	Maastricht	early medieval

4.3.1 Cranial index

Figure 4.1 Mean of cranial index



Levene's test indicates that there are no significant differences in variance among the samples examined (Levene's = 1.435, p=.130).

ANOVA indicates that there are very highly significant differences in mean cranial index among the samples examined (F=13.891, p=.000). Fifteen samples were included in this test, none of which had a very small (n<10) sample size.

The LSD (liberal) *post hoc* tests show that the earlier Iron Age samples (Wetwang and Danes' Graves) differ significantly from all Romano-British and early/late Roman Danish samples. In addition, Wetwang differs significantly from Maastricht, Maiden Castle and the mid-late Anglo-Saxon samples from Burwell and the north-east. The later Iron Age sample from Maiden Castle differs from Wetwang, the Romano-British samples from Trentholme Drive and Poundbury, and from early/late Roman Danish samples, and approaches significance from the early Anglo-Saxon sample from Bidford-on-Avon

The Romano-British samples from Trentholme Drive and Poundbury differ significantly from all other samples, but not from each other, while Cirencester differs from all samples except other Romano-British (although the difference from Poundbury approaches significance), Burwell and Maastricht.

All the earlier Anglo-Saxon samples differ significantly from all Romano-British and the early/late Roman Danish samples, while the mid-later Anglo-Saxon samples from Burwell and the north-east differ significantly from Wetwang, Trentholme Drive and Poundbury, and the Danish early/late Roman samples. The later north-east Anglo-Saxon sample also differs significantly from Cirencester. Danish early and late Roman samples are significantly different from all others except each other, and have the longest, narrowest crania of all samples.

The more conservative Tukey's HSD tests, while returning far fewer statistically significant results, generally support the pattern described above, particularly regarding the distinctive difference between the Romano-British and early Iron Age, early Anglo-Saxon and Danish samples.

In general, the cranial index does seem to vary between samples by period, Romano-British samples being distinctive due to their short broad heads, while Iron Age, early Anglo-Saxon and earlier Danish samples are longer-headed.

Table 4.32 Cranial index: Descriptive statistics

C index

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum	Maximum
					Lower Bound	Upper Bound		
wgs	283	73.5659	3.78212	.22482	73.1234	74.0085	61.31	83.62
dgd	22	74.0098	3.46635	.73903	72.4729	75.5467	67.89	80.25
mcia	46	75.2505	3.25497	.47992	74.2839	76.2171	67.00	86.98
tdy	178	76.4120	3.43005	.25709	75.9047	76.9194	68.00	87.91
pbd	49	77.2347	2.90451	.41493	76.4005	78.0690	70.41	85.00
cir	58	75.8988	3.03735	.39882	75.1002	76.6974	69.55	83.80
eneas	21	73.7528	3.52419	.76904	72.1486	75.3570	67.72	81.56
boa	30	73.6104	2.73178	.49875	72.5903	74.6305	68.39	77.78
mlm	82	74.0994	3.61435	.39914	73.3053	74.8936	65.68	86.25
bur	65	75.1384	3.49756	.43382	74.2718	76.0051	68.69	83.82
lneas	60	74.5983	4.10335	.52974	73.5383	75.6583	67.84	85.51
daner	67	71.6217	3.50837	.42862	70.7659	72.4774	63.73	79.65
danlr	53	71.7011	4.45772	.61232	70.4724	72.9298	62.78	86.21
danvik	43	74.4365	3.23521	.49336	73.4409	75.4322	67.93	82.29
maas	35	74.9812	2.82554	.47760	74.0106	75.9518	68.23	81.25
Total	1092	74.4633	3.84075	.11623	74.2353	74.6914	61.31	87.91

Table 4.33 Cranial index: ANOVA *post hoc* tests: LSD

	wgs	dgd	mcia	tdy	pbd	cir	eneas	boa	mlm	bur	lneas	daner	danlr	danvik
dgd	.573													
mcia	**.003**	.179												
tdy	**.000**	**.003**	**.049**											
pbd	**.000**	**.000**	**.007**	.152										
cir	**.000**	**.034**	.356	.340	.053*									
eneas	.816	.813	.110	**.001**	**.000**	**.018**								
boa	.948	.689	.050*	**.000**	**.000**	**.004**	.888							
mlm	.232	.916	.079	**.000**	**.000**	**.003**	.690	.520						
bur	**.001**	.199	.870	**.014**	**.002**	.237	.121	.052*	.079					
lneas	**.041**	.507	.350	**.001**	**.000**	**.047**	.349	.215	.409	.397				
daner	**.000**	**.006**	**.000**	**.000**	**.000**	**.000**	**.017**	**.011**	**.000**	**.000**	**.000**			
danlr	**.000**	**.011**	**.000**	**.000**	**.000**	**.000**	**.026**	**.019**	**.000**	**.000**	**.000**	.903		
danvik	.135	.647	.281	**.001**	**.000**	**.041**	.471	.329	.615	.316	.820	**.000**	**.000**	
maas	**.027**	.316	.736	**.030**	**.004**	.228	.211	.122	.220	.833	.613	**.000**	**.000**	.501

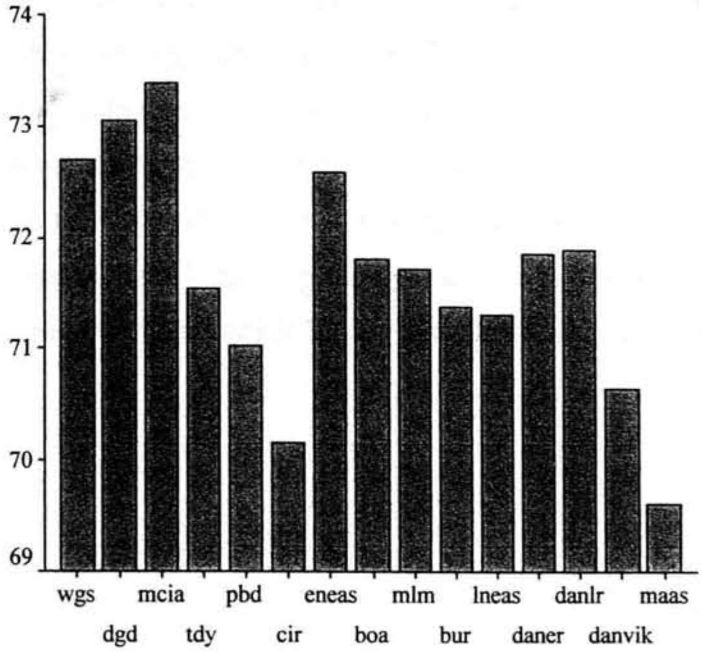
Table 4.34 Cranial index: ANOVA *post hoc* tests: Tukey's HSD

	wgs	dgd	mcia	tdy	pbd	cir	eneas	boa	mlm	bur	lneas	daner	danlr	danvik
dgd	1.000													
mcia	.164	.991												
tdy	**.000**	.160	.814											
pbd	**.000**	**.033**	.296	.984										
cir	**.001**	.721	1.000	1.000	.835									
eneas	1.000	1.000	.959	.081	**.015**	.539								
boa	1.000	1.000	.819	**.006**	**.001**	.217	1.000							
mlm	.997	1.000	.915	**.000**	**.000**	.176	1.000	1.000						
bur	.087	.994	1.000	.463	.115	.998	.968	.829	.914					
lneas	.773	1.000	1.000	**.048**	**.011**	.807	1.000	.996	1.000	1.000				
daner	**.005**	.287	**.000**	**.000**	**.000**	**.000**	.519	.409	**.002**	**.000**	**.000**			
danlr	**.036**	.399	**.000**	**.000**	**.000**	**.000**	.638	.554	**.012**	**.000**	**.002**	1.000		
danvik	.977	1.000	.999	.075	**.015**	.772	1.000	1.000	1.000	1.000	1.000	**.005**	**.016**	
maas	.650	1.000	1.000	.683	.216	.997	.996	.969	.997	1.000	1.000	**.001**	**.002**	1.000

Significant (at $p<.05$) p values for each comparison are in **bold** type. Those which approach significance have an *.
wgs, dgd, mcia = IA; tdy, pbd, cir = RB; eneas, boa, mlm = early AS; bur, lneas = later AS daner, danlr, danvik = Danish

4.3.2 Cranial length-height index

Figure 4.2 Mean of cranial length-height index



Levene's test indicates that there are no significant differences in variance among the samples examined (Levene's = 1.7, p=.051). However, this statistic does approach significance, so Welch's robust test for equality of means was also used.

Both tests indicate that there are very highly significant differences in mean cranial length-height index among the samples examined (ANOVA F=4.8, p=.000; Welch = 4.563, p=.000). Fifteen samples were included in this test, of which two had particularly small sample sizes (Danes' Graves n=8, early north-east Anglo-Saxon n=8).

The LSD (liberal) *post hoc* tests indicate that most Iron Age samples differ significantly from all the Romano-British, later Anglo-Saxon, Danish Viking and Maastricht samples, having higher skulls than these groups, relative to length. Maiden Castle differs significantly from all others, except from other Iron Age samples and early north-east Anglo-Saxon and Bidford-on-Avon samples.

Romano-British samples differ, on the whole, from Iron Age samples, but not from British Anglo-Saxon and Danish/Maastricht samples, except for Cirencester which is, or comes close to, significantly different from all British Anglo-Saxon and Danish early/late Roman samples.

Mid- and later Anglo-Saxon samples differ significantly from Iron Age samples, Cirencester and Maastricht, and early Anglo-Saxon samples differ significantly only from Maastricht.

The most notable pattern to emerge from this test, which is also evident from the more conservative Tukey's HSD tests, is the distinctiveness of two of the British Iron Age samples (Wetwang and Maiden Castle) from Romano-British, Danish Viking and Maastricht samples. The Iron Age samples all have higher skulls relative to length (including Danes' Graves, although this difference does not achieve statistical significance – possibly due to its relatively small sample size), and the Romano-British, Danish Viking and Maastricht samples have lower skulls.

Table 4.35 Cranial length-height index: Descriptive statistics

CLH index

					95% Confidence Interval for Mean			
	N	Mean	Std. Deviation	Std. Error	Lower Bound	Upper Bound	Minimum	Maximum
wgs	241	72.6986	2.95178	.19014	72.3240	73.0731	63.45	78.57
dgd	8	73.0560	3.61375	1.27765	70.0349	76.0772	67.60	77.84
mcia	43	73.3873	2.60559	.39735	72.5854	74.1892	68.75	79.10
tdy	137	71.5406	3.37577	.28841	70.9703	72.1110	62.94	79.12
pbd	49	71.0334	3.08701	.44100	70.1467	71.9201	63.30	76.34
cir	48	70.1592	3.15407	.45525	69.2434	71.0751	64.30	77.37
eneas	8	72.5831	3.97559	1.40558	69.2594	75.9068	67.51	77.84
boa	19	71.8048	2.82826	.64885	70.4416	73.1680	66.75	76.86
mlm	41	71.7158	2.63912	.41216	70.8828	72.5488	65.72	76.88
bur	52	71.3756	3.29330	.45670	70.4588	72.2925	64.85	80.11
lneas	40	71.3197	3.81679	.60349	70.0990	72.5403	61.93	80.22
daner	36	71.8636	3.64514	.60752	70.6303	73.0970	65.79	79.07
danlr	33	71.9118	3.35487	.58401	70.7222	73.1013	67.03	79.65
danvik	39	70.6406	3.68292	.58974	69.4468	71.8345	57.51	76.11
maas	30	69.6022	4.32522	.78967	67.9871	71.2173	60.10	79.07
Total	824	71.7993	3.34065	.11638	71.5709	72.0278	57.51	80.22

Table 4.36 Cranial length-height index: ANOVA *post hoc* tests: LSD

	wgs	dgd	mcia	tdy	pbd	cir	eneas	boa	mlm	bur	lneas	daner	danlr	danvik
dgd	.759													
mcia	.199	.791												
tdy	**.001**	.199	**.001**											
pbd	**.001**	.102	**.001**	.347										
cir	**.000**	**.019**	**.000**	**.011**	.184									
eneas	.921	.770	.519	.376	.210	.050*								
boa	.247	.359	.076	.739	.378	.061	.569							
mlm	.073	.284	**.018**	.761	.320	**.020**	.488	.921						
bur	**.008**	.172	**.003**	.754	.596	.061	.326	.621	.615					
lneas	**.013**	.167	**.004**	.704	.678	.094	.314	.591	.582	.935				
daner	.149	.346	**.038**	.594	.243	**.017**	.570	.949	.842	.487	.465			
danlr	.191	.340	**.049**	.555	.229	**.017**	.599	.909	.796	.457	.437	.951		
danvik	**.000**	.055*	**.000**	.126	.572	.491	.123	.199	.138	.284	.352	.103	.097	
maas	**.000**	**.007**	**.000**	**.003**	.057*	.460	**.021**	**.021**	**.007**	**.017**	**.028**	**.005**	**.005**	.187

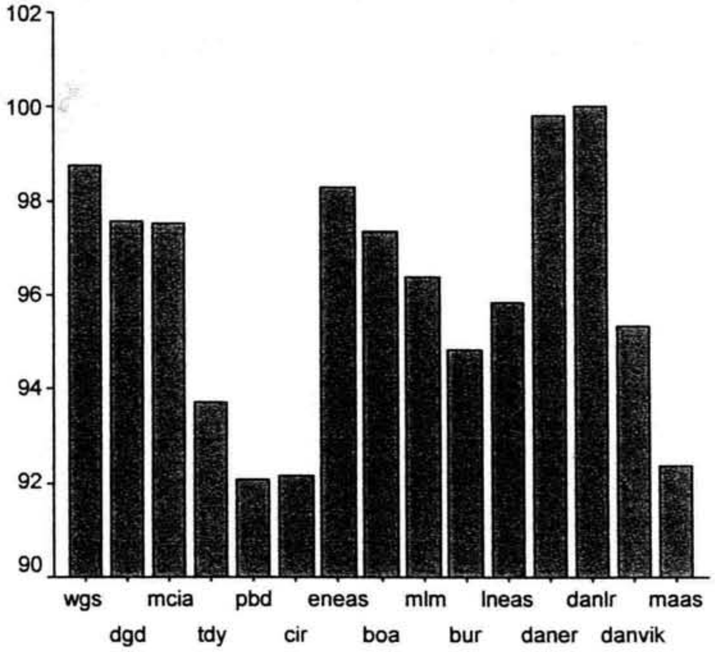
Table 4.37 Cranial length-height index: ANOVA *post hoc* tests: Tukey's HSD

	wgs	dgd	mcia	tdy	pbd	cir	eneas	boa	mlm	bur	lneas	daner	danlr	danvik
dgd	1.000													
mcia	.994	1.000												
tdy	.060	.994	.076											
pbd	.072	.950	**.039**	1.000										
cir	**.000**	.558	**.000**	.410	.992									
eneas	1.000	1.000	1.000	1.000	.996	.821								
boa	.998	1.000	.908	1.000	1.000	.865	1.000							
mlm	.899	.999	.542	1.000	1.000	.620	1.000	1.000						
bur	.324	.990	.150	1.000	1.000	.864	1.000	1.000	1.000					
lneas	.445	.989	.195	1.000	1.000	.940	1.000	1.000	1.000	1.000				
daner	.983	1.000	.746	1.000	.998	.525	1.000	1.000	1.000	1.000	1.000			
danlr	.993	1.000	.816	1.000	.997	.520	1.000	1.000	1.000	1.000	1.000	1.000		
danvik	**.020**	.842	**.011**	.971	1.000	1.000	.969	.994	.978	.999	1.000	.951	.944	
maas	**.000**	.318	**.000**	.168	.849	1.000	.580	.576	.296	.524	.667	.235	.234	.993

Significant (at $p<.05$) p values for each comparison are in **bold** type. Those which approach significance have an *.
wgs, dgd, mcia = IA; tdy, pbd, cir = RB; eneas, boa, mlm = early AS; bur, lneas = later AS daner, danlr, danvik = Danish

4.3.3 Cranial breadth-height index

Figure 4.3 Mean of cranial breadth-height index



Levene's test indicates that there are no significant differences in variance among the samples examined (Levene's = 1.536, p=.092).

ANOVA indicates that there are very highly significant differences in mean cranial breadth-height index among the samples examined (F=14.071, p=.000). Fifteen samples were included in this test, of which two had particularly small sample sizes (Danes' Graves n=8, early north-east Anglo-Saxon n=6).

The LSD (liberal) *post hoc* tests indicate that all British Iron Age samples differ significantly from all Romano-British samples and Maastricht. Wetwang also differs significantly from all later British Anglo-Saxon samples and Danish Vikings, and Maiden Castle also differs from Burwell and Maastricht.

With the exception of Trentholme Drive (which does not differ significantly from Burwell or Danish Vikings), all Romano-British samples differ from all other samples except Maastricht, in having lower skulls relative to breadth.

All early and later British Anglo-Saxon samples differ from all Romano-British samples (except Burwell/Trentholme Drive, as mentioned above). Early Anglo-Saxon samples also differ from Maastricht, while later Anglo-Saxon samples differ significantly or approach significant difference from Wetwang, Danish early/late Roman and Maastricht.

The most notable pattern to emerge from these multiple comparisons, which is confirmed by Tukey's HSD tests, is the difference between the group of Romano-British samples and the British Iron Age, early Anglo-Saxon and Danish early/late Roman samples.

Table 4.38 Cranial breadth-height index: Descriptive statistics

CBH index

					95% Confidence Interval for Mean			
	N	Mean	Std. Deviation	Std. Error	Lower Bound	Upper Bound	Minimum	Maximum
wgs	242	98.7530	5.78591	.37193	98.0204	99.4857	83.78	123.33
dgd	8	97.5841	5.29450	1.87189	93.1578	102.010	85.82	102.92
mcia	40	97.5324	4.06214	.64228	96.2333	98.8316	89.51	104.44
tdy	137	93.7394	4.80916	.41087	92.9269	94.5519	78.71	108.82
pbd	49	92.0712	4.78137	.68305	90.6978	93.4446	80.27	102.17
cir	50	92.1756	5.33529	.75452	90.6593	93.6919	80.80	103.70
eneas	6	98.2880	3.94774	1.61166	94.1451	102.431	93.66	103.85
boa	18	97.3562	4.21250	.99290	95.2614	99.4510	89.16	103.86
mlm	41	96.3789	4.18019	.65284	95.0595	97.6984	87.82	104.20
bur	52	94.8287	4.92954	.68360	93.4563	96.2011	86.01	103.76
lneas	35	95.8374	6.40871	1.08327	93.6360	98.0389	83.56	111.85
daner	34	99.8232	5.29756	.90852	97.9748	101.672	88.28	110.69
danlr	32	99.9939	5.74966	1.01641	97.9210	102.067	87.94	110.85
danvik	37	95.3046	5.76081	.94707	93.3838	97.2253	82.88	108.33
maas	27	92.3552	6.93124	1.33392	89.6132	95.0971	77.56	107.41
Total	808	96.2073	5.91997	.20826	95.7985	96.6161	77.56	123.33

Table 4.39 Cranial breadth-height index: ANOVA *post hoc* tests: LSD

	wgs	dgd	mcia	tdy	pbd	cir	eneas	boa	mlm	bur	lneas	daner	danlr	danvik
dgd	.543													
mcia	.181	.980												
tdy	**.000**	**.048**	**.000**											
pbd	**.000**	**.007**	**.000**	.061										
cir	**.000**	**.008**	**.000**	.077	.923									
eneas	.833	.807	.747	**.042**	**.007**	**.008**								
boa	.285	.920	.908	**.007**	**.000**	**.000**	.712							
mlm	**.009**	.560	.332	**.006**	**.000**	**.000**	.414	.518						
bur	**.000**	.175	**.016**	.211	**.010**	**.012**	.134	.084	.165					
lneas	**.003**	.405	.171	**.039**	**.002**	**.002**	.300	.328	.660	.388				
daner	.275	.287	.067	**.000**	**.000**	**.000**	.517	.114	**.006**	**.000**	**.002**			
danlr	.217	.252	.053*	**.000**	**.000**	**.000**	.473	.094	**.004**	**.000**	**.002**	.897		
danvik	**.000**	.274	.068	.114	**.006**	**.007**	.205	.182	.376	.679	.673	**.000**	**.000**	
maas	**.000**	**.015**	**.000**	.219	.825	.888	**.014**	**.002**	**.002**	.051*	**.011**	**.000**	**.000**	**.030**

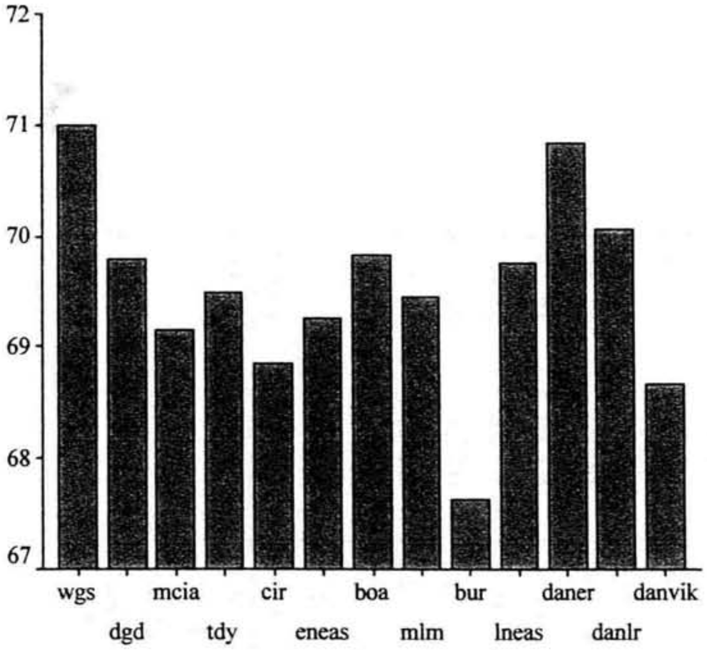
Table 4.40 Cranial breadth-height index: ANOVA *post hoc* tests: Tukey's HSD

	wgs	dgd	mcia	tdy	pbd	cir	eneas	boa	mlm	bur	lneas	daner	danlr	danvik
dgd	1.000													
mcia	.992	1.000												
tdy	**.000**	.811	**.007**											
pbd	**.000**	.308	**.000**	.865										
cir	**.000**	.333	**.000**	.909	1.000									
eneas	1.000	1.000	1.000	.773	.313	.340								
boa	.999	1.000	1.000	.307	**.027**	**.034**	1.000							
mlm	.351	1.000	1.000	.263	**.013**	**.017**	1.000	1.000						
bur	**.000**	.991	.512	.996	.377	.437	.976	.924	.988					
lneas	.149	1.000	.990	.753	.095	.117	.999	1.000	1.000	1.000				
daner	.999	.999	.882	**.000**	**.000**	**.000**	1.000	.962	.261	**.002**	.121			
danlr	.996	.998	.831	**.000**	**.000**	**.000**	1.000	.940	.214	**.002**	.097	1.000		
danvik	**.022**	.999	.887	.963	.261	.307	.995	.992	1.000	1.000	1.000	**.030**	**.023**	
maas	**.000**	.493	**.009**	.996	1.000	1.000	.471	.128	.141	.826	.410	**.000**	**.000**	.679

Significant (at $p<.05$) p values for each comparison are in **bold** type. Those which approach significance have an *.
wgs, dgd, mcia = IA; tdy, pbd, cir = RB; eneas, boa, mlm = early AS; bur, lneas = later AS daner, danlr, danvik = Danish

4.3.4 Fronto-parietal index

Figure 4.4 Mean of fronto-parietal index



Levene's test indicates that there are no significant differences in variance among the samples examined (Levene's = .850, p=.599).

ANOVA indicates that there are very highly significant differences in mean fronto-parietal index among the samples examined (F=6.272, p=.000).

Thirteen samples (no Poundbury or Maastricht) were included in this test, none of which had a very small (n<10) sample size.

The LSD (liberal) *post hoc* tests indicate that most of the significant or nearly significant differences are between Wetwang and all other samples except Bidford-on-Avon and Danish early/late Romans; and Burwell and all other samples except Danish Vikings. The Romano-British samples from Trentholme Drive and Cirencester, and the Anglo-Saxon sample from Morant's London Museums, also differ significantly from Danish Early Romans. The distinctiveness of Wetwang's broader and Burwell's narrower foreheads are emphasised by the results of Tukey's HSD tests. Apart from these, however, and while there is clearly much variation between samples, no clear temporal patterns are evident.

Table 4.41 Fronto-parietal index: Descriptive statistics

FP index

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum	Maximum
					Lower Bound	Upper Bound		
wgs	263	70.9895	3.49234	.21535	70.5654	71.4135	61.68	84.03
dgd	20	69.7997	3.37812	.75537	68.2187	71.3807	63.12	73.76
mcia	47	69.1466	3.53056	.51498	68.1100	70.1832	59.18	78.22
tdy	152	69.4843	3.19064	.25879	68.9730	69.9957	59.72	76.92
cir	60	68.8429	3.16983	.40922	68.0240	69.6617	62.31	80.10
eneas	19	69.2613	2.57603	.59098	68.0197	70.5029	63.70	73.69
boa	28	69.8361	3.87289	.73191	68.3343	71.3378	63.64	79.77
mlm	79	69.4510	3.47326	.39077	68.6731	70.2290	60.00	77.31
bur	59	67.6200	2.96166	.38558	66.8482	68.3918	60.06	73.96
lneas	54	69.7587	3.51462	.47828	68.7994	70.7180	63.04	77.24
daner	61	70.8298	3.32167	.42530	69.9791	71.6805	63.43	77.34
danlr	52	70.0589	3.75595	.52086	69.0133	71.1046	58.67	78.33
danvik	41	68.6596	3.96361	.61901	67.4085	69.9107	59.72	77.37
Total	935	69.8413	3.52905	.11541	69.6148	70.0678	58.67	84.03

Table 4.42 Fronto-parietal index: ANOVA *post hoc* tests: LSD

	wgs	dgd	mcia	tdy	cir	eneas	boa	mlm	bur	lneas	daner	danlr
dgd	.133											
mcia	**.001**	.474										
tdy	**.000**	.698	.554									
cir	**.000**	.278	.648	.218								
eneas	**.033**	.623	.902	.789	.642							
boa	.090	.971	.398	.617	.204	.571						
mlm	**.000**	.684	.629	.944	.299	.828	.608					
bur	**.000**	**.014**	**.022**	**.000**	.051*	.069	**.005**	**.002**				
lneas	**.016**	.963	.369	.612	.153	.585	.923	.610	**.001**			
daner	.742	.242	**.011**	**.009**	**.001**	.081	.203	**.018**	**.000**	.094		
danlr	.073	.773	.185	.295	.061	.384	.781	.319	**.000**	.651	.232	
danvik	**.000**	.221	.505	.170	.791	.526	.160	.229	.135	.121	**.002**	.050*

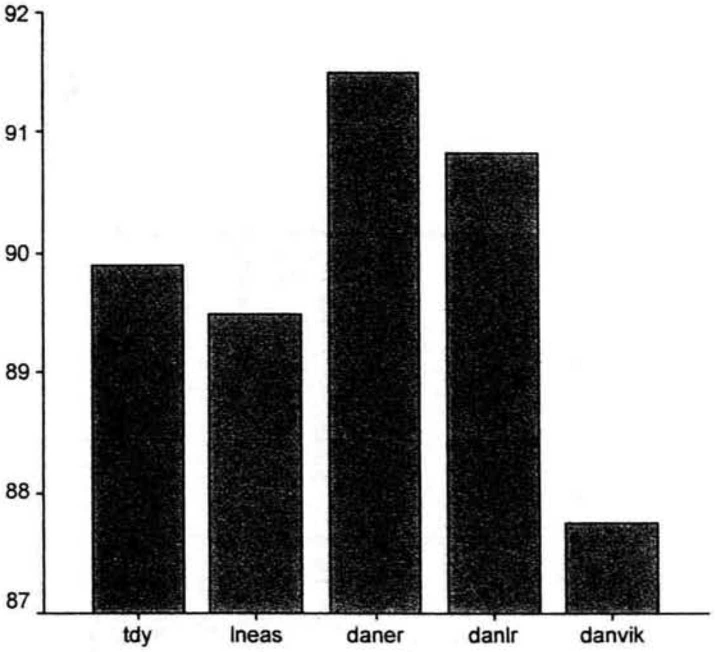
Table 4.43 Fronto-parietal index: ANOVA *post hoc* tests: Tukey's HSD

	wgs	dgd	mcia	tdy	cir	eneas	boa	mlm	bur	lneas	daner	danlr
dgd	.956											
mcia	**.038**	1.000										
tdy	**.001**	1.000	1.000									
cir	**.001**	.997	1.000	.991								
eneas	.643	1.000	1.000	1.000	1.000							
boa	.895	1.000	1.000	1.000	.989	1.000						
mlm	**.027**	1.000	1.000	1.000	.998	1.000	1.000					
bur	**.000**	.398	.528	**.023**	.763	.839	.191	.091				
lneas	.436	1.000	1.000	1.000	.970	1.000	1.000	1.000	**.049**			
daner	1.000	.994	.350	.313	.072	.874	.988	.467	**.000**	.903		
danlr	.852	1.000	.983	.998	.807	1.000	1.000	.999	**.012**	1.000	.993	
danvik	**.004**	.992	1.000	.978	1.000	1.000	.974	.993	.957	.943	.084	.758

Significant (at $p<.05$) *p* values for each comparison are in **bold** type. Those which approach significance have an *.
wgs, dgd, mcia = IA; tdy, pbd, cir = RB; eneas, boa, mlm = early AS; bur, lneas = later AS daner, danlr, danvik = Danish

4.3.5 Total facial index

Figure 4.5 Mean of total facial index



Levene's test indicates that there are no significant differences in variance among the samples examined (Levene's = 2.445, p=.051). However, this statistic does approach significance, so Welch's robust test for equality of means was also used.

Both tests indicate that there are no significant differences in mean total facial index among the samples examined (ANOVA F=.631, p=.641; Welch = .644, p=.636).

Only five samples were included in this test (Trentholme Drive, later north-east Anglo-Saxon and the three Danish samples), of which one had a particularly small sample size (Danish Viking n=8).

As there are no statistically significant differences between samples (and none approaches significance), no *post hoc* test results have been presented, and no statistical analysis can be presented, although the chart above suggests that the two earlier Danish samples have narrower faces than the Danish Viking and British samples.

Table 4.44 Total facial index: Descriptive statistics

TF index

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean Lower Bound	95% Confidence Interval for Mean Upper Bound	Minimum	Maximum
tdy	53	89.8968	5.03838	.69207	88.5081	91.2856	79.58	101.67
lneas	11	89.4784	3.55033	1.07047	87.0933	91.8636	82.93	94.62
daner	13	91.5101	4.77162	1.32341	88.6267	94.3936	83.46	98.39
danlr	24	90.8308	8.56312	1.74794	87.2149	94.4467	77.24	117.39
danvik	8	87.7369	6.46791	2.28675	82.3296	93.1442	76.92	96.67
Total	109	90.0941	5.92268	.56729	88.9697	91.2186	76.92	117.39

4.3.6 Upper facial index

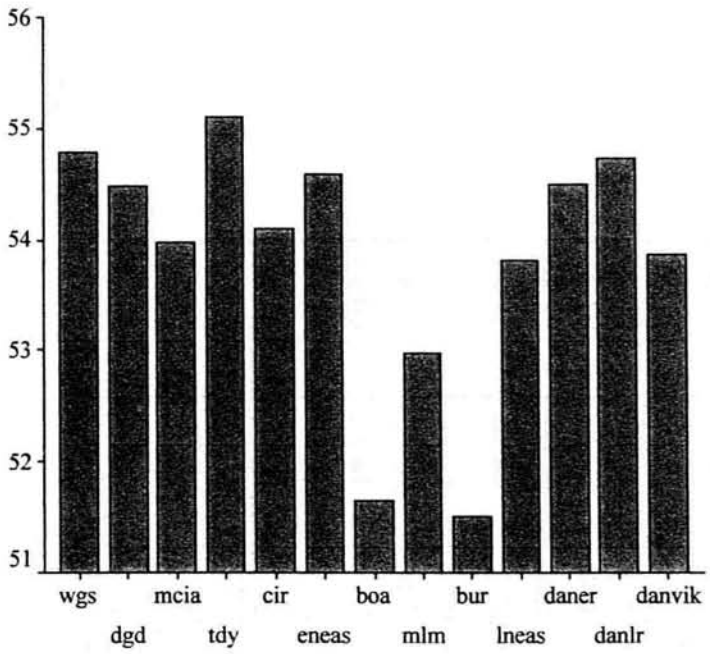


Figure 4.6 Mean of upper facial index

Levene's test indicates that there are no significant differences in variance among the samples examined (Levene's = 1.218, *p*=.268).

ANOVA indicates that there are very highly significant differences in mean upper facial index among the samples examined (*F*=2.440, *p*=.005).

Thirteen samples were included in this test (no Poundbury or Maastricht), of which two had particularly small sample sizes (Danes' Graves *n*=7, early north-east Anglo-Saxon *n*=4).

The LSD (liberal) *post hoc* tests indicate that most of the statistically significant differences involve Bidford-on-Avon, Burwell and (to a lesser extent) Morant's London Museums sample, which have broader faces compared to British Iron Age, Romano-British and Danish early and late Roman samples. All of the significant differences between Bidford-on-Avon and these groups become non-significant, however, when the more conservative Tukey's HSD is applied, and the only significant differences which remain are between Burwell and the samples from Trentholme Drive and Wetwang. No temporal or geographic patterns are evident from these results.

Table 4.45 Upper facial index: Descriptive statistics

UF index

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum	Maximum
					Lower Bound	Upper Bound		
wgs	128	54.7742	4.30709	.38070	54.0209	55.5275	44.71	77.71
dgd	7	54.4739	3.56354	1.34689	51.1781	57.7696	51.13	59.66
mcia	20	53.9679	3.71258	.83016	52.2304	55.7054	47.35	60.32
tdy	72	55.1084	3.25193	.38324	54.3443	55.8726	43.88	61.86
cir	18	54.0948	3.96439	.93442	52.1234	56.0663	40.73	59.42
eneas	4	54.5823	4.17756	2.08878	47.9348	61.2297	49.26	58.56
boa	16	51.6485	2.69537	.67384	50.2122	53.0847	47.06	57.46
mlm	25	52.9675	4.67938	.93588	51.0359	54.8990	46.19	63.03
bur	26	51.4956	4.33729	.85061	49.7437	53.2475	42.42	60.77
lneas	19	53.8154	2.78090	.63798	52.4751	55.1558	47.06	58.62
daner	22	54.4937	3.38928	.72260	52.9910	55.9964	48.84	60.48
danlr	29	54.7216	4.60241	.85465	52.9709	56.4722	47.29	69.57
danvik	11	53.8730	2.45094	.73899	52.2264	55.5195	49.65	58.33
Total	397	54.2115	4.00532	.20102	53.8163	54.6067	40.73	77.71

Table 4.46 Upper facial index: ANOVA *post hoc* tests: LSD

	wgs	dgd	mcia	tdy	cir	eneas	boa	mlm	bur	lneas	daner	danlr
dgd	.844											
mcia	.393	.769										
tdy	.563	.683	.250									
cir	.492	.828	.921	.327								
eneas	.923	.965	.775	.794	.822							
boa	**.003**	.113	.079	**.002**	.070	.182						
mlm	**.036**	.369	.396	**.019**	.353	.445	.294					
bur	**.000**	.075	**.035**	**.000**	**.031**	.144	.902	.181				
lneas	.321	.704	.903	.202	.829	.722	.104	.478	.051*			
daner	.757	.991	.664	.520	.749	.967	**.028**	.184	**.009**	.581		
danlr	.948	.881	.509	.654	.595	.947	**.012**	.102	**.002**	.434	.837	
danvik	.465	.751	.949	.331	.883	.757	.148	.524	.093	.969	.668	.541

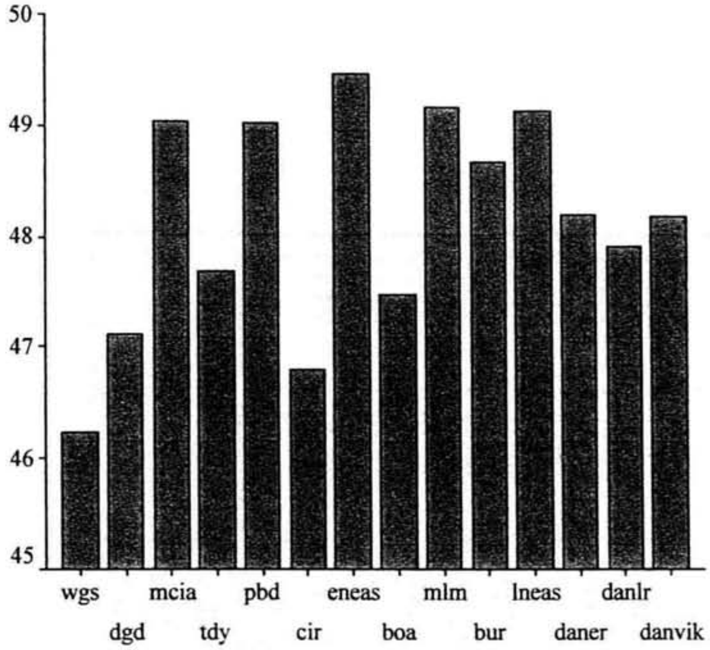
Table 4.47 Upper facial index: ANOVA *post hoc* tests: Tukey's HSD

	wgs	dgd	mcia	tdy	cir	eneas	boa	mlm	bur	lneas	daner	danlr
dgd	1.000											
mcia	1.000	1.000										
tdy	1.000	1.000	.995									
cir	1.000	1.000	1.000	.999								
eneas	1.000	1.000	1.000	1.000	1.000							
boa	.125	.932	.866	.076	.841	.982						
mlm	.659	1.000	1.000	.480	.999	1.000	.998					
bur	**.008**	.857	.650	**.005**	.619	.963	1.000	.982				
lneas	.999	1.000	1.000	.988	1.000	1.000	.920	1.000	.758			
daner	1.000	1.000	1.000	1.000	1.000	1.000	.585	.983	.290	1.000		
danlr	1.000	1.000	1.000	1.000	1.000	1.000	.366	.916	.113	1.000	1.000	
danvik	1.000	1.000	1.000	.999	1.000	1.000	.966	1.000	.899	1.000	1.000	1.000

Significant (at $p<.05$) p values for each comparison are in **bold** type. Those which approach significance have an *.
wgs, dgd, mcia = IA; tdy, pbd, cir = RB; eneas, boa, mlm = early AS; bur, lneas = later AS daner, danlr, danvik = Danish

4.3.7 Nasal index

Figure 4.7 Mean of nasal index



Levene's test indicates that there are no significant differences in variance among the samples examined (Levene's = 1.119, *p*=.340).

ANOVA indicates that there are very highly significant differences in mean nasal index among the samples examined (*F*=2.897, *p*=.000). Fourteen samples were included in this test, of which one had a particularly small sample size (early north-east Anglo-Saxon *n*=7).

The LSD (liberal) *post hoc* tests indicate that Wetwang is significantly or nearly significantly different from all other samples except Danes' Graves, Cirencester and Bidford-on-Avon. Cirencester is also significantly different from Morant's London Museums sample and later north-east Anglo-Saxons.

When the more conservative Tukey's HSD is applied, however, the sole remaining significant differences are between Wetwang and Poundbury, Morant's London Museums and later north-east Anglo-Saxons.

No clear patterns of difference are evident from these results.

Table 4.48 Nasal index: Descriptive statistics

N index

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum	Maximum
					Lower Bound	Upper Bound		
wgs	147	46.2417	4.37120	.36053	45.5292	46.9542	32.94	59.08
dgd	14	47.1129	3.91205	1.04554	44.8542	49.3717	40.00	54.17
mcia	27	49.0236	5.09152	.97986	47.0095	51.0378	41.18	61.64
tdy	70	47.6890	4.59899	.54968	46.5924	48.7856	38.46	59.65
pbd	49	49.0145	4.27061	.61009	47.7878	50.2411	42.31	57.43
cir	29	46.8001	3.53766	.65693	45.4544	48.1457	38.73	53.04
eneas	7	49.4582	2.04682	.77362	47.5652	51.3512	47.06	53.19
boa	28	47.4785	4.44528	.84008	45.7548	49.2021	40.37	58.64
mlm	38	49.1514	3.99685	.64838	47.8377	50.4652	41.76	58.01
bur	44	48.6604	3.96256	.59738	47.4557	49.8651	39.47	59.09
lneas	41	49.1131	4.43980	.69338	47.7117	50.5144	38.18	59.21
daner	23	48.1817	5.55915	1.15916	45.7777	50.5856	40.00	60.00
danlr	33	47.8990	4.09990	.71370	46.4452	49.3528	41.51	58.14
danvik	29	48.1742	3.99017	.74096	46.6565	49.6920	38.46	55.32
Total	579	47.7752	4.42805	.18402	47.4138	48.1366	32.94	61.64

Table 4.49 Nasal index: ANOVA *post hoc* tests: LSD

	wgs	dgd	mcia	tdy	pbd	cir	eneas	boa	mlm	bur	lneas	daner	danlr
dgd	.473												
mcia	**.002**	.181											
tdy	**.022**	.650	.175										
pbd	**.000**	.148	.993	.101									
cir	.572	.825	.056*	.354	**.030**								
eneas	.056*	.243	.813	.304	.800	.146							
boa	.167	.797	.187	.828	.135	.555	.280						
mlm	**.000**	.133	.907	.095	.884	**.028**	.863	.122					
bur	**.001**	.245	.732	.245	.694	.073	.651	.260	.609				
lneas	**.000**	.137	.934	.096	.914	**.028**	.846	.125	.969	.631			
daner	**.047**	.468	.498	.637	.448	.254	.496	.565	.398	.668	.410		
danlr	**.048**	.570	.318	.819	.254	.320	.388	.706	.225	.446	.232	.810	
danvik	**.029**	.452	.464	.613	.409	.228	.482	.545	.361	.639	.373	.995	.803

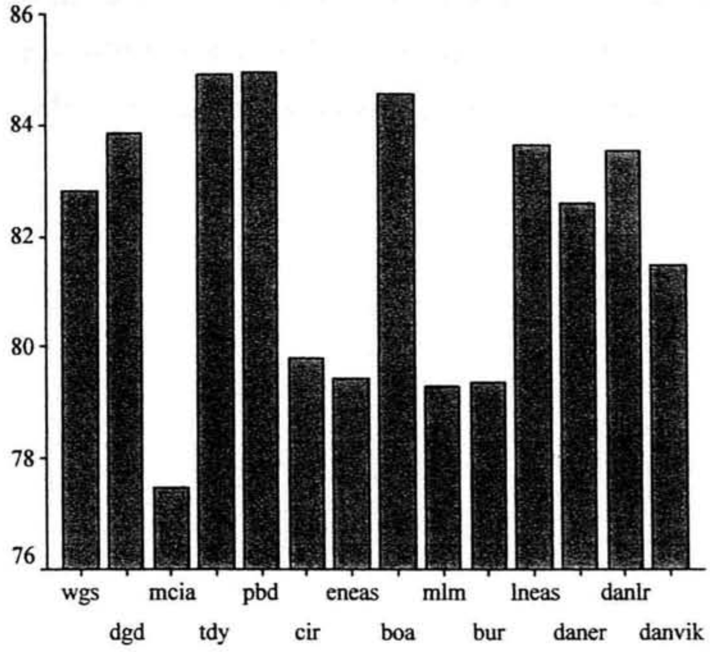
Table 4.50 Nasal index: ANOVA *post hoc* tests: Tukey's HSD

	wgs	dgd	mcia	tdy	pbd	cir	eneas	boa	mlm	bur	lneas	daner	danlr
dgd	1.000												
mcia	.120	.988											
tdy	.557	1.000	.986										
pbd	**.009**	.976	1.000	.935									
cir	1.000	1.000	.816	1.000	.645								
eneas	.816	.997	1.000	.999	1.000	.975							
boa	.984	1.000	.989	1.000	.968	1.000	.998						
mlm	**.017**	.967	1.000	.924	1.000	.630	1.000	.958					
bur	.072	.997	1.000	.997	1.000	.879	1.000	.998	1.000				
lneas	**.014**	.969	1.000	.926	1.000	.631	1.000	.960	1.000	1.000			
daner	.770	1.000	1.000	1.000	1.000	.997	1.000	1.000	1.000	1.000	1.000		
danlr	.777	1.000	.999	1.000	.997	.999	1.000	1.000	.995	1.000	.996	1.000	
danvik	.635	1.000	1.000	1.000	1.000	.995	1.000	1.000	1.000	1.000	1.000	1.000	1.000

Significant (at $p<.05$) p values for each comparison are in **bold** type. Those which approach significance have an *.
wgs, dgd, mcia = IA; tdy, pbd, cir = RB; eneas, boa, mlm = early AS; bur, lneas = later AS daner, danlr, danvik = Danish

4.3.8 Orbital index

Figure 4.8 Mean of orbital index



Levene's test indicates that there are significant differences in variance among the samples examined (Levene's = 1.976, p=.021).

Welch's test indicates that there are very highly significant differences in mean orbital index among the samples examined (F=8.666, p=.000). Fourteen samples were included in this test, of which one had a particularly small sample size (early north-east Anglo-Saxon n=9).

Because of the significantly unequal variances between samples indicated by Levene's test, Games-Howell *post hoc* tests were used to conduct multiple comparisons between samples for the orbital index. These tests indicate that the early Iron Age samples differ significantly or nearly significantly from Maiden Castle, Morant's London Museums and Burwell. Maiden Castle also differs significantly from Bidford-on-Avon, later north-east Anglo-Saxon and Danish early and late Roman samples. In addition to the above, Trentholme Drive and Poundbury both differ significantly from Maiden Castle, Cirencester, Morant's London Museums sample and Burwell. Bidford-on-Avon also differs significantly from both Morant's London Museums sample and Burwell.

No readily apparent patterns of difference by period or geography are evident in this set of comparisons. However, with the exception of Maiden Castle, the earlier (Iron Age and Romano-British samples) tend to have narrower orbits compared, with the exception of Bidford-on-Avon and later north-east Anglo-Saxons, to the later Romano-British and Anglo-Saxon samples which have wider orbits. All the Danish samples, including the Vikings, have narrower orbits.

Table 4.51 Orbital index: Descriptive statistics

O index

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean		Minimum	Maximum
					Lower Bound	Upper Bound		
wgs	168	82.8080	6.44070	.49691	81.8269	83.7890	68.05	103.79
dgd	13	83.8673	3.63500	1.00817	81.6707	86.0639	76.32	89.47
mcia	29	77.4735	4.29112	.79684	75.8412	79.1057	69.73	86.03
tdy	77	84.9312	5.96929	.68026	83.5764	86.2861	70.45	100.00
pbd	49	84.9554	6.52719	.93246	83.0806	86.8303	73.81	105.41
cir	33	79.8029	5.29305	.92140	77.9260	81.6797	67.15	92.31
eneas	9	79.4279	3.98964	1.32988	76.3611	82.4946	74.37	85.49
boa	30	84.5494	5.78339	1.05590	82.3899	86.7090	72.64	97.37
mlm	39	79.3100	4.09456	.65565	77.9827	80.6373	70.82	87.06
bur	41	79.3708	4.29693	.67107	78.0145	80.7271	69.77	89.87
lneas	40	83.6170	6.67487	1.05539	81.4823	85.7518	71.43	100.00
daner	35	82.6031	5.86364	.99114	80.5889	84.6174	72.50	100.00
danlr	41	83.5354	6.74277	1.05304	81.4071	85.6637	71.11	97.30
danvik	34	81.4889	5.75114	.98631	79.4822	83.4955	67.44	95.24
Total	638	82.4683	6.19441	.24524	81.9867	82.9498	67.15	105.41

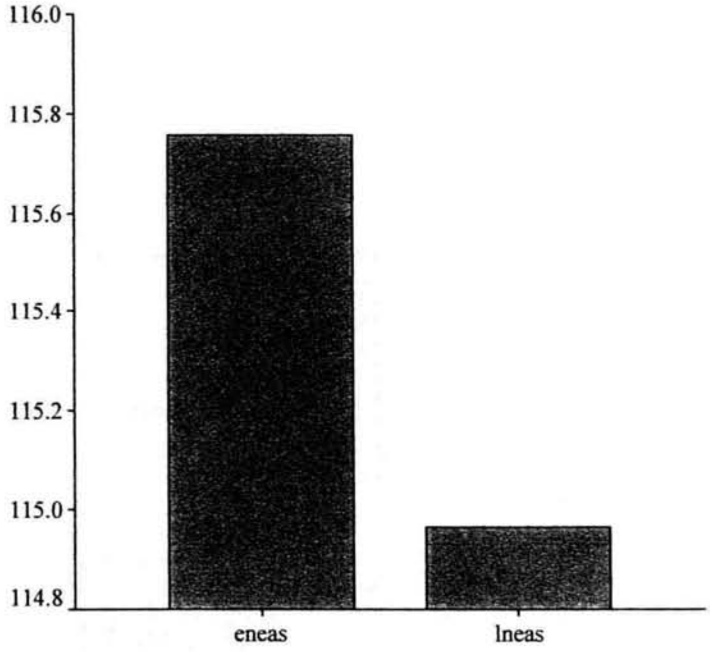
Table 4.52 Orbital index: ANOVA *post hoc* tests: Games-Howell

	wgs	dgd	mcia	tdy	pbd	cir	eneas	boa	mlm	bur	lneas	daner	danlr
dgd	.999												
mcia	**.000**	**.002**											
tdy	.401	1.000	**.000**										
pbd	.743	1.000	**.000**	1.000									
cir	.223	.199	.812	**.002**	**.012**								
eneas	.541	.376	.985	.091	.116	1.000							
boa	.962	1.000	**.000**	1.000	1.000	.067	.213						
mlm	**.004**	**.044**	.876	**.000**	**.000**	1.000	1.000	**.007**					
bur	**.006**	.051*	.858	**.000**	**.000**	1.000	1.000	**.009**	1.000				
lneas	1.000	1.000	**.001**	.999	1.000	.288	.472	1.000	.052*	.063			
daner	1.000	1.000	**.010**	.799	.899	.719	.796	.985	.267	.304	1.000		
danlr	1.000	1.000	**.002**	.997	.999	.319	.499	1.000	.061	.073	1.000	1.000	
danvik	.994	.907	.114	.216	.387	.992	.988	.686	.849	.878	.968	1.000	.977

Significant (at $p<.05$) p values for each comparison are in **bold** type. Those which approach significance have an *.
wgs, dgd, mcia = IA; tdy, pbd, cir = RB; eneas, boa, mlm = early AS; bur, lneas = later AS daner, danlr, danvik = Danish

4.3.9 Maxillo-alveolar index

Figure 4.9 Mean of maxillo-alveolar index



Levene's test indicates that there are no significant differences in variance among the samples examined (Levene's = .204, p=.654).

ANOVA indicates that there are no significant differences in mean maxillo-alveolar index among the samples examined (F=.035, p=.853).

Only two samples were included in this test (early and later north-east Anglo-Saxon), of which one had a particularly small sample size (early north-east Anglo-Saxon n=4).

As there are no significant differences between samples, no *post hoc* test results are presented.

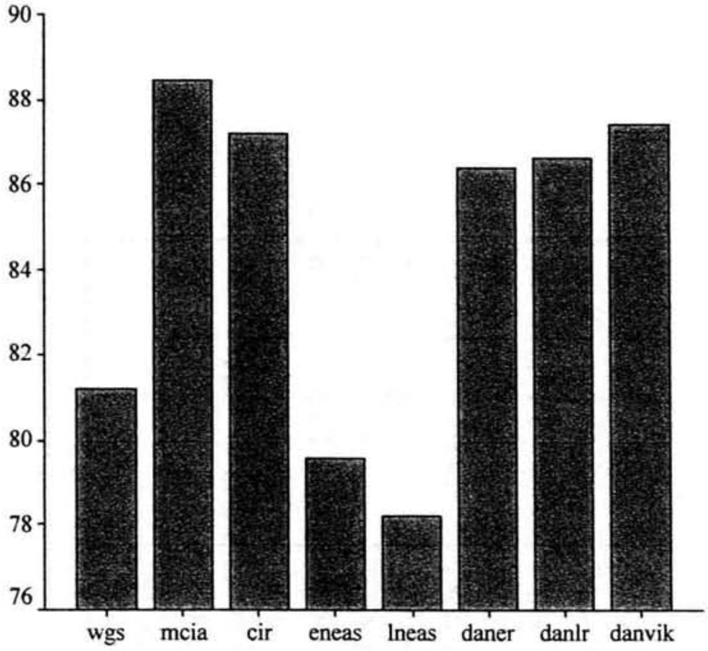
Table 4.53 Maxilloalveolar index: Descriptive statistics

MA index

	N	Mean	Std. Deviation	Std. Error	95% Confidence Interval for Mean Lower Bound	95% Confidence Interval for Mean Upper Bound	Minimum	Maximum
eneas	4	115.755	7.48277	3.74139	103.848	127.662	105.10	122.61
lneas	35	114.965	8.06660	1.36351	112.194	117.736	99.03	130.43
Total	39	115.046	7.91834	1.26795	112.479	117.613	99.03	130.43

4.3.10 Palatal index

Figure 4.10 Mean of palatal index



Levene's test indicates that there are no significant differences in variance among the samples examined (Levene's = 2.004, *p*=.055). However, this statistic approaches significance, so Welch's robust test for equality of means was also used.

Both tests indicate that there are very highly significant differences in mean palatal index among the samples examined (ANOVA *F*=7.072, *p*=.000; Welch = 7.732, *p*=.000).

Eight samples were included in this test, of which one had a particularly small sample size (early north-east Anglo-Saxon *n*=7).

The LSD (liberal) *post hoc* tests indicate that both Wetwang and later north-east Anglo-Saxons have significantly narrower palates than all other samples except early north-east Anglo-Saxons. Maiden Castle and Cirencester are also significantly or nearly significantly different from both early and later north-east Anglo-Saxons, in having broader palates. Early north-east Anglo-Saxons are also significantly different from Danish early and late Romans.

When the more conservative Tukey's HSD test is applied, however, the majority of these comparisons become non-significant, although the distinction of Wetwang and north-east later Anglo-Saxons remains evident .

Table 4.54 Palatal index: Descriptive statistics

P index

					95% Confidence Interval for Mean			
	N	Mean	Std. Deviation	Std. Error	Lower Bound	Upper Bound	Minimum	Maximum
wgs	140	81.1879	8.15153	.68893	79.8258	82.5501	60.00	105.45
mcia	20	88.4564	5.39829	1.20709	85.9299	90.9828	78.18	97.19
cir	13	87.1736	7.14865	1.98268	82.8537	91.4935	76.47	101.70
eneas	7	79.5602	6.85835	2.59221	73.2173	85.9031	71.89	92.79
lneas	42	78.2112	11.35205	1.75166	74.6736	81.7487	58.02	117.07
daner	24	86.3781	6.95745	1.42018	83.4403	89.3160	72.92	100.00
danlr	23	86.6442	5.86986	1.22395	84.1059	89.1825	73.81	94.87
danvik	24	87.4408	8.28959	1.69211	83.9404	90.9412	71.43	107.32
Total	293	82.8497	8.83533	.51617	81.8338	83.8656	58.02	117.07

Table 4.55 Palatal index: ANOVA *post hoc* tests: LSD

	wgs	mcia	cir	eneas	lneas	daner	danlr
mcia	**.000**						
cir	**.013**	.663					
eneas	.611	**.015**	.050*				
lneas	**.041**	**.000**	**.001**	.689			
daner	**.005**	.406	.780	.056*	**.000**		
danlr	**.004**	.473	.854	**.048**	**.000**	.912	
danvik	**.001**	.685	.925	**.027**	**.000**	.656	.741

Table 4.56 Palatal index: ANOVA *post hoc* tests: Tukey HSD

	wgs	mcia	cir	eneas	lneas	daner	danlr
mcia	**.007**						
cir	.199	1.000					
eneas	1.000	.220	.506				
lneas	.450	**.000**	**.016**	1.000			
daner	.088	.991	1.000	.536	**.003**		
danlr	.069	.996	1.000	.492	**.003**	1.000	
danvik	**.016**	1.000	1.000	.341	**.000**	1.000	1.000

Significant (at $p<.05$) p values for each comparison are in **bold** type. Those which approach significance have an *
wgs, dgd, mcia = IA; tdy, pbd, cir = RB; eneas, boa, mlm = early AS; bur, lneas = later AS daner, danlr, danvik = Danish

4.3.11 ANOVA: Summary

Examination of Levene's test results as a whole indicated that differences in variance were significant only for the orbital index. Some of the test results (for cranial length- and breadth- height, total facial and palatal indices) fall just outside of the critical *p* values, and may reflect the small sizes of some samples involved.

Analyses pertaining to the cranial index resulted in the distinctiveness of Romano-British samples' medium, as opposed to long, skulls in comparison to most other samples, being confirmed statistically. The very long skulls of Danish early and late Roman samples were also significantly different from all except each other, using liberal *post hoc* tests, although the differences between these samples and Danes' Graves, Bidford-on-Avon and early north-east Anglo-Saxons became non-significant when Tukey's test was used.

While no clear patterns of difference in the cranial length-height index were observed in the descriptive analyses, statistically significant differences between Iron Age and Romano-British samples were evident from the ANOVA results.

In analyses of cranial breadth-height indices, while Iron Age samples appeared different from the others in descriptive analyses (falling into the 'high' rather than 'medium' skull category), in the ANOVA the lower skulls of Romano-British samples were again found to be consistently distinct, not only from the Iron Age samples, but also from early Anglo-Saxons, most later Anglo-Saxon and most Danish samples. Mid- and later Anglo-Saxon samples were also notably different as a group from Danish early and late Roman samples.

Finally, in terms of patterns of difference not identified in the descriptive analyses, the fronto-parietal index analysis showed that both Wetwang and Burwell were consistently distinct; the former from all except Bidford-on-Avon and Danish early and late Romans, and the latter from all except Danish Vikings.

No notable patterns of difference were observed from analyses of the total facial, upper facial, nasal, orbital, maxillo-alveolar or palatal indices.

The ANOVA results again confirm the overall differences of Romano-British samples, in terms of indices involving the vault, rather than the facial skeleton, and indicate, as a whole, that temporal pooling is justified. However, some regional differences are apparent in differences between results for same-period samples, particularly for Iron Age and Anglo-Saxon periods, while Romano-British samples appear rather more morphologically homogenous for many indices.

4.4 Introduction to multivariate results

In this section, the results of the multivariate analyses are presented. Manova analyses for both separate and pooled groups are presented in section 4.5. Biodistance matrices, hierarchical cluster analysis dendrograms and principal coordinates plots are presented in section 4.6, Mantel matrix correlation analyses in section 4.7 and Relethford-Blangero analyses in section 4.8.

4.5 MANOVA

Multivariate analyses of variance (MANOVA) have been used to ascertain firstly that multivariate differences exist between groups used in this study, and secondly to identify which variables out of the eight used in the biodistance analyses contribute significantly to differences between groups.

Variables included comprise:

- z-GOL (maximum cranial length)
- z-XCB (maximum cranial breadth)
- z-BBH (maximum cranial height)
- z-BNL (basi-nasal length)
- z-OBH (orbital height)
- z-OBB (orbital breadth)
- z-NLH (nasal height)
- z-NLB (nasal breadth)

Results below are presented firstly for 'separate groups', which are actually a combination of single-site samples and pooled samples from both Britain and Denmark, and secondly for 'pooled groups', where the separate groups have been pooled by period into country-wide samples representing Britain and Denmark.

For both these analyses, pooled sex groups (and thus also sex-standardised z-scores) have been used, to better reflect the samples used in the majority of subsequent analyses, and to improve sample sizes.

4.5.1 Separate samples

Twelve separate samples were included in this analysis. The Danes' Graves and north-east early Anglo-Saxon samples were not included, due to their small size when reduced to a multivariate dataset (*n*=5).

Table 4.57 lists the samples included and their size.

Table 4.57 Summary of samples

Sample	Code	Period	*n*
Wetwang / Garton Slack	wgs	IA	130
Maiden Castle	mcia	IA	21
Trentholme Drive	tdy	RB	59
Poundbury	pbd	RB	49
Cirencester	cir	RB	17
Bidford-on-Avon	boa	Early AS	16
Morant's London Museums	mlm	Early/mid- AS	21
Burwell	bur	Mid-AS	34
North-east later Anglo-Saxons	nelas	Later AS	15
Danish early Roman	daner	ER	16
Danish late Roman	danlr	LR	21
Danish Viking	danvik	Viking	25

The following results were obtained: Box's M (test for equality of covariance matrices) = 576.845, F=1.242, p=0.001. Because of the inequality of covariance matrices, the test used in this analysis was Pillai's Trace, which is more robust in the event of Box's M yielding a significant result. Pillai's trace = 0.728, F=3.751, p=.000. MANOVA therefore indicates that there is at least one very highly significant multivariate difference between one or more of the groups used in this analysis. The results of the tests for between-subjects effects indicate which variables demonstrate significant difference(s) between groups, and are tabulated below.

Table 4.58 Test of between-subjects effects

Variable	Levene's (*p*)	*F* (*p*)
z-GOL	0.723 (.717)	1.977 (.029)
z-XCB	0.570 (.690)	6.161 (.000)
z-BBH	0.423 (.946)	4.006 (.000)
z-BNL	3.142 (.000)	5.463 (.000)
z-OBH	0.653 (.783)	3.201 (.000)
z-OBB	2.347 (.008)	5.879 (.000)
z-NLH	1.708 (.069)	2.759 (.002)
z-NLB	0.789 (.651)	2.867 (.001)

Levene's test indicates that the variance of basi-nasal length and orbital breadth was statistically different between some sites. Nasal height also comes close to significance. Tests of between-subjects effects indicate that all variable means differ significantly among sites.

4.5.2 Pooled samples

Seven pooled groups were included in this analysis. Groups were pooled to produce British samples by period for comparison with Danish samples by period. Table 4.59 indicates which groups were included and the sample size for each group.

Table 4.59 Summary of samples

Sample	Code	*n*
UK Iron Age	ukia	156
UK Romano-British	ukrb	125
UK early Anglo-Saxon	ukeas	39
UK eater Anglo-Saxon (incl. Burwell)	uklas	49
Danish early Roman	daner	16
Danish late Roman	danlr	21
Danish Viking	danvik	25

The following results were obtained: Box's M = 306.337, *F*=1.262, *p*=0.006. Pillai's Trace = 0.452, *F*=4.303, *p*=.000. MANOVA therefore indicates both inequality of covariance matrices and that there is at least one significant multivariate difference between one or more of the groups included in this analysis. The results of the tests for between-subjects effects indicate which variables demonstrate significant difference(s) between groups, and are tabulated below.

Table 4.60 Test of between-subjects effects

Variable	**Levene's (*p*)**	***F* (*p*)**
z-GOL	1.307 (.252)	1.807 (.096)
z-XCB	1.008 (.419)	9.980 (.000)
z-BBH	0.214 (.972)	6.227 (.000)
z-BNL	0.972 (.444)	5.867 (.000)
z-OBH	0.556 (.765)	4.634 (.000)
z-OBB	2.693 (.014)	4.250 (.000)
z-NLH	1.707 (.118)	3.426 (.003)
z-NLB	0.636 (.702)	3.695 (.001)

Levene's test indicates that the variance of orbital breadth was statistically different between some samples. Tests of between-subjects effects show that all variable means are significantly different, with the exception of z-GOL.

4.5.3 MANOVA: summary

Multivariate analyses of variance indicate that for both pooled and un-pooled sample sets, with females and males pooled, there are significant differences among groups for all but one of the eight variables which form the basis for the R matrix analyses to follow. The sole exception (z-GOL) is significant for un-pooled samples only. Tests of homogeneity of variance indicate that for pooled samples only one variable (z-OBB) differed significantly in variance among samples while in the analysis of un-pooled samples three variables (z-BNL, z-OBB and z-NLH) differed significantly among samples, probably due to smaller sample sizes in the latter analysis.

4.6 Biodistance analyses

In this section the biodistance (d^2) matrices produced by RMET are presented, along with hierarchical cluster analysis (HCA) dendrograms and principal coordinates (PCO) plots, which allow hypotheses 2a to 2c to be tested.

The HCA dendrograms and PCO plots aid interpretation of the matrices via representation of group relationships in two dimensions. Although HCA (UPGMA) dendrograms and PCO plots both provide two dimensional representations of the biological distance matrices, they differ in that the former is group forcing, but the latter is not, and so give different perspectives. The PCO plots also allow group relationships to be examined in three dimensions, if necessary. In most cases plots for coordinates one and two only have been presented, as these contain the bulk of the variation. When the number of samples in an analysis is increased, however, the third coordinate tends to contain more information and, where this is the case, plots for coordinates one and two, and two and three have been presented.

Within this subsection analyses are presented firstly for temporally and sex pooled (UK) groups. In order to aid interpretation, analyses are then presented by period and for separate sexes. Then, analyses are presented for separate samples, all periods together and by separate period, in order to investigate within-UK differences in biodistance relationships. Separate sex analyses have also been presented for un-pooled samples where necessary, but because of the small size of some sex-specific samples, these have been kept to a minimum.

Individual sample sizes and the codes used in the HCA dendrograms and PCO plots can be found in tables 4.57 and 4.59 above. Where analyses have been conducted for females and males separately, codes are prefixed with an ‘f’ or an ‘m’.

All analyses have been based on RMET analyses which use the eight variables detailed in section 4.5, a heritability of .55, with correction for sampling bias requested.

4.6.1 Pooled samples: UK only: all periods: pooled sex

In this subsection biodistance analysis results are presented for UK sex-pooled samples, pooled geographically and by temporal period, excluding Danish samples.

Examination of the d^2 matrix (table 4.61) shows that the UK Iron Age sample is closest to UK early Anglo-Saxons and most distant from UK later Anglo-Saxons. The UK Romano-British samples are less close to all other samples overall, but are closest to UK early Anglo-Saxons, and most distant from UK later Anglo-Saxons. UK early Anglo-Saxons are closest to UK later Anglo-Saxons, and are moderately close to both UK Romano-British and Iron Age samples.

The HCA dendrogram (figure 4.11) reasonably accurately reflects these relationships. The PCO plot (figure 4.12) also represents these relationships reasonably well, in terms of the general lack of very close relationships between any of the samples, and also emphasises the distinctiveness of the UK Romano-British sample on coordinate two. The Iron Age and Anglo-Saxon samples are spread evenly across coordinate one, with the Romano-British sample being closest to the early Anglo-Saxon sample on this coordinate.

In the next two subsections, these geographically pooled samples are examined for females and males separately, in order to examine whether there are sex-specific differences evident in relationships through time within the UK.

Table 4.61 Biological distance (d^2) matrix derived from the unbiased R matrix

	ukeas	uklas	ukrb
uklas	0.094414		
ukrb	0.129502	0.166442	
ukia	0.125062	0.227086	0.179648

Figure 4.11 Hierarchical cluster analysis dendrogram

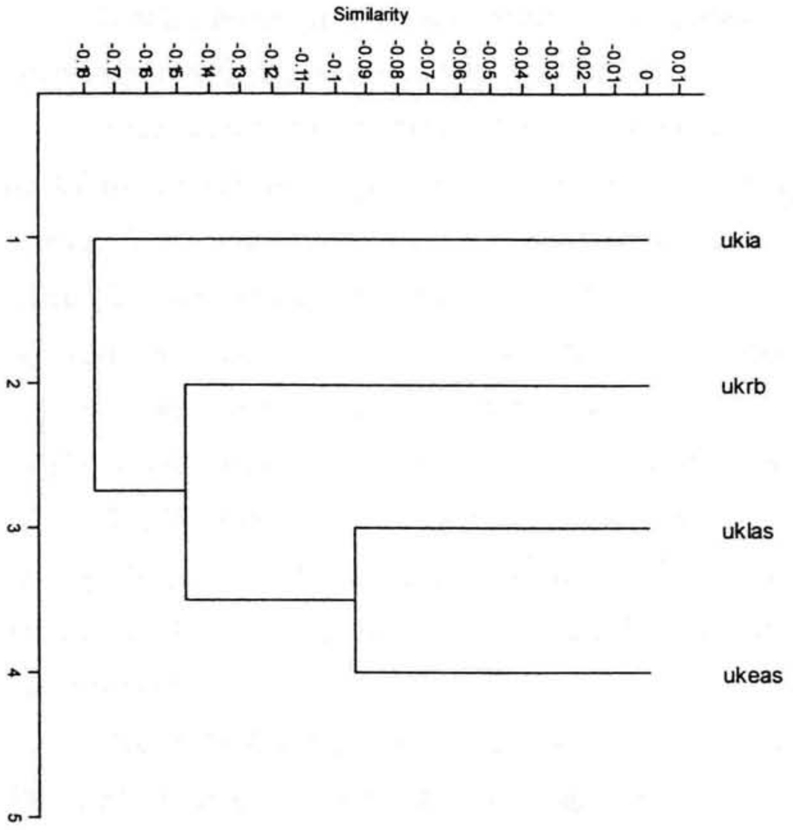
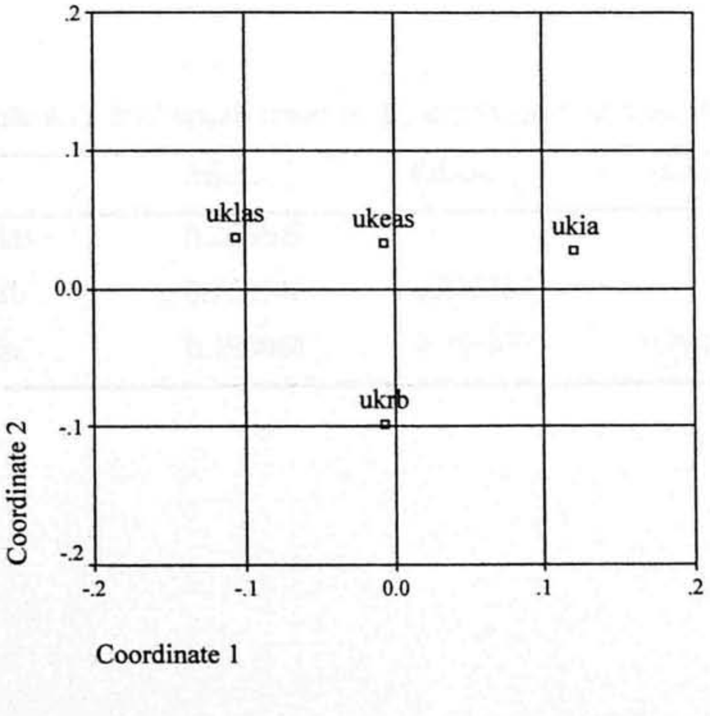


Figure 4.12 Principal coordinates plot: axes 1 (66.03%) and 2 (32.56%)



4.6.2 Pooled samples: UK only: all periods: females

In this subsection biodistance analysis results are presented for UK female samples, pooled geographically and by temporal period, excluding Danish samples.

Examination of the d^2 matrix (table 4.62) indicates that, compared to the sex pooled biodistance matrix (table 4.61 above), the overall magnitude of the distances between female samples is larger. In contrast to the sex pooled sample, the closest female UK early Anglo-Saxon relationships are with UK Romano-British and Iron Age females, and their most distant with UK later Anglo-Saxon females. As with the sex pooled sample, however, Iron Age females' closest relationship is with UK early Anglo-Saxons, and their most distant with UK later Anglo-Saxon females.

The HCA dendrogram (figure 4.13) represents these relationships well, placing UK early Anglo-Saxon females closest to UK Romano-British and Iron Age females, whilst later Anglo-Saxon females are the least similar to all the other samples overall.

The PCO plot (figure 4.14) resembles an inverted mirrored version of the PCO plot for sex-pooled samples, reflecting the lack of any very close relationships between samples, and again emphasising the distinctiveness of the Romano-British sample on coordinate two, and the spread of the other three samples across coordinate one.

Table 4.62 Biological distance (d^2) matrix derived from the unbiased R matrix

	fukeas	fuklas	fukrb
fuklas	0.263609		
fukrb	0.155146	0.233335	
fukia	0.190068	0.396877	0.261525

Figure 4.13 Hierarchical cluster analysis dendrogram

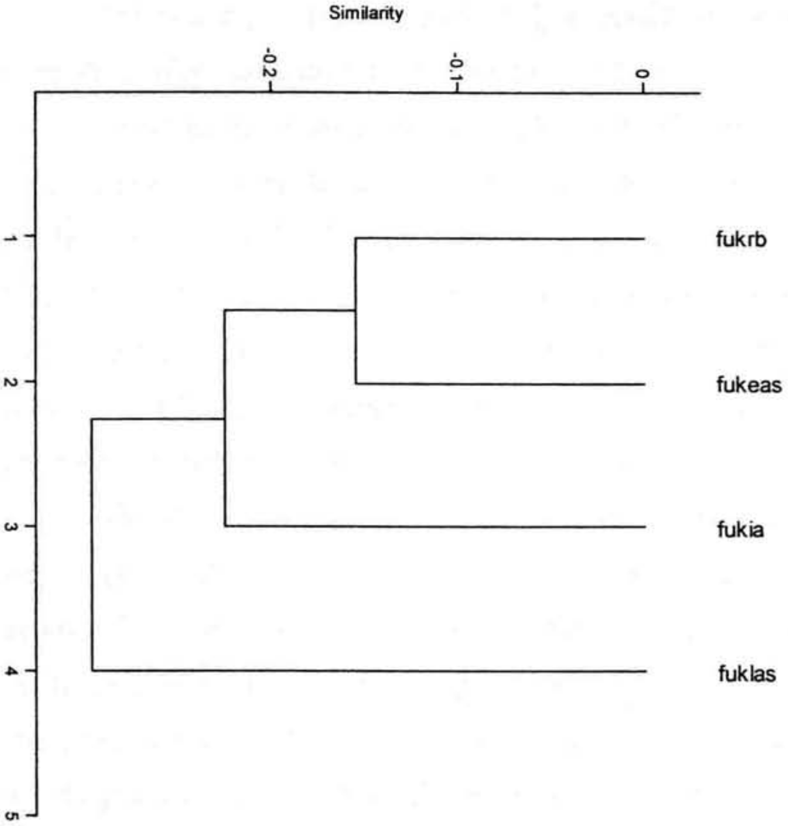
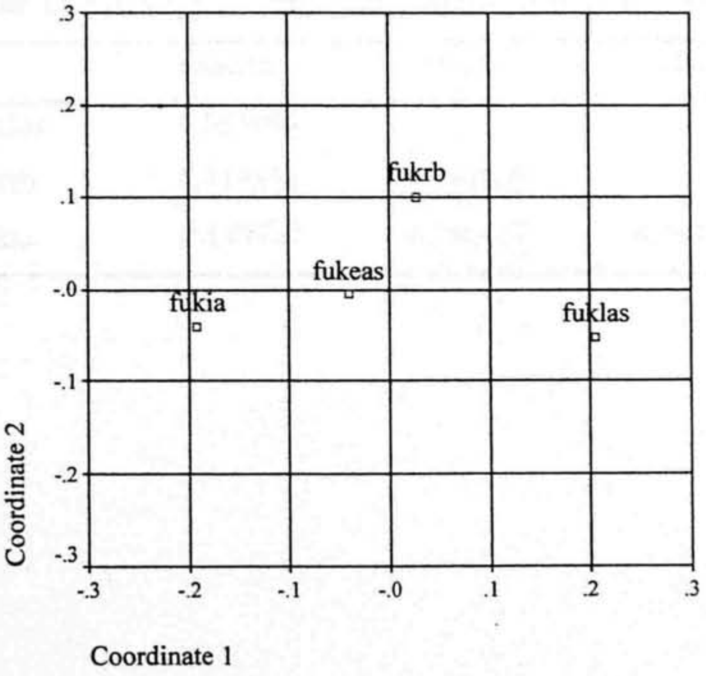


Figure 4.14 Principal coordinates plot: axes 1 (78.93%) and 2 (14.11%)



4.6.3 Pooled samples: UK only: all periods: males

In this subsection biodistance analysis results are presented for UK male samples, pooled geographically and by temporal period, excluding Danish samples.

Examination of the d^2 matrix (table 4.63) indicates that on the whole, the magnitude of the male distances is very similar to that for the sex pooled samples (table 4.61). This probably reflects the dominance of males over females, in terms of number of individuals, in the pooled sex analysis. Additionally, the overall patterning of relationships for male only samples is the same as for pooled samples, although the early Anglo-Saxon sample is relatively closer to UK later Anglo-Saxon males, and more distant from UK Iron Age males in this analysis.

The HCA dendrogram and PCO plots reflect the overall patterning discussed above. The HCA dendrogram (figure 4.15) is a near replica of the dendrogram produced for pooled sexes (figure 4.11), although it does reflect the changes in relative distances between the samples. The PCO plot (figure 4.16) is also similar to that produced for pooled sex samples (figure 4.12), although as with the HCA dendrogram, it emphasises the closer relationship between early and later Anglo-Saxons.

Table 4.63 Biological distance (d^2) matrix derived from the unbiased R matrix

	mukeas	muklas	mukrb
muklas	0.055964		
mukrb	0.119311	0.142620	
mukia	0.149927	0.200427	0.191733

Figure 4.15 Hierarchical cluster analysis dendrogram

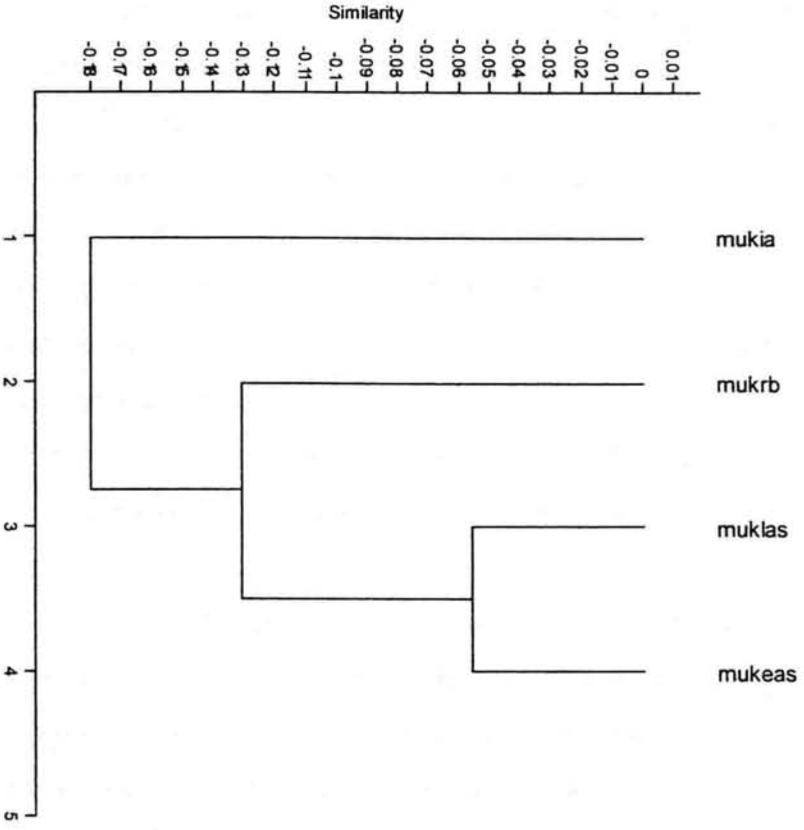
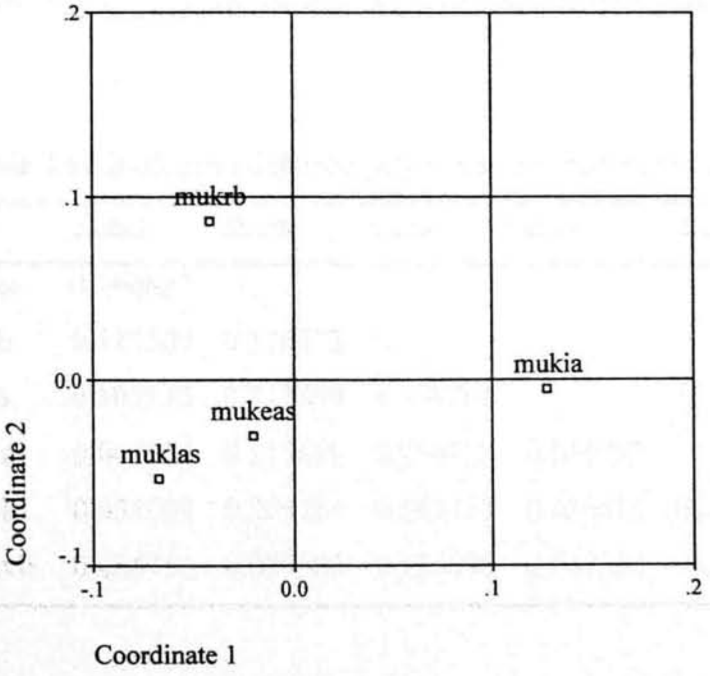


Figure 4.16 Principal coordinates plot: axes 1 (66.5%) and 2 (32.94%)



4.6.4 Pooled samples: all periods: pooled sex

In this subsection biodistance analysis results are presented for UK and Danish sex-pooled samples, pooled by period.

Examination of the d^2 matrix (table 4.64) indicates that early UK Anglo-Saxons are closest to all Danish samples, and only moderately close to the Iron Age and Romano-British UK samples. Later UK Anglo-Saxons are closest to Danish Vikings, but are relatively distant from all other samples, particularly Danish early and late Roman and UK Iron Age. The UK Iron Age sample, however, is closer even than the early Anglo-Saxons to all the Danish samples, and relatively more distant from later UK Anglo-Saxon and Romano-British samples. The UK Romano-British sample is closest overall to early Anglo-Saxons, but is relatively distant from all the UK and Danish samples.

The HCA dendrogram (figure 4.17) provides a reasonable two dimensional representation of the d^2 matrix, demonstrating the similarity of UK Iron Age, early Anglo-Saxon and Danish samples, and the overall dissimilarity of the Romano-British sample. In contrast the PCO plot (figure 4.18) does not accurately represent the d^2 matrix.

In the next four subsections the biodistance analyses for Iron Age / Romano-British periods and Romano-British /Anglo-Saxon periods are presented, for separate sexes, in order to examine sex specific relationships through these periods.

Table 4.64 Biological distance (d^2) matrix derived from the unbiased R matrix

	ukeas	uklas	ukrb	ukia	daner	danlr
uklas	0.100857					
ukrb	0.117569	0.170572				
ukia	0.107373	0.213800	0.168761			
daner	0.041054	0.215690	0.256723	0.036937		
danlr	0.051098	0.205754	0.192353	0.036515	0.000000	
danvik	0.064750	0.039383	0.136896	0.040586	0.059039	0.050388

Figure 4.17 Hierarchical cluster analysis dendrogram

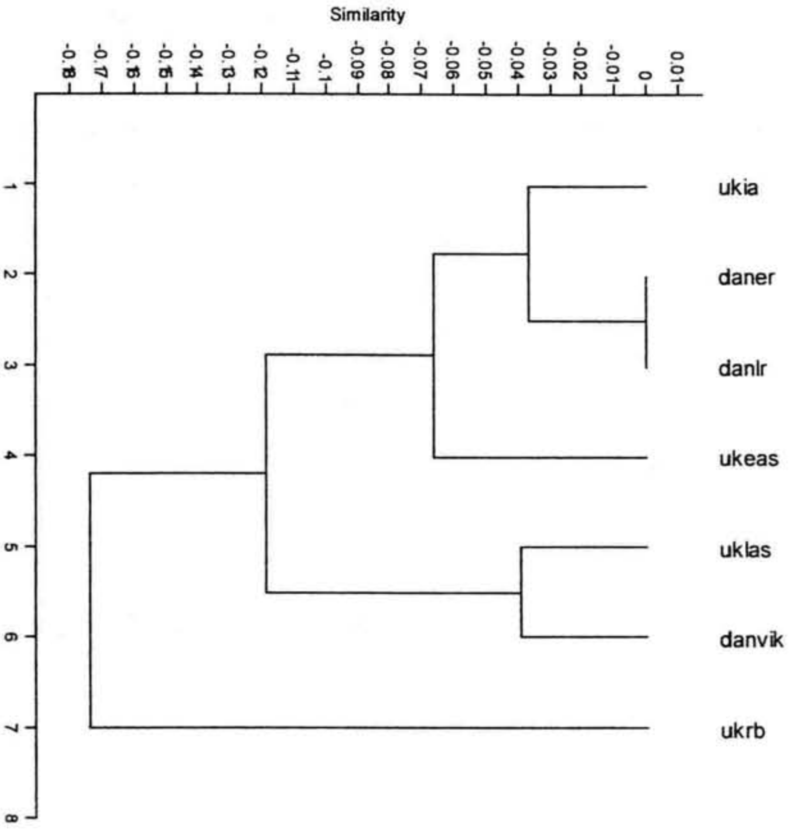
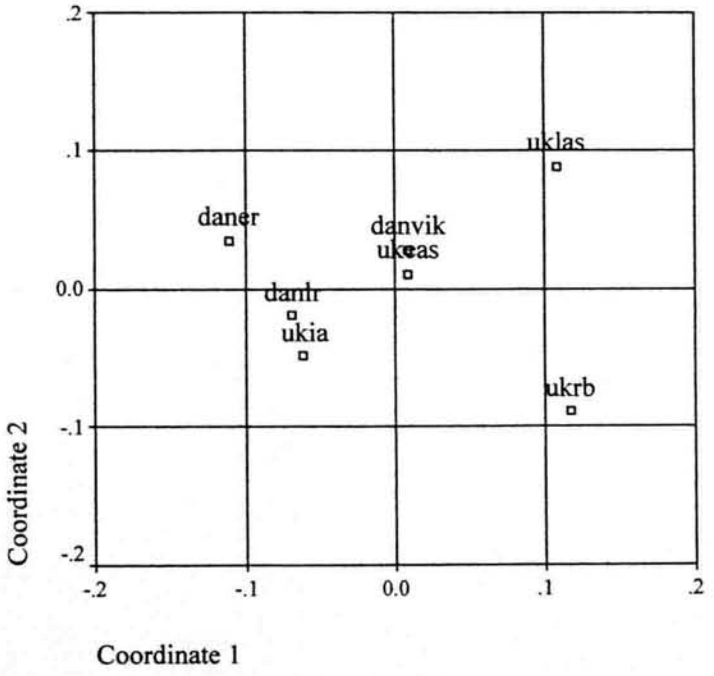


Figure 4.18 Principal coordinates plot: axes 1 (51.18%) and 2 (22.9%)



4.6.5 Pooled samples: Iron Age and Romano-British: females

In this subsection the biodistance analyses for Iron Age, Romano-British and Danish females have been presented. Danish early and late Roman samples represent the nearest-to-contemporary comparative samples for these periods.

Examination of the d^2 matrix (table 4.65) indicates that the closest relationships are between UK Iron Age females and Danish early and late Romans. UK Romano-British females are very distant from all other samples.

The HCA dendrogram (figure 4.19) accurately represents these relationships, as does the PCO plot (figure 4.20), although in the latter relationships are distorted somewhat due to coordinate two, which represents only 1.37% of the variance.

Table 4.65 Biological distance (d^2) matrix derived from the unbiased R matrix

	fukrb	fukia	fdaner
fukia	0.330330		
fdaner	0.366927	0.000000	
fdanlr	0.331809	0.047913	0.039196

Figure 4.19 Hierarchical cluster analysis dendrogram

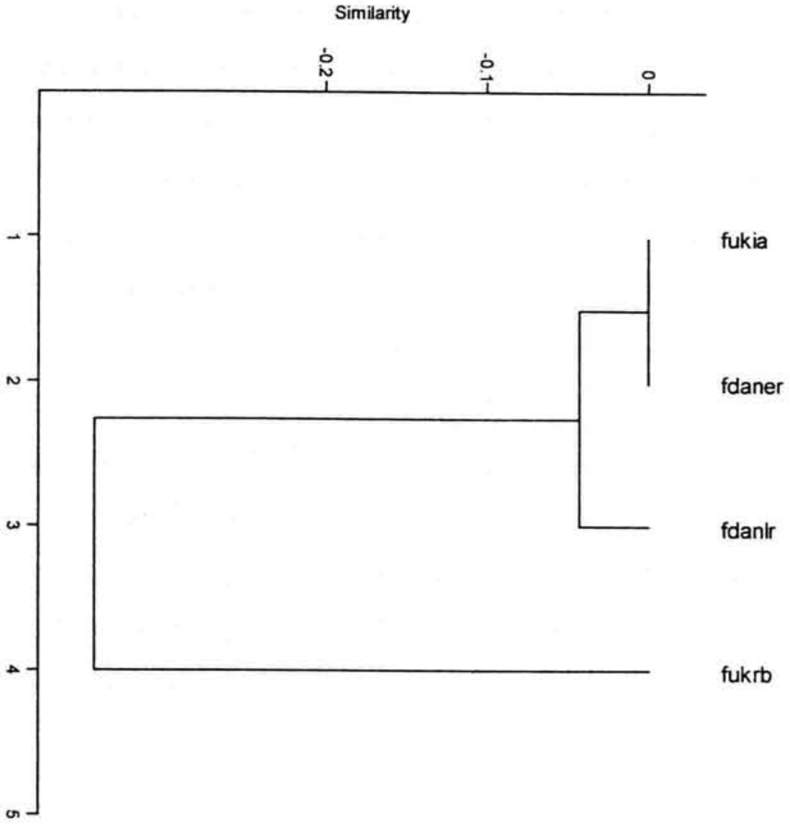
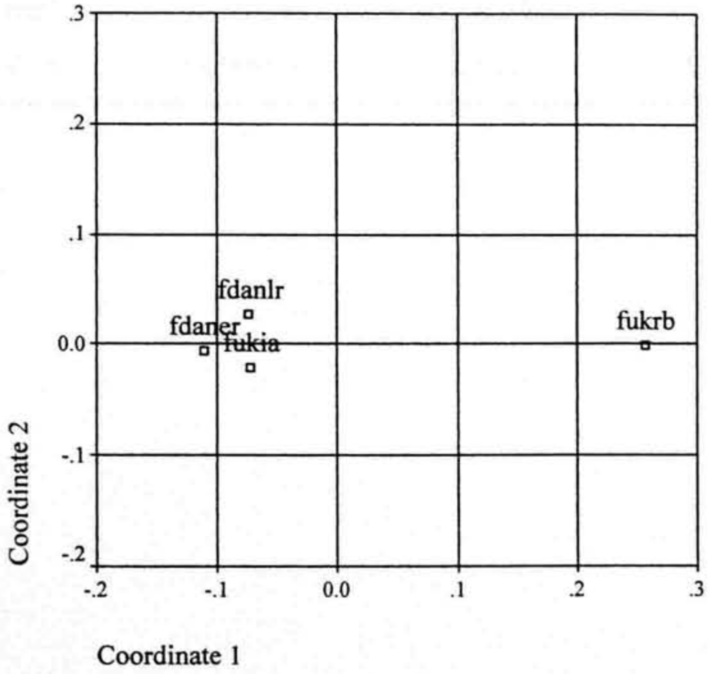


Figure 4.20 Principal coordinates plot: axes 1 (97.66%) and 2 (1.37%)



4.6.6 Pooled samples: Iron Age and Romano-British: males

In this subsection the biodistance analyses for Iron Age, Romano-British and Danish males have been presented. Danish early and late Roman samples represent the nearest-to-contemporary comparative samples for these periods.

Examination of the d^2 matrix (table 4.66) indicates that, as with the female samples, the closest relationships are between UK Iron Age males and Danish early and late Roman males. The UK Romano-British sample is most dissimilar to all the other samples, although the magnitude of this dissimilarity is less than in the case of Romano-British females, and UK Romano-British males are closer to the UK Iron Age than they are to the Danish samples.

The HCA dendrogram (figure 4.21) reflects these relationships well, as does the PCO plot (figure 4.22) although, as with the analysis of female samples, in the latter relationships are distorted somewhat due to coordinate two, which in this case represents only 1.85% of the variance.

Table 4.66 Biological distance (d^2) matrix derived from the unbiased R matrix

	mukrb	mukia	mdaner
mukia	0.158336		
mdaner	0.288298	0.048827	
mdanlr	0.246879	0.068516	0.000000

Figure 4.21 Hierarchical cluster analysis dendrogram

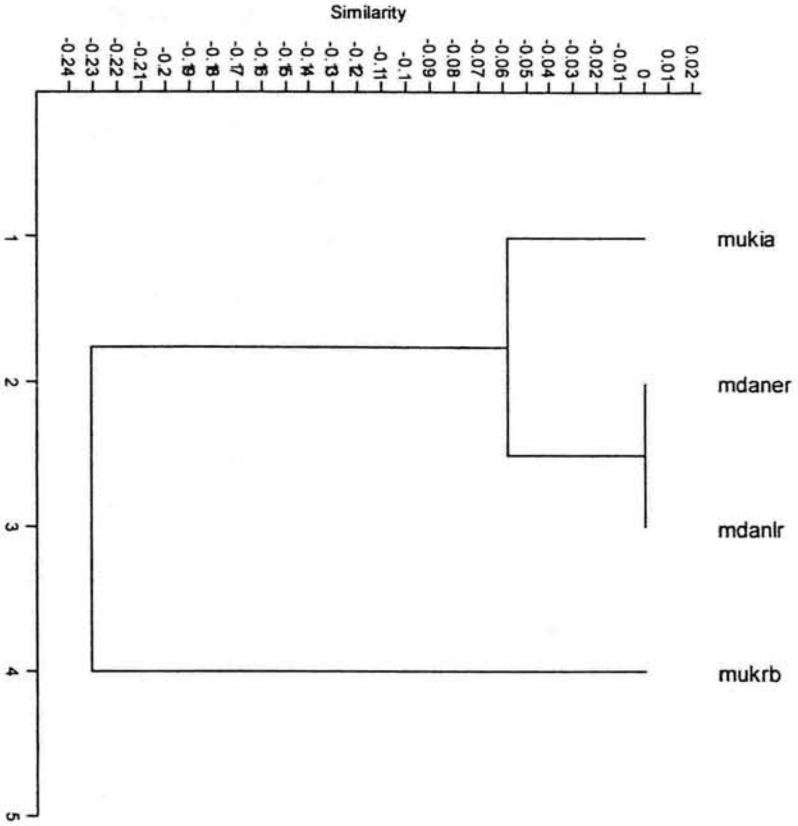
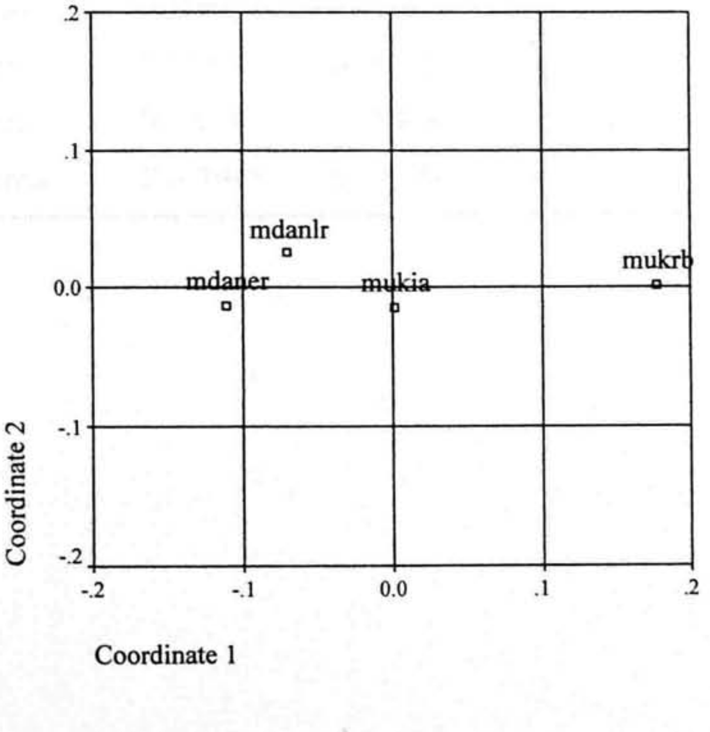


Figure 4.22 Principal coordinates plot: axes 1 (87.67%) and 2 (1.85%)



4.6.7 Pooled samples: Romano-British and Anglo-Saxon: females

In this subsection the biodistance results for Romano-British, Anglo-Saxon and Danish females have been presented. Danish late Roman and Viking samples represent the nearest-to-contemporary samples for the Romano-British period and Anglo-Saxon periods respectively.

Examination of the d^2 matrix (table 4.67) shows that both early and later UK Anglo-Saxon females are closest to Danish Vikings. UK Romano-British females are generally dissimilar from all samples, but are closest to early Anglo-Saxons. Although no samples have very close relationships, of the UK samples the early Anglo-Saxon females have more similarities overall than all other samples.

The HCA dendrogram (figure 4.23) reasonably accurately represents the d^2 matrix, although the large distance between later UK Anglo-Saxon females and Danish late Roman females may have contributed to the former sample appearing more dissimilar than the matrix suggests, from all other groups. Both the HCA dendrogram and the PCO plot (figure 4.24) suggest a general lack of close clustering between any of the samples.

Table 4.67 Biological distance (d^2) matrix derived from the unbiased R matrix

	fukeas	fuklas	fukrb	fdanlr
fuklas	0.289052			
fukrb	0.150101	0.286336		
fdanlr	0.202596	0.588684	0.348182	
fdanvik	0.071947	0.150305	0.197265	0.131664

Figure 4.23 Hierarchical cluster analysis dendrogram

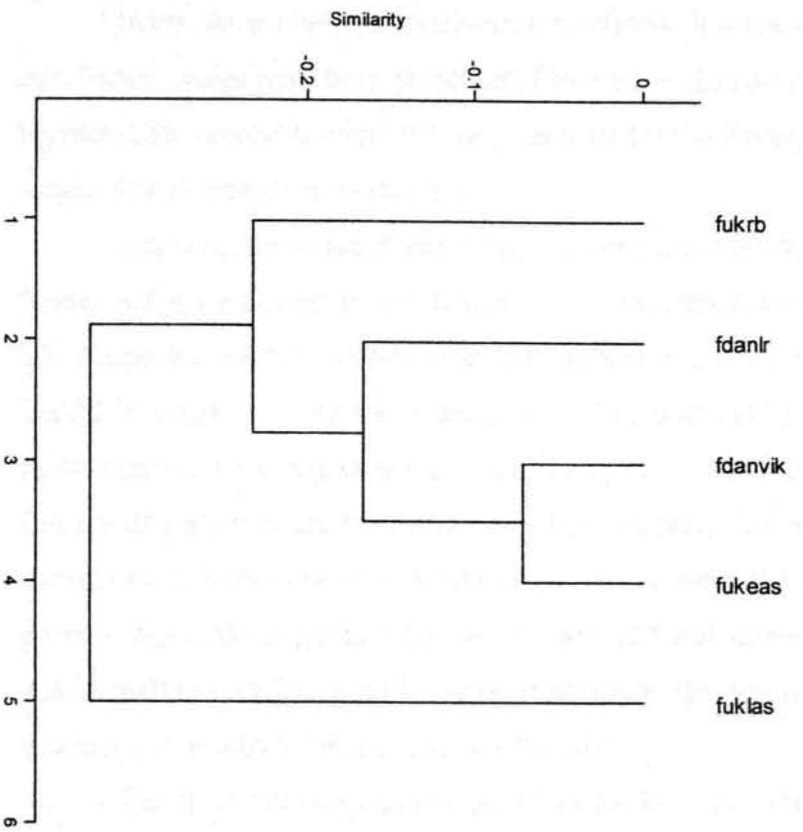
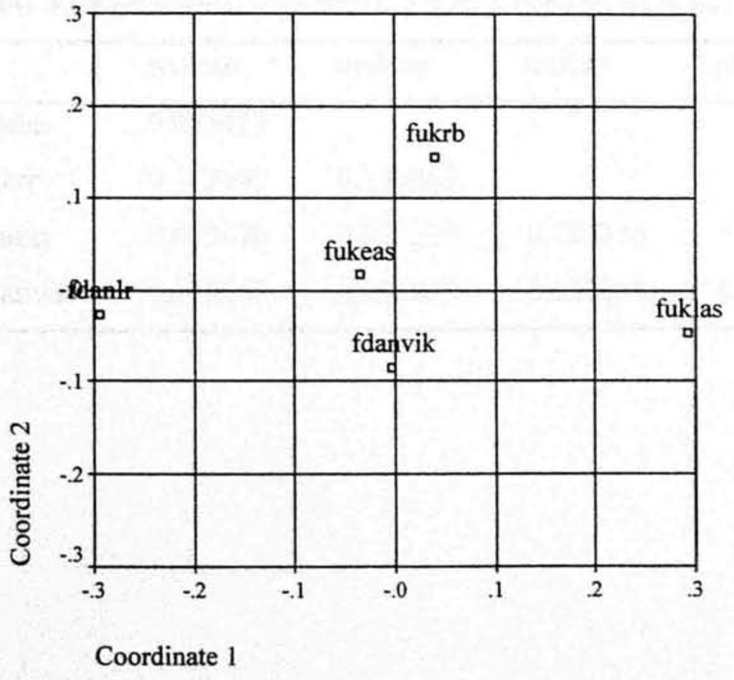


Figure 4.24 Principal coordinates plot: axes 1 (67.49%) and 2 (11.92%)



4.6.8 Pooled samples: Romano-British and Anglo-Saxon: males

In this subsection the biodistance results for Romano-British, Anglo-Saxon and Danish males have been presented. Danish late Roman and Viking samples represent the nearest-to-contemporary samples for the Romano-British period and Anglo-Saxon periods respectively.

Examination of the d^2 matrix (table 4.68) indicates that early UK Anglo-Saxon males are closest to later UK Anglo-Saxons and Danish late Romans. Later UK Anglo-Saxons are closest to Danish late Romans, early UK Anglo-Saxons and Danish Vikings. As in previous analyses, UK Romano-British males are not particularly close to any samples, and UK Anglo-Saxons are more similar to the Danish samples than are the Romano-British samples. The overall pattern of relationships in this matrix is not dissimilar to that derived for females of these periods, especially regarding the dissimilarity of the Romano-British sample. Additionally overall, as seen in previous analyses, the absolute magnitude of the distances is smaller for males than for females.

The HCA dendrogram (figure 4.25) and PCO plot (figure 4.26) both emphasise the closer relationship between Anglo-Saxon and Danish late Roman samples, and the relative dissimilarity of the Romano-British and Danish Viking samples.

Table 4.68 Biological distance (d^2) matrix derived from the unbiased R matrix

	mukeas	muklas	mukrb	mdanlr
muklas	0.053419			
mukrb	0.112190	0.130863		
mdanlr	0.073020	0.052239	0.159336	
mdanvik	0.113267	0.093875	0.133334	0.162929

Figure 4.25 Hierarchical cluster analysis dendrogram

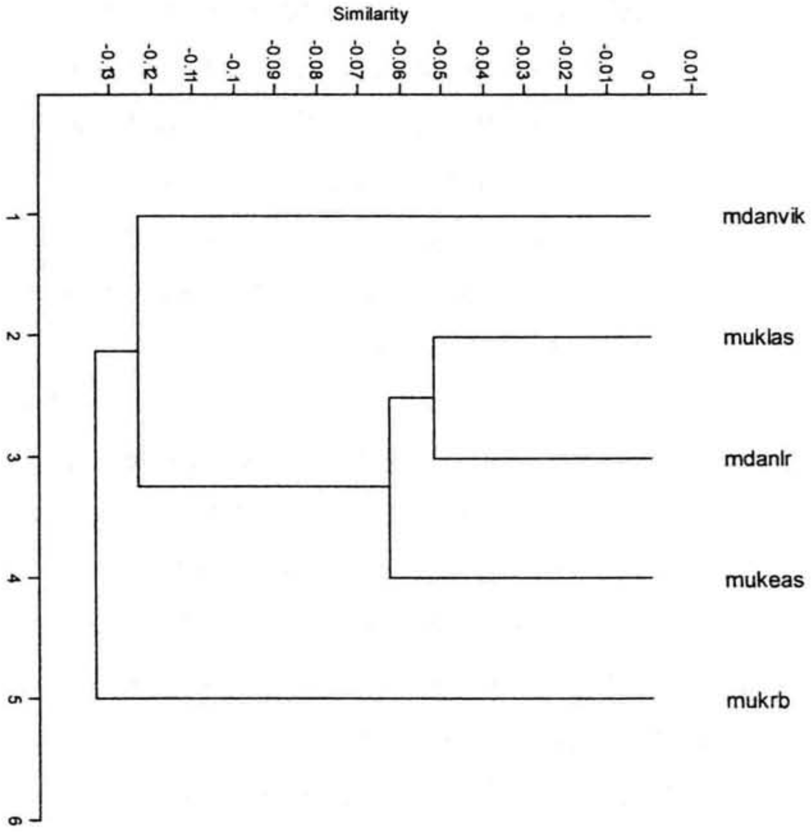
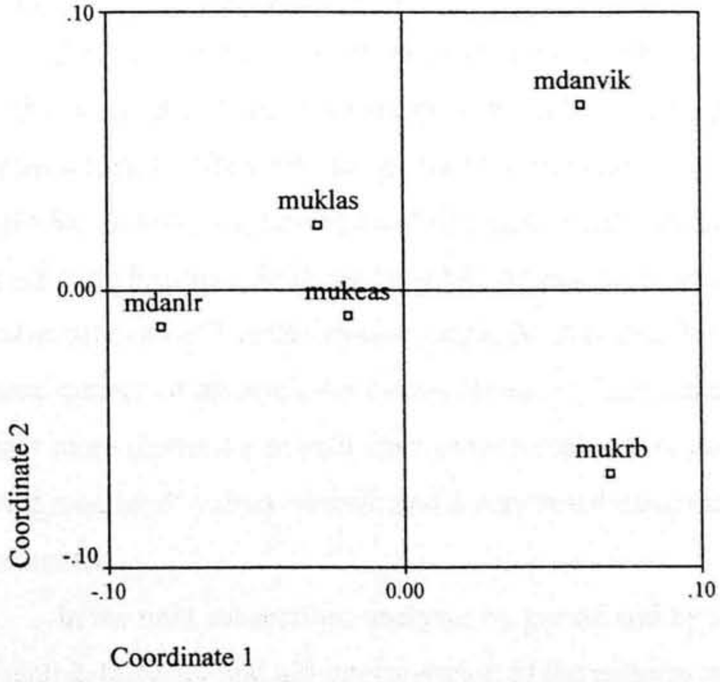


Figure 4.26 Principal coordinates plot: axes 1 (57.72%) and 2 (34.38%)



4.6.9 Separate samples: all periods: pooled sex

In this subsection, all possible sex-pooled samples have been compared in a single biodistance analysis, in order to investigate firstly whether or not un-pooled samples demonstrate the same patterns of relatedness as pooled samples, and secondly what, if any, regional variability is evident in relationships between groups.

The large size of the d^2 matrix (table 4.69) means that it is rather difficult to examine without the aid of reference to the HCA dendrogram and PCO plot. However, the previously discovered pattern of greater Iron Age, Anglo-Saxon and Danish relatedness, in contrast to Romano-British samples, is evident, and the relationships discussed below are reasonably well represented in both the HCA dendrogram (figure 4.27) and PCO plot (figure 4.28).

A distinction is seen in the relatively large d^2 between the two Iron Age samples of Wetwang and Maiden Castle. Wetwang's similarities to Danish samples and the early Anglo-Saxon sample from Bidford-on-Avon contrast with Maiden Castles greater similarity to Morant's London Museums sample, and general dissimilarity from Romano-British, Danish and other Anglo-Saxon samples.

On the whole, Romano-British samples are much closer to each other than they are to any other groups, Poundbury being very close to both Trentholme Drive and Cirencester, although the latter two are much less similar. Unlike Trentholme Drive and Poundbury, Cirencester is also very close to Danish Vikings, Burwell and Morant's London Museums sample.

Early Anglo-Saxon Bidford-on-Avon is much closer to all Danish samples and Wetwang, than to all other samples, including other Anglo-Saxons, whereas Morant's London Museums sample is only moderately close to Danish and other Anglo-Saxon samples, having most similarities with Maiden Castle, Cirencester and Danish early Romans. With the later UK Anglo-Saxon sample split into its constituent parts of later north-east Anglo-Saxons and Burwell, it is clear that a general pattern of dissimilarity exists. However, later north-east Anglo-Saxons appear more dissimilar overall from other samples than does Burwell, the latter having smaller d^2 values overall, and a very small distance from Danish Vikings and Cirencester.

In the next subsections analyses by period and by sex (for some periods) are presented, to verify and aid interpretation of the patterns noted above.

Table 4.69 Biological distance (d^2) matrix derived from the unbiased R matrix

	lneas	tdy	pbd	mlm	daner	danlr	danvik	wgs	boa	bur	mcia
tdy	0.351306										
pbd	0.170213	0.052742									
mlm	0.196905	0.215314	0.166454								
daner	0.362784	0.243290	0.335340	0.097487							
danlr	0.333469	0.177728	0.265503	0.121246	0.000000						
danvik	0.198951	0.183484	0.164934	0.126812	0.055498	0.047632					
wgs	0.415266	0.152557	0.272155	0.270196	0.061659	0.048168	0.057618				
boa	0.318621	0.160120	0.198018	0.123997	0.047051	0.048913	0.058803	0.082515			
bur	0.215656	0.314359	0.185637	0.112460	0.196342	0.198862	0.033446	0.249648	0.153076		
mcia	0.354804	0.338141	0.329087	0.036746	0.104227	0.181754	0.138635	0.241263	0.159873	0.138633	
cir	0.134057	0.147382	0.066178	0.096560	0.208389	0.184477	0.038733	0.199070	0.139385	0.042820	0.187734

Figure 4.27 Hierarchical cluster analysis dendrogram

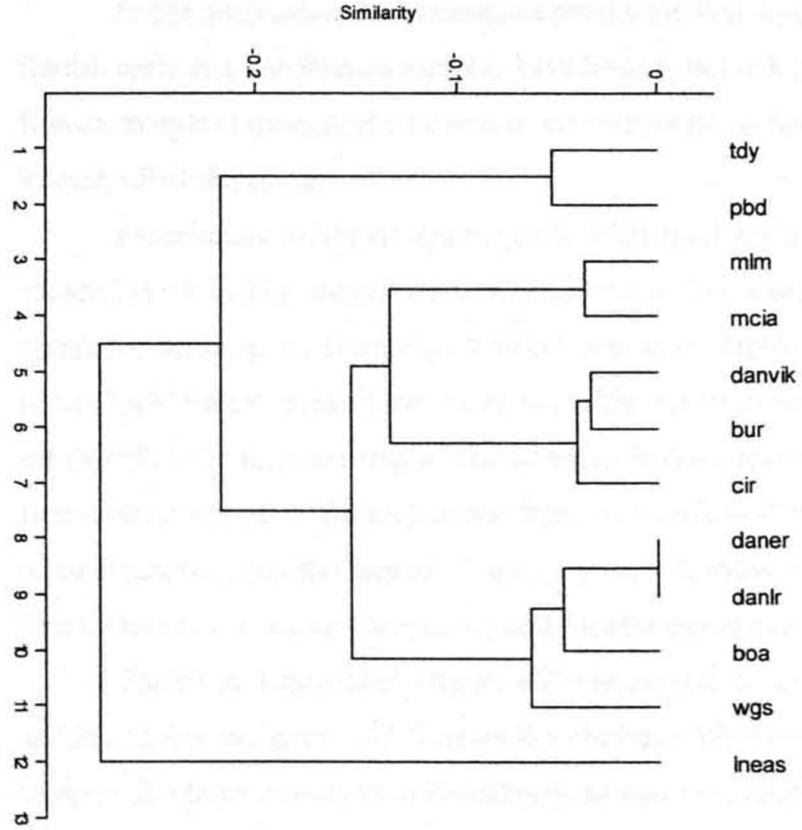
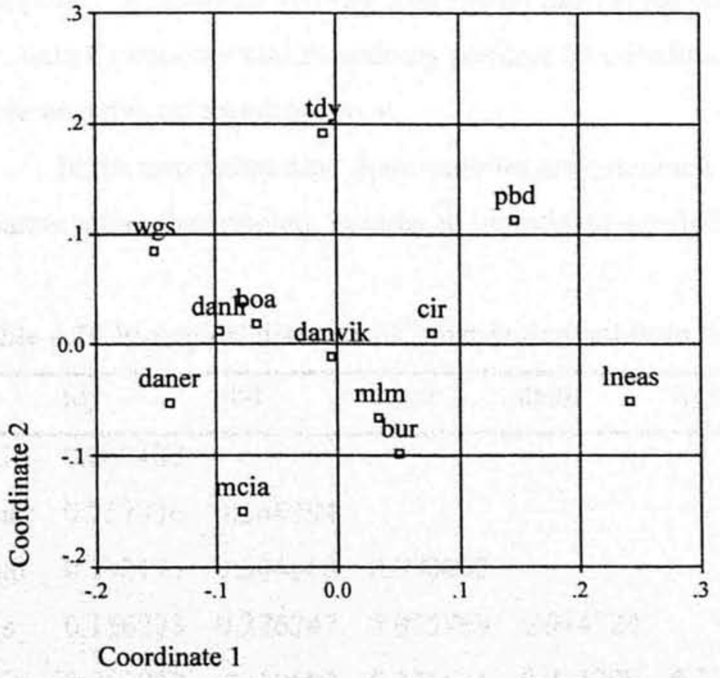


Figure 4.28 Principal coordinates plot: axes 1 (40.34%) and 2 (26.25%)



4.6.10 Separate samples: Iron Age and Romano-British: pooled sex

In this subsection the biodistance results for Iron Age, Romano-British and Danish early and late Roman samples have been presented. Danish early and late Roman samples represent the nearest-to-contemporary samples for the Iron Age and Romano-British periods.

Examination of the d^2 matrix (table 4.70) confirms the patterns seen in subsection 4.6.9. The distinction between Iron Age Wetwang and Maiden Castle remains in terms of the former's overall closeness to Danish samples. Maiden Castle is relatively distant from all other samples, although its closest relationship is with the Danish early Roman sample. The Romano-British samples remain more distant from Danish samples, although of the three, Trentholme Drive has the smallest d^2, while Poundbury has the largest. Poundbury is close to both Cirencester and Trentholme Drive, while Cirencester and Trentholme Drive are relatively distant.

The HCA dendrogram (figure 4.29) represents these relationships accurately, and in contrast to figure 4.27, Cirencester clusters with the other Romano-British samples due to its closeness to Poundbury, so that the dendrogram clearly indicates Iron Age/Danish and Romano-British clusters. This pattern is also evident from the PCO plot (figure 4.30), where Wetwang and the Danish samples plot together on the negative side of coordinate one, with Maiden Castle removed from this group on coordinate two. Romano-British samples all plot on the positive side of coordinate one, with Cirencester and Poundbury positive on coordinate two, and Trentholme Drive negative on coordinate two.

In the next subsection these samples are examined with males and females separate rather than pooled, in order to investigate sex differences.

Table 4.70 Biological distance (d^2) matrix derived from the unbiased R matrix

	tdy	pbd	daner	danlr	wgs	mcia
pbd	0.067482					
daner	0.257836	0.366394				
danlr	0.192175	0.304068	0.000000			
wgs	0.156273	0.276247	0.055769	0.044724		
mcia	0.352032	0.319802	0.121631	0.201299	0.231292	
cir	0.195364	0.074988	0.255809	0.243345	0.226051	0.175576

Figure 4.29 Hierarchical cluster analysis dendrogram

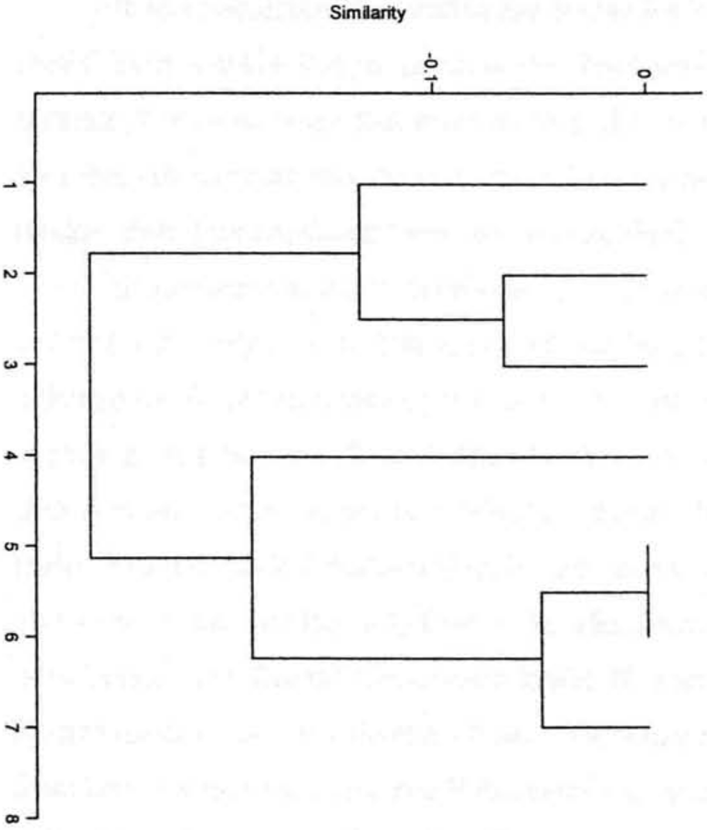
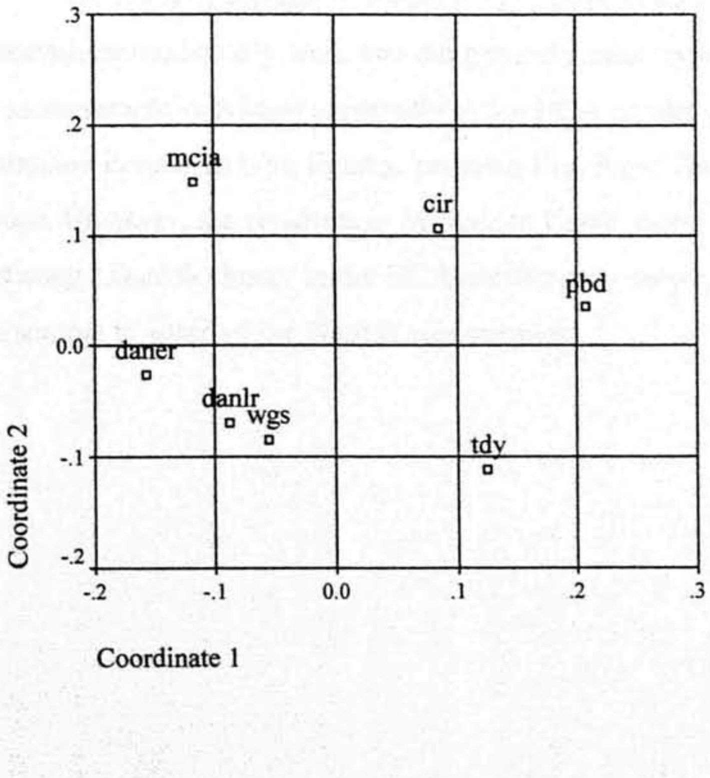


Figure 4.30 Principal coordinates plot: axes 1 (56.31%) and 2 (29%)



4.6.11 Separate samples: Iron Age and Romano-British: separate sex

In this subsection the biodistance results for Iron Age, Romano-British and Danish early and late Roman samples have been presented, with males and females separate. It must be noted that when males and females are not pooled, sample sizes for some sub-samples become very small. In this case, small samples (*n*<10) include females from Maiden Castle (*n*=9) and female Danish early Romans (*n*=6).

Examination of the d^2 matrix (table 4.71) indicates that Wetwang females and males are very close to both early and late Danish Roman females and males, although for Wetwang females particularly, the distance from Danish males is slightly greater than from Danish females. Wetwang females and males are very similar to each other, but are both relatively distant from Maiden Castle females and males. Maiden Castle females and males are close to each other, and females are also very close to Danish early Roman females. Maiden Castle males are close to both Danish early Roman females and males. Neither are very close to Danish late Roman males or females. Females from Trentholme Drive are very close to males from both Trentholme Drive and Poundbury. Females from Poundbury are closest to males from Cirencester. Males from Poundbury are closest to both males and females from Trentholme Drive, and to males from Cirencester, and are closer to all of these than they are to females from Poundbury.

The HCA dendrogram (figure 4.31) and PCO plot (4.32) represent these relationships moderately well, and the general similarity of females and males from the same sample is evident especially in the HCA dendrogram. Again, a clear distinction is seen, in both figures, between Iron Age / Danish and Romano-British groups. However, the remoteness of Maiden Castle males and females from the Wetwang / Danish cluster in the HCA dendrogram does not reflect the closeness of this sample to some of the Danish sub-samples.

Table 4.71 Biological distance (d^2) matrix derived from the unbiased R matrix

	ftdy	fpbd	fdaner	fdanlr	fwgs	fmcia	mtdy	mpbd	mdaner	mdanlr	mwgs	mmcia
fpbd	0.188965											
fdaner	0.209120	0.435341										
fdanlr	0.121282	0.500195	0.022377									
fwgs	0.122185	0.458588	0.005369	0.028949								
fmcia	0.483880	0.533087	0.078631	0.357722	0.299748							
mtdy	0.000000	0.167120	0.186944	0.151713	0.120113	0.388560						
mpbd	0.050193	0.102210	0.216967	0.248014	0.166799	0.328083	0.012305					
mdaner	0.260519	0.554598	0.000000	0.000000	0.098455	0.271835	0.259739	0.326990				
mdanlr	0.245409	0.397358	0.000000	0.062688	0.117479	0.257627	0.237069	0.269611	0.000000			
mwgs	0.182913	0.445464	0.000000	0.042172	0.040649	0.263961	0.201476	0.257014	0.092116	0.076375		
mmcia	0.313886	0.388114	0.027092	0.162516	0.170926	0.024789	0.229878	0.194623	0.081560	0.125528	0.219880	
mcir	0.227352	0.070400	0.191224	0.321423	0.237197	0.303926	0.163543	0.083947	0.321274	0.216419	0.249901	0.145107

Figure 4.31 Hierarchical cluster analysis dendrogram

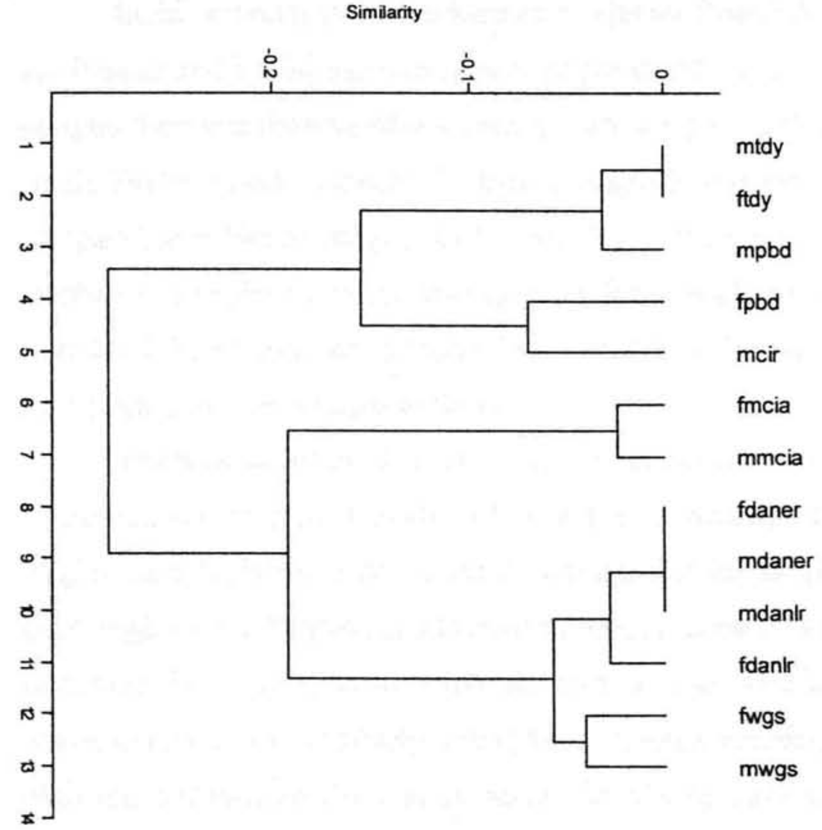
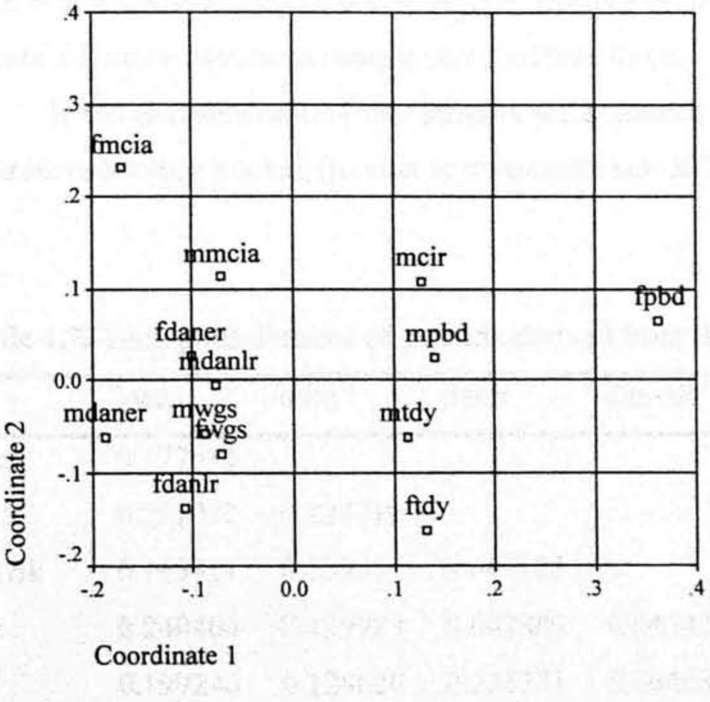


Figure 4.32 Principal coordinates plot: axes 1 (47.1%) and 2 (22.47%)



4.6.12 Separate samples: Anglo-Saxon: pooled sex

In this subsection the biodistance results for British Anglo-Saxon and Danish late Roman and Viking samples have been presented. Danish late Roman and Viking samples represent the nearest-to-contemporary samples for the early and later Anglo-Saxon periods respectively. British Anglo-Saxon samples only have been compared with Danish samples in this, and the next, analysis, in order to restrict the numbers of samples involved, thus allowing for a detailed comparison of British-Danish relationships in this period (since Iron Age and Romano-British relationships have already been examined in detail).

Examination of the d^2 matrix (table 4.72) indicates that the relationships seen in subsection 4.6.9 remain evident. The smallest distances are seen between early Anglo-Saxon Bidford-on-Avon and Danish late Roman samples, and between mid-later Anglo-Saxon Burwell and Danish Vikings. Morant's London Museums sample is moderately close (or distant) from all other samples. The later north-east Anglo-Saxon sample is also relatively distant from all other samples, although it is closer to other mid and later Anglo-Saxons and Danish Vikings, and more distant from early Anglo-Saxon Bidford-on-Avon and Danish late Romans.

The HCA dendrogram (figure 4.33) accurately represents these relationships, while the PCO plots (figure 4.34 and 4.35) emphasise the distinctiveness of later north-east Anglo-Saxons on coordinate one, Burwell on coordinate two, and Morant's London Museums sample on coordinate three.

In the next subsection these samples are examined with males and females separate rather than pooled, in order to investigate sex differences.

Table 4.72 Biological distance (d^2) matrix derived from the unbiased R matrix

	lneas	mlm	danlr	danvik	boa
mlm	0.177631				
danlr	0.261072	0.128719			
danvik	0.163311	0.139957	0.047183		
boa	0.240406	0.129989	0.042880	0.045421	
bur	0.199246	0.128626	0.221371	0.044034	0.159624

Figure 4.33 Hierarchical cluster analysis dendrogram

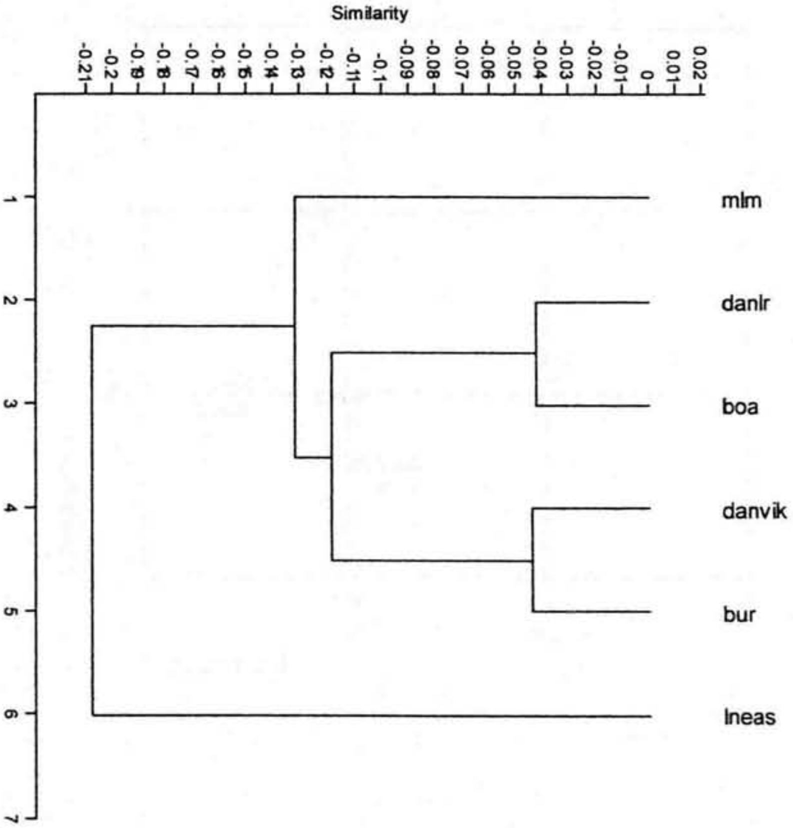


Figure 4.34 Principal coordinates plot: axes 1 (52.24%) and 2 (21.68%)

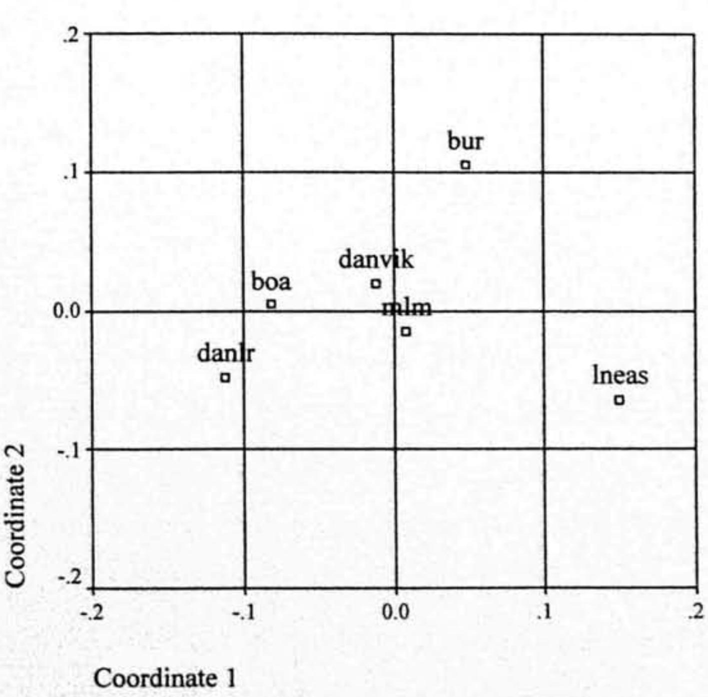
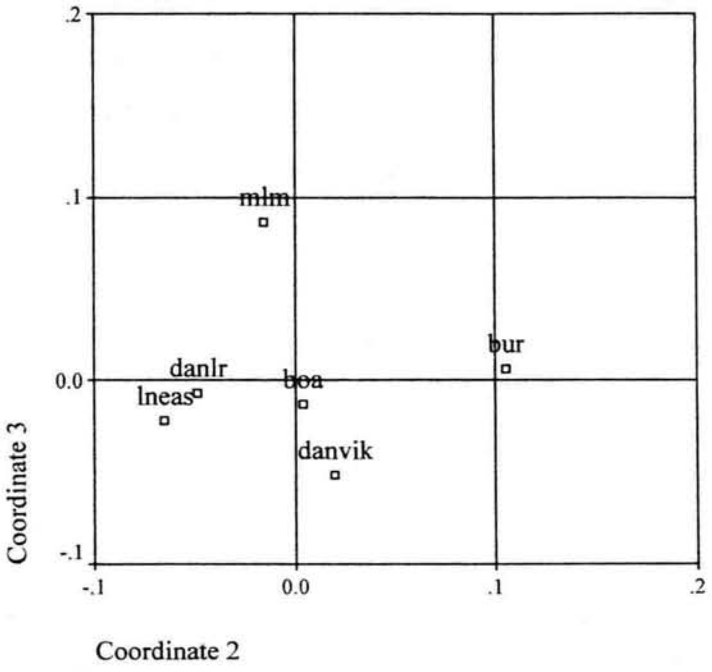


Figure 4.35 PCO axes 2 (21.68%) and 3 (12.92%)



4.6.13 Separate samples: Anglo-Saxon: separate sex

In this subsection the biodistance results for Anglo-Saxon and Danish late Roman and Viking samples have been presented, with males and females separate, and relationships will be discussed in a roughly chronological order. It must be noted that when males and females are not pooled, sample sizes for a number of sub-samples become very small. In this case, small samples (n<10) include females from Morant's London Museums sample (n=9), Bidford-on-Avon (n=6), Burwell (n=7) and Danish early Romans (n=6), and north-east later Anglo-Saxon males (n=9).

Examination of the d^2 matrix (table 4.73) indicates that relationships between Anglo-Saxon and Danish samples are very complex, and temporal / sample-specific patterns in female/male relationships are less obvious than in previous analyses.

Bidford-on-Avon females are very close to Danish Viking, Morant's London Museums and Danish late Roman females, and to all UK Anglo-Saxon and Danish late Roman males. Bidford-on-Avon males are closest to Danish Viking males and Bidford-on-Avon and Danish late Roman females. They are also moderately close to all other male Anglo-Saxon samples and to Danish Viking females.

Morant's London Museums females are most similar to females from Bidford-on-Avon, and males from the north-east Anglo-Saxon, Morant's London Museums and Danish late Roman samples. Morant's London Museums males are most similar to other males from Burwell and the north-east later Anglo-Saxon sample, to females from Bidford-on-Avon and to the Morant's London Museums and Danish Viking samples.

Burwell females are moderately or very distant from many other samples, and are close only to Burwell and north-east Anglo-Saxon males, and moderately close to male Danish late Romans and female Danish Vikings. Burwell males are close to Burwell, Bidford and Danish Viking females, and to north-east later Anglo-Saxon, Morant's London Museums and Danish late Roman and Viking males.

Most notable is the set of very large distances relating to female north-east Anglo-Saxons, in contrast to males from this sample who exhibit small to moderate distances from many other samples and, in addition to those relationships already noted, are particularly close to female Danish Vikings and male Danish late Romans. This female distinctiveness is emphasised by the HCA dendrogram (figure 4.36), and by PCO coordinate one (figure 4.37).

Table 4.73 Biological distance (d^2) matrix derived from the unbiased R matrix

	fnelas	fmlm	fdanlr	fdanvik	fboa	fbur	mnelas	mmlm	mdanlr	mdanvik	mboa
fmlm	0.584310										
fdanlr	0.797770	0.310447									
fdanvik	0.567958	0.103621	0.154131								
fboa	0.714331	0.000570	0.042057	0.000000							
fbur	0.565091	0.223133	0.692440	0.121518	0.247075						
mnelas	0.369399	0.042089	0.218218	0.011966	0.031381	0.079868					
mmlm	0.641395	0.068931	0.185187	0.075959	0.012812	0.293320	0.073143				
mdanlr	0.684550	0.062666	0.100161	0.000000	0.000000	0.196167	0.027349	0.106262			
mdanvik	0.609774	0.483167	0.170068	0.074423	0.176430	0.277938	0.155529	0.218418	0.134173		
mboa	0.644835	0.375037	0.094318	0.111134	0.086143	0.426123	0.173071	0.162524	0.159259	0.065107	
mbur	0.628516	0.157277	0.328254	0.007876	0.069022	0.029284	0.049901	0.074106	0.049706	0.100576	0.161227

Figure 4.36 Hierarchical cluster analysis dendrogram

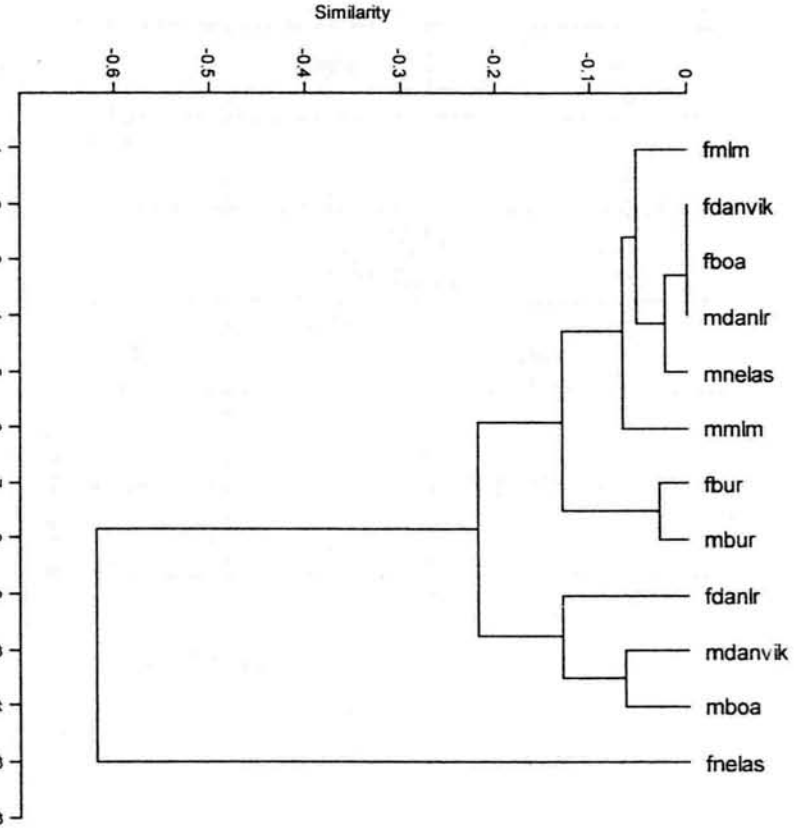


Figure 4.37 Principal coordinates plot: axes 1 (42.51%) and 2 (19%)

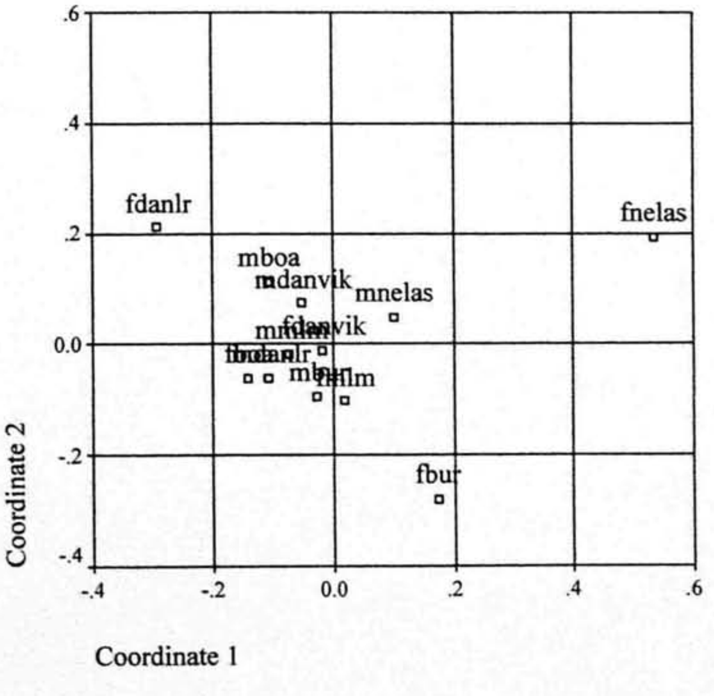
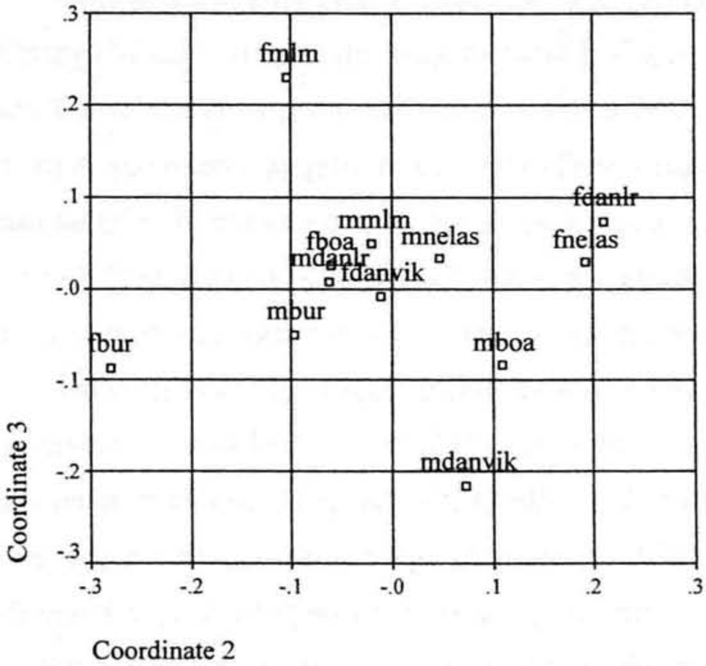


Figure 4.38 Principal coordinates plot: axes 2 (19%) and 3 (11.67%)



4.6.14 Biodistance analyses: summary

Biodistance analyses for samples at all levels of pooling indicated that, within the UK only, samples that were temporally closer were also biologically closer. When Danish samples were also considered, however, in general, both Iron Age and Anglo-Saxon samples were closer to Danish samples than to Romano-British samples. In analyses both inclusive and exclusive of Danish samples, Romano-British samples were generally distinct from all other UK and Danish samples, and this distinctiveness was particularly visible in the PCO plots.

These analyses also demonstrated that within time periods, there was considerable variation between samples in terms of the magnitude of their similarity or difference from other samples. Additionally, while patterns of relationships were quite clearly evident for the Iron Age and Romano-British periods, these patterns in the Anglo-Saxon period appeared more complex, particularly with regard to differences in female and male relationships when these sub-samples were un-pooled. It must be reiterated however, that within the Anglo-Saxon period, and particularly with regard to separate sex samples, the impact of small sample sizes particularly for females may well have impacted on the reliability of these analyses, in terms of their representitiveness.

In the next section Mantel matrix correlation tests are used to test the association between patterns of relationships deriving from the biodistance analyses, and similarities between samples in terms of their temporal, geographical and cultural characteristics.

4.7 Mantel matrix correlation analyses

In this section, results of the Mantel matrix correlation tests relating to hypotheses 3a and 3b are presented. For clarity, they are presented in tabulated form, whereby biodistance is compared to all other distance matrices.

Mantel tests have been carried out for pooled UK samples as well as for separate samples. In all cases, sexes are pooled. Results are presented firstly for pooled UK samples and then for separate samples.

4.7.1 UK only: pooled samples

Matrix correlation tests were first carried out for pooled UK populations (UK Iron Age, Romano-British, early Anglo-Saxon and later Anglo-Saxon), excluding Danish samples; sample *n* = 4. In the first test (table 4.74), Burwell was included as part of the later Anglo-Saxon sample, in the second test (table 4.75) Burwell was included as part of the early Anglo-Saxon sample, leaving north-east later Anglo-Saxons to represent later Anglo-Saxons. Sexes were pooled.

As samples were pooled geographically, and the tests were limited to UK populations, no other matrices have been compared as, since tests were limited to UK populations, and samples were pooled, biodistance / geographic or cultural distance comparisons are precluded, as the matrices constructed lack detail.

The test results indicate that there is a significant positive correlation between biodistance (d^2) and temporal distance in years. The magnitude of this correlation is large overall, and larger particularly in the second test.

Table 4.74 Mantel test results: pooled UK populations (Bur = later AS)

Bio-dist / temp-dist
$R = 0.7, R^2 = 0.49$ *p* = (0/23) = **0.000**

Table 4.75 Mantel test results: pooled UK populations (Bur = early AS)

Bio-dist / temp-dist
$R = 0.779, R^2 = 0.6068$ *p* = (0/23) = **0.000**

4.7.2 Pooled samples

Matrix correlation tests were next carried out for pooled UK populations (UK Iron Age, Romano-British, early Anglo-Saxon and later Anglo-Saxon) and Danish samples; sample $n = 7$. As in section 4.7.1, in the first test (table 4.76), Burwell was included as part of the later Anglo-Saxon sample, in the second test (table 4.77) Burwell was included as part of the early Anglo-Saxon sample, leaving north-east later Anglo-Saxons to represent later Anglo-Saxons. Sexes were pooled.

The Mantel matrix correlation test results indicate that for both sets of tests, when Danish samples are included, there is no significant correlation between biodistance and either geographical or temporal distance. However, there are significant correlations in both sets of tests between biodistance and cultural distances (although in the second test, the correlation between biodistance and cultural distance 'a' is not significant). It is evident that when Burwell is pooled with early rather than later Anglo-Saxons, the magnitude of the correlation decreases, and it become less highly significant. Similarly, when a cultural link is proposed (in cultural distance 'b') between Iron Age and Danish early Romans, in addition to the links already proposed between Anglo-Saxon and Danish samples, the magnitude of the correlation coefficient is greater, and is more highly significant than when no links between Iron Age and Danish samples are proposed (cultural distance 'a').

Table 4.76 Mantel test results: pooled UK and Danish populations (Bur = later AS)

biodistance			
geo-dist	**temp-dist**	**cult-dist 'a'**	**cult-dist 'b'**
R = -0.008 R^2 = 0.0001 p = (2451/5039) = 0.4864	R = 0.028 R^2 = 0.0008 p = (2175/5039) = 0.4316	R = 0.5469 R^2 = 0.2991 p = (194/5039) **= 0.0385**	R = 0.6268 R^2 = 0.3929 p = (40/5039) **= 0.0079**

Table 4.77 Mantel test results: pooled UK and Danish populations (Bur = early AS)

biodistance			
geo-dist	**temp-dist**	**cult-dist 'a'**	**cult-dist 'b'**
R = 0.04 R^2 = 0.0016 p = (1637/5039) = 0.3249	R = 0.0755 R^2 = 0.0057 p = (1801/5039) = 0.3574	R = 3579 R^2 = 0.1218 p = (533/5039) = 0.1058	R = 0.4474 R^2 = 0.2002 p = (168/5039) **= 0.0333**

4.7.3 UK only: separate samples

In order to examine whether the correlations seen in sections 4.7.1 and 4.7.2 apply also to un-pooled samples, Mantel matrix correlation tests were next carried out for separate UK samples (as in detailed table 4.57) excluding Danish samples. Tests involving Anglo-Saxon samples were carried out both including and excluding north-east later Anglo-Saxons, because of the large biodistances associated with females of this sample.

The results for the first set of tests (table 4.78; sample $n = 9$), which include all UK separate samples, indicate that the only significant correlation with biodistance is for cultural distance. However, the correlations for biodistance compared to both sets of temporal distance approach significance (at $p<0.1$). There is no significant correlation whatever between biodistance and geographical distance. When the same samples excluding north-east later Anglo-Saxons are examined (table 4.79; sample $n = 8$), none of the correlations is significant, and none approaches significance.

In order to look in more detail at shorter periods of time, tests were run for Iron Age and Romano-British samples only, and for Romano-British and Anglo-Saxon (both including and excluding north-east later Anglo-Saxon) samples only.

In the tests including Iron Age and Romano-British samples only (table 4.80; sample $n = 5$), the results indicate that there are no significant correlations between any of the matrices, although the correlation between biodistance and cultural distance approaches significance.

In the tests including Romano-British and Anglo-Saxon (including north-east later Anglo-Saxons) samples only (table 4.81; sample $n = 7$), there are significant correlations with biodistance for both temporal distances, and cultural distance. The correlation for biodistance and geographical distance is not significant. Excluding north-east later Anglo-Saxons (table 4.82; sample $n = 6$) from these tests results in all but temporal distance 'b' becoming non-significant, although temporal distance 'a' approaches significance, despite the absolute magnitude of these correlations increasing.

In all cases above, the magnitude of the correlations, which are all positive, is small, therefore the amount of variance in the biodistance matrices explained by even the significant correlations with other matrices, is relatively little.

Table 4.78 Mantel test results: separate samples (inc nelas)

biodistance			
geo-dist	**temp-dist 'a'**	**temp-dist 'b'**	**cult-dist**
R = 0.1059 R^2 = 0.0112 p = (492+1)/(999+1) = 0.493	R = 0.3923 R^2 = 0.1539 p = (94+1)/(999+1) = 0.095	R = 0.4022 R^2 = 0.1618 p = (76+1)/(999+1) = 0.077	R = 0.2642 R^2 = 0.0698 p = (43+1)/(999+1) **= 0.044**

Table 4.79 Mantel test results: separate samples (exc nelas)

biodistance			
geo-dist	**temp-dist 'a'**	**temp-dist 'b'**	**cult-dist**
R = 0.2247 R^2 = 0.0505 p = (227+1)/(999+1) = 0.2280	R = 0.1743 R^2 = 0.0304 p = (164+1)/(999+1) = 0.1650	R = 0.1868 R2 = 0.0349 p = (174+1)/(999+1) = 0.175	R = 0.2224 R^2 = 0.0495 p = (181+1)/(999+1) = 0.182

Table 4.80 Mantel test results: UK Iron Age and Romano-British samples

biodistance			
geo-dist	**temp-dist 'a'**	**temp-dist 'b'**	**cult-dist**
R = 0.1879 R^2 = 0.0353 p = (36/119) = 0.3025	R = 0.4843 R^2 = 0.2346 p = (15/119) = 0.1261	R = 0.4682 R^2 = 0.2192 p = (15/119) = 0.1261	R = 0.6547 R^2 = 0.4286 p = (9/119) = 0.0756

Table 4.81 Mantel test results: UK Romano-British and all Anglo-Saxon samples

biodistance			
geo-dist	**temp-dist 'a'**	**temp-dist 'b'**	**cult-dist**
R = -0.0468 R^2 = 0.0022 p = (2790/5039) = 0.5537	R = 0.4591 R^2 = 0.2108 p = (93/5039) **= 0.0185**	R = 0.4644 R^2 = 0.2156 p = (116/5039) = **0.023**	R = 0.3590 R^2 = 0.1289 p = (178/5039) **= 0.0353**

Table 4.82 Mantel test results: UK Romano-British and Anglo-Saxon samples exc

biodistance			
geo-dist	**temp-dist 'a'**	**temp-dist 'b'**	**cult-dist**
R = 0.1062 R^2 = 0.0113 p = (235/719) = 0.3268	R = 0.4966 R^2 = 0.2466 p = (44/719) = 0.0612	R = 0.5549 R^2 = 0.3079 p = (27/719) = **0.0376**	R = 0.3827 R^2 = 0.1464 p = (104/719) = 0.1446

4.7.4 Separate samples

In this set of Mantel matrix correlation tests, all separate samples were included together with Danish samples, both including (table 4.83; sample $n = 12$) and excluding (table 4.84; sample $n = 11$) north-east later Anglo-Saxons, because of the large biodistances associated with females of this sample.

The test results indicate that for both sets of tests, the sole significant correlations are between biodistance and both cultural distances (cultural distance 'a' is not significant, but is close to significance, when north-east later Anglo-Saxons are excluded), although this is more highly significant for the test including the north-east later Anglo-Saxon sample. There are no significant or nearly significant correlations between biodistance and either temporal or geographic distances.

As previously, when Iron Age/Danish links are proposed in cultural matrix 'b', the magnitude of the correlation coefficient is larger, and more highly significant than for cultural matrix 'a', although none of the significant correlations is very large in magnitude.

Table 4.83 Mantel test results: separate UK samples (inc nelas) and Danish samples

biodistance				
geo-dist	**temp-dist 'a'**	**temp-dist 'b'**	**cult-dist 'a'**	**cult-dist 'b'**
R = -0.0652 R^2 = 0.0043 p = (558+1)/(999+1) = 0.5590	R = 0.0947 R^2 = 0.009 p = (398+1)/(999+1) = 0.3990	R = 0.0954 R^2 = 0.0091 p = (360+1)/(999+1) = 0.3610	R = 0.2862 R^2 = 0.0819 p = (14+1)/(999+1) **= 0.015**	R = 0.3119 R^2 = 0.0973 p = (9+1)/(999+1) **= 0.01**

Table 4.84 Mantel test results: separate UK samples (exc nelas) and Danish samples

biodistance				
geo-dist	**temp-dist 'a'**	**temp-dist 'b'**	**cult-dist 'a'**	**cult-dist 'b'**
R = -0.0472 R^2 = 0.0022 p = (500+1)/(999+1) = 0.501	R = -0.1156 R^2 = 0.0134 p = (761+1)/(999+1) = 0.762	R = -0.1203 R^2 = 0.0145 p = (782+1)/(999+1) = 0.783	R = 0.3084 R^2 = 0.0951 p = (58+1)/(999+1) = 0.059	R = 0.3394 R^2 = 0.1152 p = (48+1)/(999+1) **= 0.049**

4.7.5 Mantel analyses: summary

The Mantel matrix correlation tests carried out here indicate that the characteristics which correlate significantly with the relationships derived from the biodistance analysis differ for both pooled and un-pooled samples, and also across time periods.

When UK pooled-sex and sub-sample samples were examined, the observation that samples closer in time were also closer biologically was confirmed, and this association was found to be statistically significant. However, when Danish samples were added, neither geographical nor temporal distance correlated with biodistance, indicating that neither isolation by distance nor temporal distance can explain biological relationships, and the only significant correlation was between biodistance and cultural affinity.

When un-pooled samples were examined across the whole time period from the Iron Age to the later Anglo-Saxon period, excluding Danish samples, significant or near significant correlations were found between all distance matrices except that describing geographic distance (however when the north-east later Anglo-Saxon sample was removed none of the correlations remained significant). Examining these samples within shorter time periods indicated that from the Iron Age to the Romano-British period, only correlations between biodistance and cultural affinity neared significance. Between the Romano-British and Anglo-Saxon period, however, temporal distance correlated most significantly with biodistance, as did cultural distance (but again, only when north-east later Anglo-Saxons were included). When Danish samples were added to the separate samples analyses, the sole significant correlation was between biodistance and cultural affinity, with no significant correlation between biodistance and either geographical or temporal distance.

Overall, relationships within the UK only can be best explained by temporal distance and cultural affinities, while, when relationships with Danish samples are taken into account, cultural affinities are most significant.

In the next section Relethford-Blangero analyses are conducted in order to investigate differences between samples in terms of their relative heterogeneity, and consequently the level of extra-regional / extra-sample gene flow they received.

4.8 Relethford-Blangero analyses

In this subsection, the results of the Relethford-Blangero analyses relating to null hypothesis 4 – that there are no differences in genetic within-group variation – are presented. Tables are presented first, which indicate the samples being compared, the distance of each from the centroid, and the observed, expected and residual variance. Secondly, plots are presented, which, for each analysis, plot each sample in terms of its distance from the centroid, and its observed variance. The line running (usually diagonally) through each plot indicates the line of expected variance in relation to distance from the centroid.

Analyses have been conducted for 'coherent' (i.e. geographically and temporally un-pooled) single-site samples, firstly for single periods (Iron Age, Romano-British and Anglo-Saxon), then for adjacent periods (Iron Age to Romano-British and Romano-British to Anglo-Saxon), then for single periods with sexes separate. The latter two groups of analyses can only be considered experimental, as the first violates the assumption of panmixia (i.e. that samples are panmictic - form a potential mating network), and the second divides samples into separate female and male 'populations' for comparison (the implications of comparing females and males of the same sample in the same analysis, however, are unknown).

4.8.1 Analyses by period

In this set of analyses, the results from the Relethford-Blangero analyses for separate periods, with sexes pooled, are presented.

The results of the Relethford-Blangero analysis for Iron Age samples (table 4.85 and figure 4.39) indicate that of the two Iron Age samples, Wetwang has a large positive residual, and Maiden Castle an equally large negative residual, suggesting that Wetwang has received more gene flow than Maiden Castle, either from a source outside the UK, or from a source within the UK, but not sampled here.

The results of the Relethford-Blangero analysis for Romano-British samples (table 4.86 and figure 4.40) indicate that all of the samples have residuals which are close to zero, particularly in the case of Trentholme Drive, suggesting that they are near equilibrium in terms of extra-regional gene flow. However, Poundbury has a slightly more positive residual, and Cirencester a slightly more negative residual, suggesting that these two sites have received slightly more and slightly less extra-regional gene flow respectively.

The results of the Relethford-Blangero analysis for Anglo-Saxon samples (table 4.87 and figure 4.41) indicate that both samples have residuals which are close to zero, suggesting that they are similar in terms of extra-regional gene flow, although Bidford-on-Avon's residual is slightly positive whereas Burwell's residual is slightly negative.

Table 4.85 Relethford-Blangero analysis: Iron Age samples

Population	r(ii)	Observed *V*	Expected *V*	Residual
wgs	0.060553	1.007	0.905	0.102
mcia	0.040589	0.822	0.924	-0.102

Table 4.86 Relethford-Blangero analysis: Romano-British samples

Population	r(ii)	Observed *V*	Expected *V*	Residual
tdy	0.059994	0.949	0.956	-0.007
pbd	0.010026	1.038	1.007	0.031
cir	0.050959	0.941	0.965	-0.024

Table 4.87 Relethford-Blangero analysis: Anglo-Saxon samples

Population	r(ii)	Observed *V*	Expected *V*	Residual
boa	0.074275	0.961	0.951	0.011
bur	0.090820	0.923	0.934	-0.011

Figure 4.39 Pooled sex: Iron Age samples

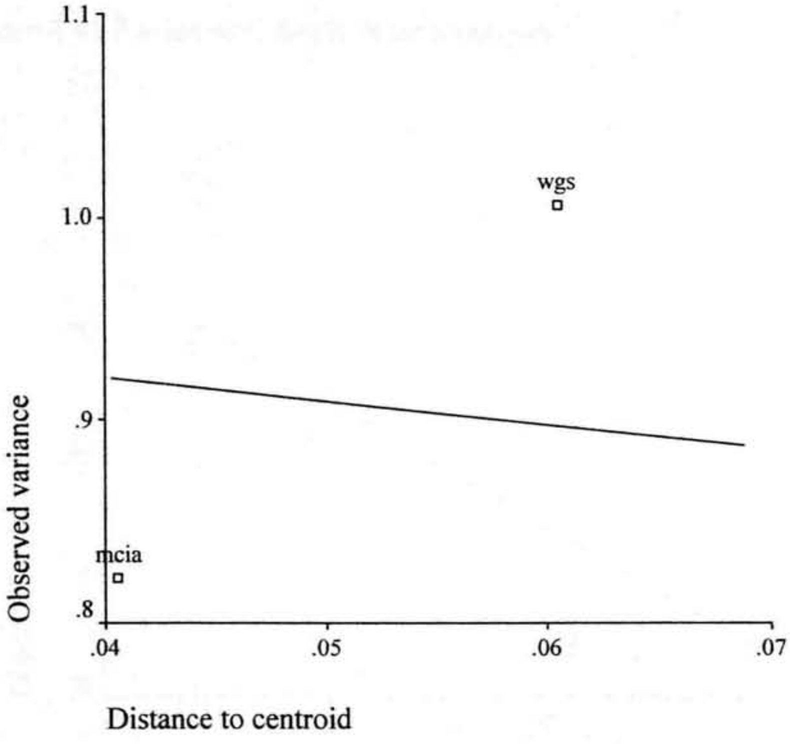


Figure 4.40 Pooled sex: Romano-British samples

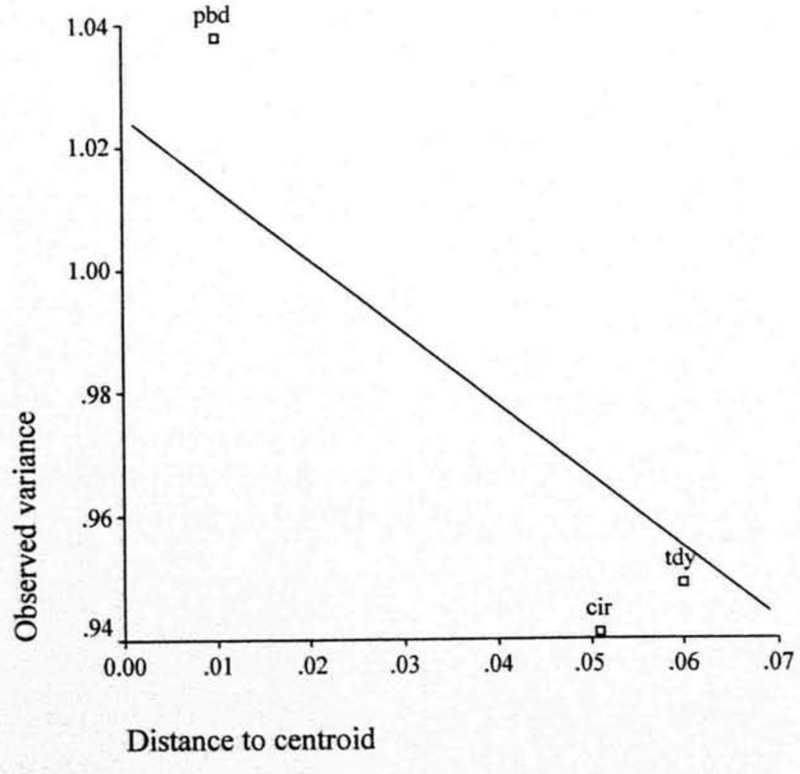
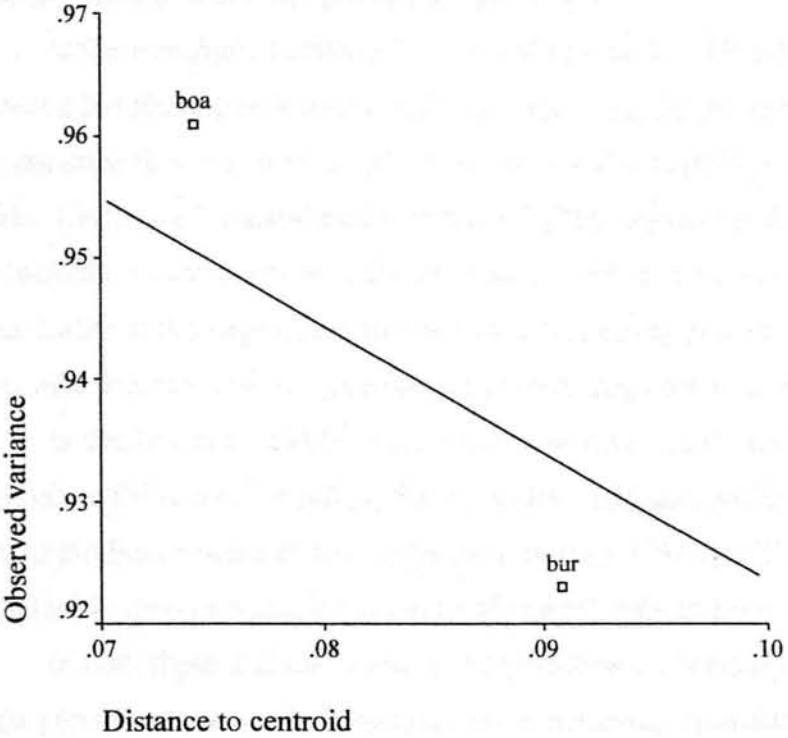


Figure 4.41 Pooled sex: Anglo-Saxon samples



4.8.2 Analyses for adjacent periods

In this set of analyses, the results from the Relethford-Blangero analyses for adjacent periods, with sexes pooled, are presented.

In the Iron Age / Romano-British analysis (table 4.88 and figure 4.42) Wetwang has the largest positive residual, suggesting the greatest level of extra-regional gene flow into this sample. Poundbury has a slightly positive residual and Maiden Castle and Trentholme Drive have slightly negative residuals, suggesting that these three samples received similar, near average, levels of gene flow. Cirencester has the largest negative residual, suggesting greater homogeneity, and a lower than average level of gene flow from extra-regional sources.

In the Romano-British / Anglo-Saxon analysis (table 4.89 and figure 4.43) Trentholme Drive and Poundbury have positive residuals, while Cirencester and both Anglo-Saxon samples have negative residuals (although Bidford-on-Avon is very close to zero), suggesting greater and lesser levels of gene flow respectively.

In both these analyses, patterns of gene flow are similar to those seen in the single period analyses, indicating that even considering these samples across time periods, the relative pattern of residuals remains the same.

Table 4.88 Relethford-Blangero analysis: Iron Age and Romano-British samples

Population	r(ii)	Observed *V*	Expected *V*	Residual
wgs	0.097922	0.994	0.869	0.125
mcia	0.128457	0.806	0.840	-0.034
tdy	0.075028	0.863	0.891	-0.028
pbd	0.060816	0.924	0.905	0.019
cir	0.045125	0.838	0.920	-0.082

Table 4.89 Romano-British and Anglo-Saxon samples

Population	r(ii)	Observed *V*	Expected *V*	Residual
tdy	0.120898	0.928	0.888	0.041
pbd	0.050744	1.007	0.959	0.048
cir	0.038075	0.910	0.972	-0.062
boa	0.094082	0.914	0.915	-0.001
bur	0.122257	0.861	0.886	-0.026

Figure 4.42 Pooled sex: Iron Age and Romano-British samples

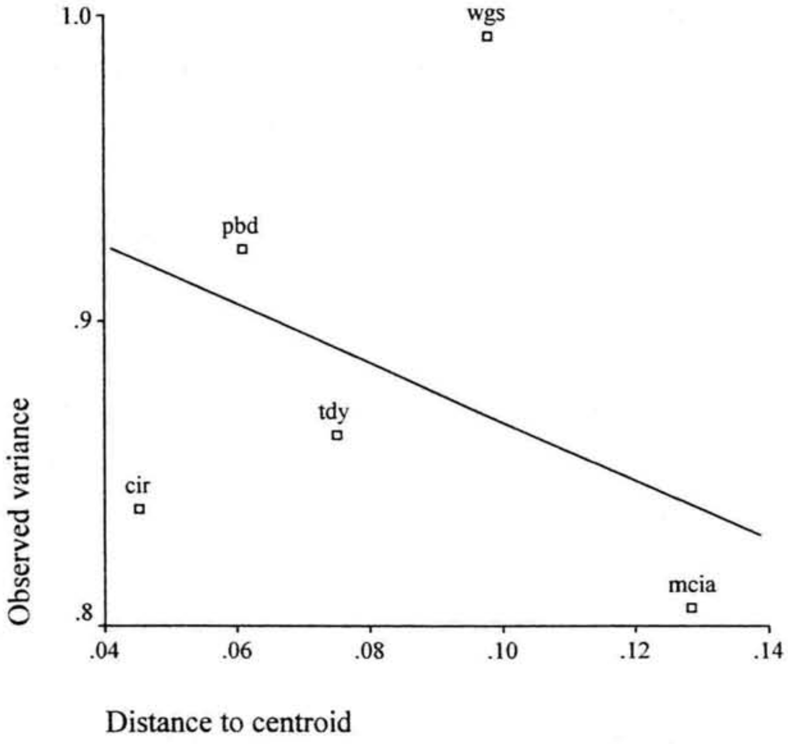
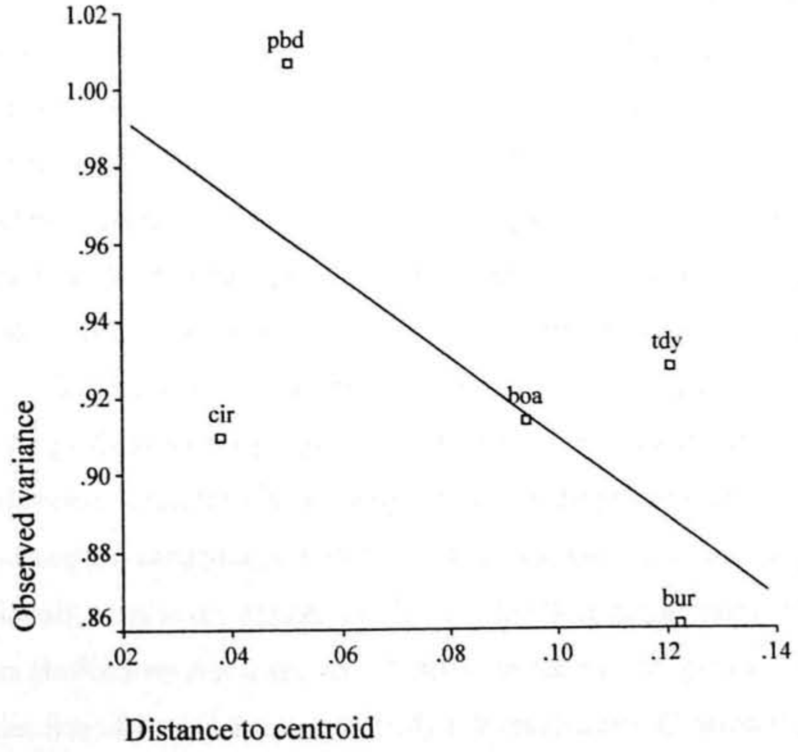


Figure 4.43 Pooled sex: Romano-British and Anglo-Saxon samples



4.8.3 Analyses by sex

In this set of analyses, the results from the Relethford-Blangero analyses for separate periods, with sexes un-pooled, are presented. The aim of these analyses was to compare differences in sex-specific homogeneity or heterogeneity, and thus in sex-specific levels of extra-regional (or extra-sample) gene flow.

In table 4.90 and figure 4.44 the results of the Relethford-Blangero analysis for Iron Age female and male sub-samples are presented. Both Wetwang samples have relatively large positive residuals, while both Maiden Castle samples have relatively large negative residuals. This suggests that both females and males from Wetwang received greater than average levels of extra-regional gene flow, while females and males from Maiden Castle received less than average extra-regional gene flow. It may be noteworthy that both female samples have relatively greater positive / less negative residuals compared to their respective males, possibly indicating that females of this period were more heterogeneous than males.

In table 4.91 and figure 4.45 the results of the Relethford-Blangero analysis for Romano-British female and male sub-samples are presented. Females from Poundbury have the greatest positive residual, suggesting a greater than average level of gene flow. Males from Poundbury and Trentholme Drive have only slightly positive residuals, and females from Trentholme Drive and males from Cirencester have moderately negative residuals, suggesting slightly more and moderately less gene flow into these samples respectively. Unlike in the Iron Age analysis, there is no clear indication of a pattern of greater or lesser female or male heterogeneity, with most samples being near average, and Poundbury females having the largest positive, and Trentholme Drive females the largest negative, residuals.

In table 4.92 and figure 4.46 the results of the Relethford-Blangero analysis for Anglo-Saxon female and male sub-samples are presented. In this analysis, Bidford-on-Avon females have by far the largest positive residual, while all other sub-samples, particularly males from Bidford-on-Avon, have large negative residuals, suggesting greater and lesser gene flow respectively. Females and males from Bidford-on-Avon are very different in their heterogeneity, while females and males from Burwell are similar in their homogeneity. Caution must be exercised in interpreting this analysis, however, as the female Bidford-on-Avon sample is small (*n*=6), and the apparent heterogeneity of this sample may therefore be due to sampling effects.

Table 4.90 Relethford-Blangero analysis: Iron Age females and males

Population	r(ii)	Observed *V*	Expected *V*	Residual
f wgs	0.065500	1.006	0.897	0.109
m wgs	0.080422	0.973	0.883	0.090
f mcia	0.068545	0.849	0.894	-0.045
m mcia	0.032786	0.775	0.928	-0.154

Table 4.91 Relethford-Blangero analysis: Romano-British females and males

Population	r(ii)	Observed *V*	Expected *V*	Residual
f tdy	0.052802	0.882	0.949	-0.066
f pbd	0.055088	1.020	0.946	0.074
m tdy	0.022091	0.997	0.980	0.018
m pbd	0.008157	1.005	0.993	0.012
m cir	0.069268	0.895	0.932	-0.037

Table 4.92 Relethford-Blangero analysis: Anglo-Saxon females and males

Population	r(ii)	Observed *V*	Expected *V*	Residual
f boa	0.208285	1.368	0.894	0.473
f bur	0.197620	0.799	0.906	-0.108
m boa	0.143047	0.722	0.968	-0.246
m bur	0.046135	0.957	1.077	-0.120

Figure 4.44 Separate sex: Iron Age samples

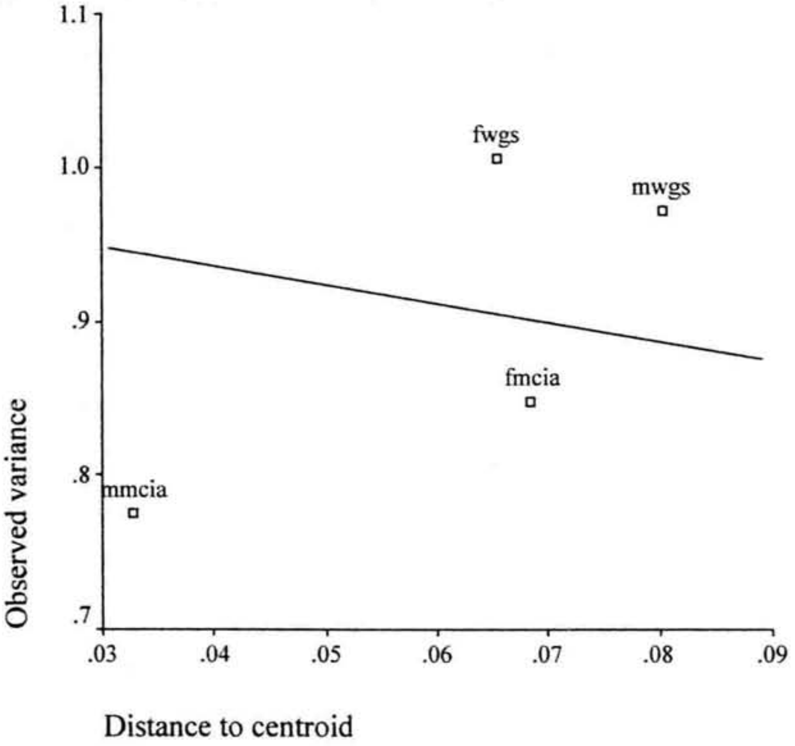


Figure 4.45 Separate sex: Romano-British samples

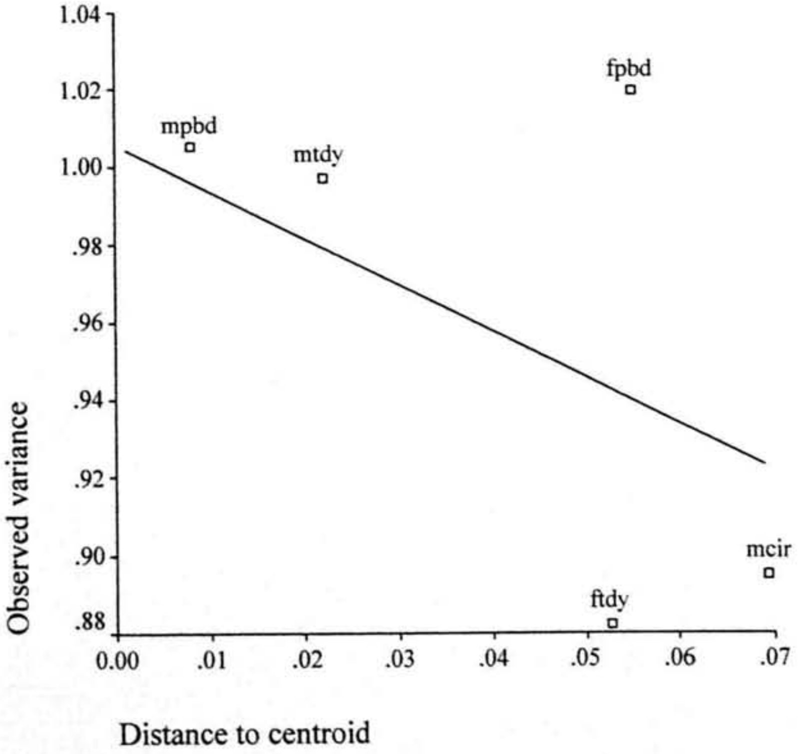
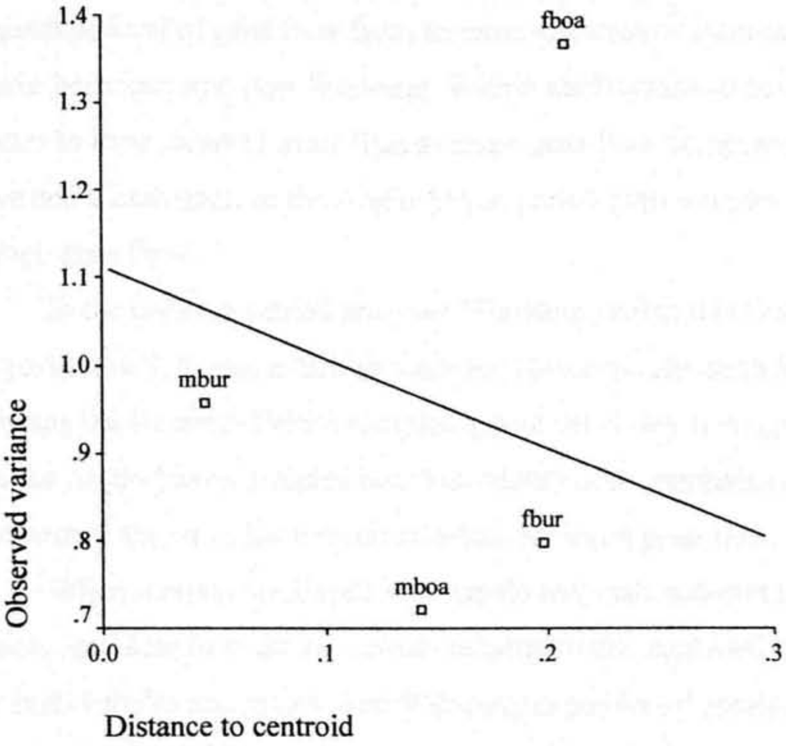


Figure 4.46 Separate sex: Anglo-Saxon samples



4.8.4 Relethford-Blangero analyses: summary

Of all the samples included in within-period Relethford-Blangero analyses, the greatest level of gene flow from an extra-regional or extra-sample source appears to have been into Iron Age Wetwang. Within the Romano-British period Poundbury appears to have received more than average gene flow compared to Trentholme Drive and Cirencester. In the Anglo-Saxon period both samples have received near average gene flow.

In the between-period analyses Wetwang retains this distinctiveness in comparison with Romano-British samples. However, although in comparison with Wetwang the Romano-British samples appear relatively homogenous, in comparison with the Anglo-Saxon samples both Poundbury and Trentholme Drive (but not Cirencester) appear to have received relatively more gene flow.

When samples were split into female and male sub-samples and compared, it appears (and bear in mind the caveats relating to this analysis) that within the Iron Age both females and males from Wetwang experienced greater levels of gene flow than Maiden Castle females and males, and within the Romano-British period males from both Trentholme Drive and Poundbury, and (particularly) females from Poundbury experienced the greatest levels of gene flow. Within the Anglo-Saxon period females from Bidford-on-Avon appear distinctive, however as noted, this may be at least partially due to sampling effects.

Finally, some evidence of female/male differences in heterogeneity may be visible in the Relethford-Blangero analyses, particularly within the Iron Age and Romano-British periods, and between sample sites in the latter.

CHAPTER 5

DISCUSSION AND CONCLUSIONS

5.1 Introduction

In section 5.2 of this chapter, the results of analyses presented in Chapter 4 are reviewed, and discussed in terms of the hypotheses set out in Chapter 3, which address questions regarding population history in Britain, and relationships with Denmark. In section 5.3 a general discussion of these results is presented with regard to theories of biological, social and cultural change in Britain. Finally, in section 5.4, conclusions are drawn, and suggestions for further work made.

5.2 Research hypotheses

Hypothesis 1

There are observable, measurable, differences in craniofacial morphology between the Iron Age, Romano-British and Anglo-Saxon periods in Britain.

The results of the descriptive, univariate and MANOVA analyses indicate that there are considerable differences in craniofacial morphology between samples, both in a qualitative sense (based on descriptive craniofacial indices) and in a quantitative statistical sense (based on ANOVA and MANOVA results).

The results of these analyses suggest that there are broad temporal trends in craniofacial shape, although these are more visible, and more easily identifiable, in the results of analyses based on measurements which employ cranial rather than facial measurements. Some of the research concerning British population history presented in Chapter 2 suggested that there was continuity between the Iron Age and Romano-British periods, and between the Romano-British and Anglo-Saxon periods (e.g. Higham 1992, Lucy 1998, 2000, Haselgrove 1999, Esmonde Cleary 1999, Hanson 1999, Harding 2004, Tyrrell 2000). Upon analysis, however, the Romano-British samples appear distinct from all the others, in terms of both within-British and between British and Danish analyses.

In terms of sex differences, on the whole, females and males within samples have very similar craniofacial morphology, as indicated by the descriptive statistics and *t*-tests presented in section 4.3. There is also no evidence from these analyses for systematic differences in any period with regard to female and male variability (based on the standard deviations of the craniofacial indices), although, as has been noted, the small size of many of the sex-specific samples, or the nature of their composition, makes this type of analysis problematic.

The univariate analyses also allowed the findings of some previous research on cranial morphological relationships within Britain to be reassessed. The major early study done in this area (Morant 1926) suggested that Iron Age and Anglo-Saxon samples could be distinguished primarily by the greater calvarial height (but not by any of the cephalic [cranial] indices) of the latter. While univariate analyses based on single cranial measurements of the skull were not conducted here, it was found that Morant's sample would have differed significantly in cranial breadth-height index from Wetwang and in cranial length-height index from Maiden Castle, suggesting (as do results from comparisons between other samples) that regional differences in cranial morphology may be obscured by pooling across large geographic areas. Such differences are also apparent in temporal variation, particularly when early and later Anglo-Saxons are considered separately

Some differences may also be observed between the findings of this research and those of Goodman & Morant (1940), who found no distinction between Morant's Anglo-Saxon sample, and the sample from Maiden Castle. While differences were apparent in terms of statistically significant differences in some of the cranial indices in this research, however, it was also noted that these samples were more similar in the biodistance analyses than were other Iron Age / Anglo-Saxon samples. When these two samples were considered in the univariate analyses, however, the overall homogeneity of regional sub-groups of Morant's sample was confirmed. This is in contrast to the reassessment of the sample from Maiden Castle, which, whilst confirming the homogeneity of 'Belgic' and Iron Age sub-samples, indicated some differences between these and the Romano-British sub-sample.

These results indicate that hypothesis 1 should be accepted. They also indicated that, on the whole, pooling by region, sex and temporal period, in order to create samples large enough to be used in the multivariate analyses, was justified.

Hypothesis 2a

Samples will cluster according to their geographic proximity – i.e. British samples through time will be closer to other British samples than to Danish samples.

Hypothesis 2b

There is evidence for changes in British-Danish relationships, as indicated by minimum genetic distance (d^2), through time.

Hypothesis 2c

If there are differences in British-Danish relationships through time, greater similarities will be seen in the Anglo-Saxon period, compared to the Iron Age and Romano-British periods.

To investigate patterns of phenotypic change within Britain, and to test hypotheses regarding change through time, multivariate analyses were used. Primary among these was the calculation of minimum genetic distances (d^2) used to investigate population relationships within Britain over time, and between Britain and Denmark over time. Hypothesis 2a related to the expectation that, if acculturation models of change in the Anglo-Saxon period (and indeed in the Iron Age) were correct (e.g. Todd 1985, Higham 1992, Lucy 1998, 2000, Haselgrove 1999, Tyrrell 2000, Harding 2004), British samples would be more similar to each other than they were to Danish samples, and there would be a clear British-Danish distinction, based on a model of geographical isolation, and a general lack of significant gene flow between the two. In contrast, hypothesis 2b proposed that if 2a was rejected, period-specific differences in British-Danish relationships would be observed. Hypothesis 2c proposed that, if 2a was rejected, and 2b accepted, a model of migration-based change between the Romano-British and Anglo-Saxon periods (e.g. Welch 1992, Burmeister 2000) might be supported if greater similarities between Britain and Denmark in the Anglo-Saxon period than in preceding periods was observed.

When British only, UK pooled, samples were analysed, there was a clear indication that, overall, populations closer in time were closer biologically than those which were more distant. However when Danish samples were included in the analysis, the pattern of biological relationships changed, although a certain degree of temporal patterning remained, in that earlier UK samples were closer to earlier Danish samples, and later UK samples closer to later Danish samples. As with the univariate analyses, in both pooled-group and un-pooled sample analyses, the Romano-British sample(s) proved to be anomalous, in terms of their overall lack of similarities with Danes compared to Iron Age and Anglo-Saxon samples. The relationship between temporal and biological distance identified in the British-only analyses remained, therefore, when Danish samples were included, however, the expectation that British samples would be more similar to one another than to Danish samples was not sustained.

These findings apply equally to separate female and male samples, for both pooled and un-pooled samples, and for analyses within restricted time periods, although the patterns are somewhat clearer for males than females, and the genetic distances for pooled samples suggest that overall females were less genetically similar through time than were males. Results also indicated that within Britain, there was regional variability in terms of British-Danish relationships.

The hypothesis that samples will be more similar geographically (2a) is therefore rejected, while the hypothesis that there is temporal change in British-Danish relationships (2b) is accepted. Perhaps most importantly, in terms of theories of change which are linked to migration, hypothesis 2c can also technically be rejected, on the basis that while Anglo-Saxons are more similar to Danish samples than are Romano-British samples, so are the Iron Age samples – indeed in some analyses they are more similar to Danes than even the Anglo-Saxons. The implications of the Iron Age similarity to Danish samples will be discussed more fully in section 5.3 below.

Hypothesis 3a

Both within Britain, and between Britain and Denmark, biological relationships indicated by the minimum genetic distance (d^2) matrix can be explained by an isolation by distance (geographic continuity) model.

Hypothesis 3b

Both within Britain, and/or between Britain and Denmark, samples which are more similar temporally will be more similar biologically.

In order to investigate relationships between biodistance and other measurable features of samples, Mantel matrix correlation tests were used, primarily to test theories regarding geographic and temporal correlations with biodistance, but also to investigate associations between biodistance and cultural affinity.

None of the analyses, whether for pooled samples in comparison with Danes or for un-pooled samples both in the UK and in comparison with Danish samples, indicate that there is any significant correlation between biodistance and geographic distance. Hypothesis 3a cannot, therefore, be accepted.

For British-only samples, there is some slight indication of a geographic relationship between samples, in that the correlation coefficient, albeit small in magnitude and statistically non-significant, is positive in direction. In cases where British and Danish samples were analysed together, however, the correlation coefficient was near to zero, indicating no correlation whatever between the biodistance and geographic distance matrices. This outcome holds even when samples are analysed for pairs of time periods (Iron Age – Romano-British and Romano-British – Anglo-Saxon). This suggests that a model of isolation by distance (or geographical continuity through time) cannot explain biological relationships either within Britain, or between Britain and Denmark in this case. The results of the Mantel matrix correlation tests therefore confirm the pattern which was suggested by both the univariate and biodistance analyses. It also fails to support the conclusions drawn by Lloyd Jones (1997, 1999), who found that Romano-British and Anglo-Saxon sites were more similar geographically than temporally, and who concluded that this indicated overall geographic continuity rather than change in the Romano-British to Anglo-Saxon periods.

Hypothesis 3b proposed that, in contrast to hypothesis 3a, biodistance would correlate with temporal distance, and therefore that samples that were closer temporally would also be closer biologically. The results of the Mantel matrix correlation tests for association between biological and temporal distance were rather mixed. For UK samples only, pooled geographically and by period, biological distance was strongly and significantly associated with temporal distance, verifying the patterns observed in the relevant biodistance matrices. Temporal distance was also nearly significantly correlated with biological distance for UK separate samples (but only when north-east later Anglo-Saxons were included in the analysis), and was significantly correlated in the analysis which included Romano-British and Anglo-Saxon samples only. However, temporal distance was not significantly associated with biological distance for the Iron Age to Romano-British period only, or when Danish samples were included with either pooled or un-pooled UK samples.

The reason for this could be at least partially due to one or more of a number of factors; these include the differences between Wetwang and Maiden Castle in the former analysis, the inclusion of Romano-British samples (for which there is no evidence for a Danish link) in the latter analyses, and the late date of the Danish Viking sample which does not match easily with the slightly earlier British dates. In order to test the impact of including the Romano-British samples, repeat Mantel tests comparing biodistance with temporal distance were conducted for both pooled and separate samples, omitting Romano-British samples from the analysis. In both cases the magnitude of the correlation coefficient increased (although it is still relatively small), and the *p* value decreased compared to analyses which included Romano-British samples. In neither of the analyses, however, did the correlation become significant (pooled sample: $R=0.3355$, $R^2=0.1125$, $p=0.117$; un-pooled samples temporal matrix a: $R=0.2042$, $R^2=0.0417$, $p=0.206$, temporal matrix b: $R=0.1956$, $R^2=0.0383$, $p=0.202$).

Hypothesis 3b can therefore be accepted for some UK only analyses, but must be rejected for all analyses which include Danish samples.

Because of the lack of significant association between either geographic or temporal distance for the samples analysed, when Danish samples were included, an additional comparative matrix was designed in order to test the relationship between biological distance and socio-cultural aspects of the samples used.

The 'cultural distance' matrix described similarities or differences between samples in terms of their cultural affinities (see Chapter 2). This was not intended to inflame the 'genes = culture' debate, but rather as a means by which a model of Danish cultural relationships with British Anglo-Saxon samples could be enumerated and tested against the biological distance matrices. Because of the biological similarities of (particularly) Wetwang and Danish samples, a secondary cultural matrix was constructed which also proposed links between these samples in order to represent the possibility of a continental cultural relationship, which some have proposed may be related to migration (e.g. Stead 1965, 1991, Cunliffe 1991). It should be reiterated here, however, that a proportion of the variation described by these 'cultural matrices' represents temporal distances.

In all pooled and un-pooled analyses including Danish samples, and in the UK only analyses that included UK Romano-British and Anglo-Saxon samples only (including north-east later Anglo-Saxons), one or both of the cultural matrices was found to be significantly correlated with biodistance. While the correlation for the UK Iron Age – Romano-British only analysis was statistically non-significant, it did approach significance (*p*=0.0756), and the magnitude of the correlation was comparatively large (R=0.6547, R^2=0.4286), suggesting a substantial association between biological distance and cultural affinity in these periods. Although none of the statistically significant correlations was large in magnitude, as expected they invariably increased in magnitude, and became more highly significant, upon linking Wetwang and the pooled UK Iron Age sample with Denmark.

Null hypothesis 4

There are no differences in genetic within-group variation between the Iron Age, Romano-British and Anglo-Saxon periods in Britain.

Although the usefulness of the Relethford-Blangero method was limited in this study by the small sizes of most samples, and by theoretical constraints already discussed, a number of analyses were conducted in order to investigate differences between those samples which could be used, in terms of within-sample variation. Relethford-Blangero analyses give an indication of which populations within an analysis are more or less variable relative to the variation that would be expected based on a sample's distance to the centroid, and thus indicate whether samples have received more or less than average gene flow from an extra-regional source, or from a intra-regional source not sampled in the analysis.

In the three sets of analyses that were carried out, the first examined sex-pooled, within-period samples. The most striking result was for the Iron Age sample from Wetwang, which exhibited a large positive residual compared to Maiden Castle, indicating that it had received above average levels of gene flow from a source either outside Britain, or from a British source not sampled in the current analysis. Differences between sites in within-sample variation were not so apparent for the Romano-British period or the Anglo-Saxon period, where individual samples seem to have received near-equal amounts of gene flow, although within these analyses Poundbury and Bidford-on-Avon each exhibited higher levels of within group variation respectively.

As has been noted previously, combining samples from different time periods technically violates the assumption of panmixia, on which the Relethford-Blangero analyses are based. Nevertheless, in an exploratory capacity, analyses comparing variability within samples in adjacent time periods were conducted. It is notable that in many cases the relative positioning of samples above or below the expected variance line (but not necessarily their distance from the centroid) on the Relethford-Blangero results plots reflects very closely their positions in the plots derived from the within-period analyses. Results continued to suggest comparatively higher levels of gene flow into Wetwang and Poundbury in the Iron Age / Romano-British analysis. In the Romano-British / Anglo-Saxon analysis, however, two of the Romano-British samples, Poundbury and Trentholme Drive, seem to have experienced more gene flow than did Cirencester or the two Anglo-Saxon samples. The implication of these results is that Romano-British samples, with the exception of Cirencester, appear genetically more variable than Anglo-Saxon samples. In terms of explaining what happened during the Romano-British / Anglo-Saxon transition this result is not particularly helpful, however it may tell us something about the relatively more heterogeneous composition of Romano-British populations. Whether this heterogeneity is due to migration related to Roman activities in Britain, to environmental or social differences between Romano-British and Anglo-Saxon periods, or simply to the nature of the samples used is a matter for further research, and will be discussed further in sections 5.3 and 5.4 below.

The third set of Relethford-Blangero analyses tested within-group variation for males and females in each period separately, so that females and males were compared within the same analyses. To my knowledge, direct comparison of separate female and males sub-samples of the same sample in a single analysis has not been done before, at least in studies using cranial data, and as a result the theoretical consequences of doing so are unknown (Relethford pers. comm.). Additionally, one of the consequences of examining females and males separately is that sample sizes, particularly for females, tend to become small, and the results must therefore be less robust.

Within the Iron Age sample, the Relethford-Blangero results indicate that both females and males from Wetwang are more variable than expected, indicating greater gene flow into these samples than into Maiden Castle females and males which are both less variable than expected. This may represent support for theories that invoke migration as a cause of the development of the Arras culture seen in this area (e.g. Stead 1965, 1991, Cunliffe 1991); alternatively it may be a consequence of differences between the samples used. One of the limitations of the application of the Relethford-Blangero method in this study, which means its full potential cannot be exploited, is that it fails to take into account factors such as overall population size, which could influence the results of the analysis. Additionally, differences in the duration of use of individual cemeteries may have implications for the results of these analyses.

Within the Romano-British period, all the male samples are close to the expected level of variation, while females from Poundbury and Trentholme Drive are more and less variable relatively than expected. The results of previous analyses had all suggested that Cirencester was more homogenous than other Romano-British samples, and it might have been reasonable to suggest that this was due to the Cirencester sample being composed almost entirely of males. However, the results of this analysis indicate that, when divided by sex, Cirencester males still appear more homogenous, relative to other males, which suggests that there is some difference between these sites in terms of gene flow.

Within the Anglo-Saxon period, females from Bidford-on-Avon stand out as being very highly variable (although problems with the small size of this sample have been noted), while males from Bidford-on-Avon appear more homogenous than all the other samples. Females and males from Burwell demonstrate very similar levels of variability relative to that expected.

The results of the Relethford-Blangero analyses *may* indicate that there is evidence for both temporal and regional variation in within-group and within-sex heterogeneity through these time periods in Britain. The results, however, must be interpreted in the light of the problems which have already been discussed and therefore, at the present time, the hypothesis that within-group variation differs through time cannot be accepted or rejected with any reasonable level of confidence. These analyses do, however, suggest that this method may be valuable in future research, and this potential is discussed further in section 5.4.

5.3 General discussion

The results of the analyses which have been described above in relation to the research hypotheses, are rather difficult to interpret in the light of the usual models which have been used to explain the population history of Britain. In terms of the debate regarding the Romano-British / Anglo-Saxon transition, the results could, perhaps, be taken to support both sides of this theoretically polarised argument.

On the one hand, in response to the questions 'were the Anglo-Saxons in Britain more similar to Danish samples than were the Romano-British', and 'were the Anglo-Saxons in Britain genetically more similar to Danes than they were to the Romano-British?' then the answer to both questions is yes, they were. This finding would support models of change which emphasise the migration of substantial numbers of people from Denmark, or a genetically similar region.

However, when the similarity of Iron Age samples to the Danish samples is taken into account, the implications of the answer to the previous question become much less clear. It is difficult to determine whether the similarity of Anglo-Saxons to Danish samples was due to the movement of people in this period, or was a result of a previous migration and/or long term gene flow between the two areas, rather than a migration *per se* in the Anglo-Saxon period.

This also has the effect of making direct comparisons between the findings of this study, and that done previously, problematic, since no recent previous work has explicitly investigated the Romano-British / Anglo-Saxon transition by examining Anglo-Saxon samples in comparison to Iron Age as well as Romano-British samples. Additionally none outside the realm of archaeogenetics has considered temporally matched continental as well as British samples.

Overall, the results have more in common with those derived from archaeogenetic research, and with some studies (e.g. Härke 1990) from biological anthropology, than from recent empirical and theoretical archaeological and historical research. However, because of the focus of these 'biological' studies, none has found evidence which suggests a substantial Iron Age link with the continent, including those which have examined the Iron Age specifically (e.g. Leese 1991, Jay 2006). The results also directly conflict with those reported by Morant (1926), Brothwell and Krzanowski (1974) and Dawes (1980), who all noted the similarities between Iron Age and Romano-British samples in their studies.

It seems reasonable to propose, at this point, a number of scenarios that may be responsible for the patterns seen in the both the univariate and the multivariate analyses, with relation to the specific samples used in this analysis, and to evaluate these systematically in terms of the other evidence available.

Firstly, separate large scale migrations from the continent in both the Iron Age, and throughout the Anglo-Saxon periods, may explain the pattern of temporal similarities between the samples investigated here. As was noted in Chapter 2, migration models have, in the past, been used to explain cultural changes that occurred in both these periods, although in more recent times these have been almost universally replaced by models emphasising acculturation.

For the early Anglo-Saxon period, migration models were proposed from the very earliest research. For the Iron Age, it may be significant that both the samples use in this analysis have, at some point, been linked with continental migration. Foremost among these is Wetwang in East Yorkshire, and its relatively strong and enduring association with 'the continent', although the exact origin of this continental affiliation is vague – northern France and Switzerland have been proposed (Stead 1965, 1991, Cunliffe 1991). Of all the samples examined in this study, Wetwang has the closest genetic similarity to the early Danish samples. Although these are later in date than Wetwang, there is some evidence to suggest that relatively little biological change was occurring in Denmark in the early and later Roman periods (note the similarity between these samples in the biodistance analyses here, and see also Sellevold *et al.* 1984), and it *may* be reasonable to suggest that Danes of these periods were genetically similar to those in preceding periods. The second Iron Age sample, from Maiden Castle, has not had the same level of attention given to it in terms of migration as has Wetwang. Nevertheless, suggestions have been made that the south of England was also the recipient of reasonably large-scale migration, this time of Belgae from what is now northern France, during the Iron Age (Cunliffe 1991). The links between Belgae (or northern France / Gaul) and Germanic tribes have already been noted (Chapter 2, section 2.2.3.2).

For both Iron Age samples, then, there is some archaeological and historical evidence to suggest that there may have been significant contact with, perhaps extending to significant migration from, areas which were associated with Germanic peoples, tribes or conquest. The results presented here suggest that this contact might not have been limited to trade and small-scale population movement, and may have involved immigration on a much larger scale, although the differences between Wetwang and Maiden Castle, and the relationships of these with the Danish samples, complicate this interpretation somewhat.

An alternative explanation, which does not emphasise discrete migrations as such, would be long term, perhaps regionally variable gene flow, between one or more continental regions and Britain. This could account for transitions seen both in cultural material, and in biological relationships between Britain and Denmark. The impact of this flow may have been interrupted during the Romano-British period – perhaps by immigration of a distinct nature related to the Roman occupation of Britain or by environmental and social change. As far as I am aware, little research has been done to investigate the origins, composition and extent of Roman biological influence upon the population of Britain (although recent research done on skeletons from York by Janet Montgomery (pers. comm.), in association with York Archaeological Trust confirms that at least part of the population was composed of individuals with wide-ranging continental origins).

The archaeological evidence suggests that while initially small in number, during the reasonably long period of Britain's occupation Roman military personnel may have become integrated both socially and biologically with the 'indigenous' population (Jones 1984). As the samples used in this analysis were all from urban areas, to some degree associated with Roman military and/or civil control, the distinction of these samples as seen from the biodistance analyses may indicate changes in the genetic as well as social make up of these samples. Results from the Relethford-Blangero analyses may support this proposition, indicating relatively greater heterogeneity within these samples in some analyses.

In this explanation, then, long term gene flow, and temporal changes in this flow, between Britain and the continent accounts for both cultural / archaeological and biological relationships, via a combination of migration, cultural exchange, and, perhaps in some cases, politically induced acculturation. However, if long-term gene flow is responsible for similarities between Britain and Denmark, recent craniometric research would indicate that this did not have an origin in Neolithic or Bronze Age migrations (Loring Brace *et al*. 2006). Additionally, the genetic evidence would suggest that this was not occurring in pre- Bronze or Iron Age periods, as most studies emphasise a post-Neolithic origin for relationships between Britain and northern Europe (e.g. Wilson *et al*. 2001, Weale *et al*. 2002, Capelli *et al*. 2003), due to regional differences apparent within Europe. While most of these latter studies rule out an Iron Age origin for the patterns seen, their conclusions are based on the notion of a single wave of *Celtic* migration from a quite precisely located central

European homeland, rather than on the possibility of more localised population movements.

A third explanation might involve a combination of the two scenarios discussed already in this section, but with rather more focus on regional variability. In this explanation, long-term, low level, gene flow would account for the overall similarities between Britain and Denmark throughout these periods (with the exception of the Romano-British period which has already been discussed), with regional and temporal 'spikes' in migration perhaps also occurring. In this 'mosaic' scenario, then, overall biological and cultural similarities are explicable on the basis of long-term biological and cultural contact, while the differences between individual samples may be explained on the basis of regional variation. Regional variation has only recently begun to be taken into account in studies which examine the population history of Britain, and recent genetic studies (Capelli *et al.* 2003, Töpf *et al.* 2006) have emphasised this variation. A perspective on biological population change which emphasises regional variation begins to address some of the concerns of 'anti-migrationist' archaeologists, who have argued against the importance of large-scale migration on the basis of variation seen in the archaeological evidence. The results of this study indicate that, at the level of individual samples (cemetery sites), both regional and temporal variation are evident, and therefore supports the conclusions of both archaeogeneticists, and the arguments of some archaeologists, that this should be taken into account in the design and interpretation of evidence deriving from both past and future research. It also suggests that regional variation might explain the very different conclusions to which previous researchers of this topic have come.

Going beyond the narrow focus of this study, a number of theoretical and methodological issues may be identified, discussion of which concludes this section.

One of the major questions that emerges concerns the impact of sampling on the findings which have been discussed. This is with regard not only to biological / genetic differences in this period, but also to the impact of the environmental and economic differences between samples which have been outlined above and in Chapter 2. As has been noted, one of the limitations of this research was its reliance on Romano-British samples derived solely from 'urbanised' areas of Britain.

The question of environmental continuity, and issues regarding the relationship between environment and phenotype, have already been discussed in this thesis (Chapter 2). The majority of work done indicates, and focuses on, considerable environmental and, to an extent, economic continuity from the Iron Age to the Anglo-Saxon period in Britain (e.g. Higham 1992, Lucy 1998, 2000, Haselgrove 1999, Esmonde Cleary 1999, Hanson 1999, Harding 2004, Tyrrell 2000). However, the Roman period remains distinctive, particularly for its social, environmental and economic differences. Urban settlements, trade, and the biological, social, cultural and technological effects of the Roman occupation of Britain all contribute significantly to this distinctiveness. Nevertheless, many researchers now emphasise continuity rather than change, especially with regard to rural populations.

The similarities of British Iron Age and Anglo-Saxon samples to each other, and of both to Danish samples, suggests a close genetic relationship, and possible explanations for this have already been discussed in this chapter. The distinctiveness of the Romano-British samples, however, might suggest that they were profoundly genetically different from preceding and subsequent populations. Alternatively, it may indicate that environmental and economic change in this period led to morphological changes which, in this research, and in combination with the inevitable increase in heterogeneity expected in urban samples, give the impression of genetic distinctiveness.

However, on the basis of the research done here, the fact that all three Romano-British samples included in this research appear so similar (although the sample from Cirencester seems slightly distinct in some analyses), indicates a high degree of homogeneity in this period. This homogeneity exists despite the samples being somewhat distant from one another in both time and space. Details regarding the specific samples (see section 3.3.3) suggest that Poundbury, in particular, represented an indigenous civilian population, individuals from which were buried – as was the custom – in the large cemetery associated with a major settlement. This depiction contrasts somewhat with Trentholme Drive and Cirencester, which were both strongly associated with Roman legions and government; samples from which some (Wenham 1968, Wells 1982) have suggested may not represent the 'normal' indigenous population of Britain.

Despite this contrast, however, there is no substantial evidence from the biodistance analyses conducted here to suggest that the population of Poundbury differed biologically from the populations of the other two Romano-British sites. In these analyses, Poundbury remains just as distant from Iron Age, Anglo-Saxon and Danish samples as Trentholme Drive and Cirencester. Additionally, while Poundbury in general, and Poundbury females in particular, appeared somewhat more genetically variable than the other two samples, this could be explained on the basis that it served a different type of community – individuals from rural areas as well as from the town itself, perhaps. These findings suggest that whatever the cause of the overall Romano-British distinctiveness, it could apply to the Romano-British population of Britain in general, and is not necessarily due solely and directly to the occupation of towns by Roman military or administrative personnel.

Previous research has noted the impact of environmental change on craniofacial form (see Chapter 2, section 2.8), and at times the importance of its plasticity has been stressed to the exclusion of other analyses of craniofacial form (Boas 1912). However, recent research suggests that the impact of environmental change on the phenotype does not obscure population relationships (e.g. Sparks 2001, Relethford 2004b), and although changes in economic strategy produce changes in craniofacial form, the variation which exists remains representative of historical relationships (González-José *et al.* 2005). The question which must, therefore, be asked, is whether or not the changes in environment, economy and lifestyle between the Iron Age and Romano-British periods were sufficient to be held responsible for the distinctiveness of Romano-British samples in this research?

The implications of the 'Romano-British difference' for the main Romano-British / Anglo-Saxon question addressed in this research are unclear. With regard to the central question of this research – that which addresses population relationships between Britain and Denmark, particularly in the Anglo-Saxon period – the distinctiveness of the Romano-British samples should not detract from the implications of the finding of close British / Danish relationships in the Iron Age and Anglo-Saxon periods. These relationships are apparent despite considerable geographical, and to a lesser extent temporal, distances between the regions, and this in itself is worthy of both note, and further investigation.

What can be concluded is that on the basis of this research there is certainly not continuity between the Iron Age / Romano-British and Romano-British / Anglo-Saxon periods in Britain. Answers to the questions identified above must ultimately lie in further research; on the genetic make up of urban and rural Romano-British populations, on the impact of differences in environment on craniofacial morphology, and on the relationships between, and variations within, regions and temporal eras. It should also be emphasised that it is not enough to concentrate solely on single, or adjacent periods in British history; where there is the possibility of long term gene flow, a much broader temporal perspective must be taken.

The finding of both regional and temporal variation in the craniofacial morphology of Britain's past populations also has implications for larger-scale studies of continental and global biodiversity. Where researchers use a single, archaeological sample as representative of 'Britain', this variability must be noted, and the historical and biological characteristics of the sample taken into account.

Another consequence of the findings of this study, which is partly a result of the rather narrow temporal and theoretical focus on the relationship between cultural and biological change, is that the models used to explain change in British pre- and early history appear inadequate. Perhaps because of the polarisation of perspectives regarding migration and acculturation, they completely fail to account for the possibility that at least some degree of biological (and hence cultural) movement may have been the norm in these periods. While this research has not been able to provide a conclusive answer to the question of what happened during the Romano-British / Anglo-Saxon transition, its findings suggest that models of both cultural and biological British-continental relationships should be reassessed.

At this stage in this discussion, the benefits and limitations of the methods used in this study should be considered. On the basis of this research, as well as that done previously, the analytical methods used – which have never before been applied with regard to British population relationships – appear more than adequate in terms of addressing the questions asked here. Population genetic analyses clearly have the potential to be applied widely, on various scales of analysis which are not limited to investigation of the problem addressed here, but which can be applied to a much broader investigation of British and European regional history. However, some limitations have emerged from this study which must first be tackled.

The limitations which constrained the execution and interpretation of this study were due not so much to constraints inherent in the methods, but rather to issues associated with the data available for analysis. This problem is common to most studies of archaeological biometric variation, where analyses involving complete datasets with no missing data must be used. As biological anthropologists rather than mathematicians, if we wish to use population genetic analyses such as those produced by RMET, it is the data limitations which must be addressed. If they can be successfully addressed, then the vast majority of the issues raised in this discussion can be tackled with a greater degree of confidence, and the full potential of the analytical methods exploited.

The effect that reducing the dataset to one where there were no individuals with missing data was the primary reason why only eight craniofacial variables were utilised in the multivariate analyses in this research, and the use of this limited number of variables is one of the major limitations of this research. In order to maximise both the size and number of samples, the variables used here were ones that are almost always recorded in assessments of human remains, and that are well standardised. With the data available, it was not possible to include a greater number of either cranial or facial measurements, due mainly to differences between suites of measurements originally recorded, and to the fragmentation of the skeletal material. However, differences between patterns seen in the univariate analyses, which examined cranial and facial indices separately, and recent research done into the heritabilities of cranial dimensions (Carson 2006), suggest that a better set of variables could be identified for use in future research.

It was possible, however, to use the data currently available to test the effects of using different suites of variables on biodistance matrices (see Appendix 3). In order to provide a controlled test of the effect of using different suites of variables, it was necessary to use a modified and reduced set of samples, which means the results are not directly comparable to the bulk of results presented in Chapter 4 here.

The results of these tests demonstrate that whilst utilising different sets of variables does result in differences in the way samples cluster in the HCA dendrograms and PCO plots, on the whole the pattern of relationships between samples remains. Simply adding more variables (from eight to twelve) does not greatly alter the clustering of samples, and indeed a Mantel test reveals an extremely strong, highly significant, positive association between biodistance matrices deriving from the eight- and twelve- variable datasets. When a suite of seven cranial vault measurements only are used, the pattern of relationships does alter – in fact it becomes more similar to the conclusions drawn out of the results presented in Chapter 4 of this thesis. However when facial measurements alone are used, the pattern of relationships alters dramatically. The Mantel test additionally reveals that while the association between matrices deriving from eight craniofacial and five facial variable sets is statistically significant, it is much smaller in magnitude than associations between the other sets of variables.

An interesting feature of the eight- and twelve- variable analyses presented in Appendix 3 is that Wetwang and Danish Vikings have small biodistances from each other, and cluster together in the HCA dendrograms. However, in the analyses based solely on cranial vault data, while the biodistances remain small, they no longer cluster together. Examination of the matrix and plots for the analysis based on facial variables may reveal the reason for this; relatively speaking Wetwang and Danish Vikings are closer than any other pair of samples, based on these variables.

The results of these exploratory analyses suggest that while analyses based on a limited number of both cranial and facial measurements are useful, and not uncommon in craniometric analyses (e.g. Brothwell & Krzanowski 1974, Schillaci & Stojanowski 2005) a choice of measurements made with the additional benefit of recent research into craniofacial heritabilities (Carson 2006), which indicated greater cranial than facial heritabilities overall, would enhance future research considerably.

An additional issue here, with regard to limitations and constraints on this study which go beyond the choice of variables used in analyses, is the availability and accessibility of skeletal material and data itself. In the earlier days of craniometric research, craniometry and research into population relationships was extremely popular in academic circles, and as a result extensive craniometric data were collected and published. In recent times, however, perhaps due to the decline of interest in metric skeletal data and analyses which focus on population history, such data is no longer published as a matter of course in excavation reports. With very few exceptions – this study being one – researchers in Britain no longer collate and analyse large bodies of skeletal metric data. This means that despite the large quantity of skeletal material which is excavated in Britain, data resulting from it tend not to be made widely available. When issues of access, post-excavation skeletal deterioration and reburial are added to this state of affairs, the situation becomes one whereby the human remains which are excavated fail to contribute to academic research, and their potential is ultimately lost.

Addressing the issues of limited data may involve making changes in the type of data which is employed (and suggestions are made in the next section of this chapter). However, the biggest difference is likely to be made by changing attitudes to the utility of biological data, its recording and dissemination, both in the archaeological literature and to – and between – academics. Publication of, and access to, skeletal data and materials has clearly not been a priority in recent times, however the research presented in this thesis should serve to illustrate the usefulness of such data to the wider archaeological and academic community, and to renew interest in skeletal and biodistance analyses.

In the next and final subsection, conclusions, and suggestions for future research which emerge from the preceding discussion, are discussed.

5.4 Conclusions and suggestions for further work

The research presented in this thesis has demonstrated that (1) both Iron Age and Anglo-Saxon samples appear genetically close to Danish samples, and that Romano-British samples are not; (2) a model of isolation by distance cannot explain the biological relationships between samples within Britain, or between Britain and Denmark; (3) a model of cultural similarity is significantly associated with biological relationships; (4) craniometric data and the analytical methods used in this research can contribute meaningfully to investigations into cultural / biological transitions in Britain (where they have not previously been used), and have the potential to help explain the association between both temporal periods and geographical regions, and between biology and culture; (5) it is essential to examine broader periods of time than have traditionally been considered, both within Britain and within Europe, when attempting to elucidate population relationships, and the potential causes of change.

All the methods used in this research, from the simple descriptive and univariate analyses, through analyses of biodistance, matrix correlation and within-group variation, contributed to the conclusions drawn, or suggested avenues for further research. It is notable that the results of relatively simple analyses of cranial indices, and complex analyses of biodistance produced broadly similar results.

There is clear potential for further work to be done in this field, and as with most research, more questions have emerged than have been answered through the course of this study. The limitations and questions identified above indicate that all the populations examined in this thesis deserve further study, and that much more data are needed, both from British and continental samples.

The distinctiveness of the Romano-British samples suggests a particular need to examine population relationships, and the impact of Roman military occupation on the genetic make-up of populations of this period. Further research needs to be done to identify a) how representative (or un-representative) Romano-British urban samples of this period are, and b) why they are different – both genetic and environmental influences may play significant roles. Similar research needs to be done on the Iron Age, due to its considerable variability within Britain.

Another question arising from this research, which has not been touched on so far, is of the difference, in both univariate and biodistance analyses, between Danish early/late Romans and Danish Vikings. Univariate research which has so far been done on these skeletal samples has noted these differences, but has explained them on the basis of environmental, rather than genetic change (Sellevold *et al.* 1984). Some archaeogenetic studies have similarly indicated that the methods used currently are unlikely to be able to distinguish between Danish Anglo-Saxon and Danish Viking migrations (Weale *et al.* 2002, Capelli *et al.* 2003). However, the results of this study, and of recent archaeogenetic work (Rudbeck *et al.* 2006 in press), albeit on a single cemetery sample from a slightly later period in Danish history (early Christian; 11th – 13th centuries AD), suggest that the population of Denmark through these periods was not as genetically homogeneous as had previously been thought, and that large scale population movement, over large geographical distances, may have been commonplace. Further research, therefore, should not be limited to comparing (for example) Danish samples against British ones, but should be extended to investigation of the population history of continental populations in general, on both individual-site and regional levels.

A major limitation of this study was the effect that reduction to a multivariate dataset (even one limited to a relatively small number of variables) had on sample sizes. This reduction was partly due to poor preservation of skeletal material, which compounded the fact that many Anglo-Saxon and rural Romano-British cemetery samples are small relative to Romano-British urban samples, and most rural Iron Age samples so rare as to have been excluded from this research.

While the effectiveness of 'modern' craniometry has been demonstrated throughout this research (as well as in research in other parts of the world), it is entirely possible that other metric approaches, such as dental metrics, could be applied, using the same or similar theoretical and methodological perspectives that have been applied here. This would at least partially circumvent the problem of poor skeletal preservation, and would also allow regional and sex-related variation to be studied on a much larger scale, via analysis of single rather than pooled samples. This would also allow the full potential of the methods used here – particularly the

Relethford-Blangero analyses – to be exploited; a particularly important consideration given the discussion of regional variability above.

Expanding the dataset available, whether based on craniometric or other metric data, would allow much more substantial research into Britain's population history to be done. It would also allow multidisciplinary studies combining, for example, biodistance and archaeogenetic and/or isotope analyses, to be conducted. With regard to biodistance / archaeogenetic studies, a careful application of the two methods could assist in resolving one of the main problems in archaeogenetics – that of identifying *when* changes in, or relationships between, populations developed. With regard to isotope analysis, biodistance methods – particularly if they could be applied to a greater proportion of individuals within a single cemetery – could assist in the identification of family groupings or other biological differences within a sample. If these analyses could be combined with comparative analyses of a much greater temporal and geographical range of samples, both within Britain and on the continent, real progress with regard to our understanding of pre- and early historic population relationships at all levels of analysis could be made.

Finally, research into population history tends to focus on one type of data. Although researchers often aim to address questions which are well-founded, and commonly posed, the use of different methods and different sites means (as has been seen in this thesis) that drawing conclusions and comparisons from the work of different researchers can be at best difficult, and at worst impossible. Collaborative multi-disciplinary research on either single or multiple cemetery sites, therefore, should also be combined with analyses based on a number of different types of data (e.g. archaeological, craniometric, dental metric / non-metric, isotope, genetic). This would be extremely beneficial methodologically, in terms of enhancing our understanding of the results produced by different data types, and would also facilitate more robust interpretations of results.

In conclusion, from the discussion of the literature, the 'new' approaches to migration, and the results emerging from new fields of analysis such as archaeogenetics and isotope analysis, as well as from this research, it is evident that current and recent perspectives on the role of migration in the population history of the British Isles should be reassessed. Considerable work remains to be done, and it is imperative that this is done with a methodological and theoretical focus free of the constraints which have limited research in recent decades.

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APPENDIX 1

MATRICES USED

A1.1 Introduction

Matrices which summarise those used in the analyses presented in section 4.7 of this thesis are presented below, for the purpose of illustrating how these matrices were constructed. Biological, geographical, temporal and cultural matrices are presented for pooled and separate samples, including both UK and Danish groups.

In these matrices, popi / popj = the pairwise comparison; bio = biodistance (d^2) derived from RMET; geo = geographic distance in kilometres; temp = temporal distance in years; 'cult a' = cultural links between samples, including Anglo-Saxon and Danish samples; 'cult b' additionally = links between Iron Age and Danish samples. In the matrices presented in section A1.4 all separate pooled sex samples are compared excluding Danes' Graves and north-east early Anglo-Saxons. The second temporal distance matrix (temp b) makes Cirencester (cir) 25 yrs older and Burwell (bur) 50 years younger. This reflects uncertainty in dating of the samples.

A1.2 Pooled samples (Burwell with later Anglo-Saxons)

popi	**popj**	**bio**	**geo**	**temp**	**cult a**	**cult b**
ukeas	uklas	0.100857	0.5	150	0.5	0.5
ukeas	ukrb	0.117569	0	250	1	1
ukeas	ukia	0.107373	0.5	750	1	1
ukeas	daner	0.041054	1	570	1	1
ukeas	danlr	0.051098	1	370	0.5	0.5
ukeas	danvik	0.06475	1	275	0.5	0.5
uklas	ukrb	0.170572	0	400	1	1
uklas	ukia	0.2138	0	900	1	1
uklas	daner	0.21569	1	670	1	1
uklas	danlr	0.205754	1	470	1	1
uklas	danvik	0.039383	1	175	0.5	0.5
ukrb	ukia	0.168761	0	500	1	1
ukrb	daner	0.256723	1	270	1	1
ukrb	danlr	0.192353	1	70	1	1
ukrb	danvik	0.136896	1	575	1	1
ukia	daner	0.036937	1	230	1	0.5
ukia	danlr	0.036515	1	430	1	1
ukia	danvik	0.040586	1	1075	1	1
daner	danlr	0	0	200	0.5	0.5
daner	danvik	0.059039	0	845	0.5	0.5
danlr	danvik	0.050388	0	645	0.5	0.5

A1.3 Pooled samples (Burwell with early Anglo-Saxons)

popi	popj	bio	geo	temp	cult a	cult b
ukeas	nelas	0.150749	0.5	150	0.5	0.5
ukeas	ukrb	0.119217	0	250	1	1
ukeas	daner	0.081929	1	570	1	1
ukeas	danlr	0.083792	1	370	0.5	0.5
ukeas	danvik	0.019373	1	275	0.5	0.5
ukeas	ukia	0.119201	0.5	750	1	1
nelas	ukrb	0.186753	0	400	1	1
nelas	daner	0.308685	1	670	1	1
nelas	danlr	0.268008	1	470	1	1
nelas	danvik	0.162567	1	175	0.5	0.5
nelas	ukia	0.324126	0	900	1	1
ukrb	daner	0.23383	1	270	1	1
ukrb	danlr	0.173766	1	70	1	1
ukrb	danvik	0.121371	1	575	1	1
ukrb	ukia	0.160106	0.5	500	1	1
daner	danlr	0	0	200	0.5	0.5
daner	danvik	0.047422	0	845	1	1
daner	ukia	0.031896	1	230	1	0.5
danlr	danvik	0.03724	0	645	0.5	0.5
danlr	ukia	0.034664	1	430	1	1
danvik	ukia	0.035515	1	1075	1	1

A1.4 Separate samples

Popi	Popj	bio	geo	temp a	temp b	cult a	cult b
lneas	tdy	0.351306	79.5	450	450	1	1
lneas	pbd	0.170213	447	400	400	1	1
lneas	mlm	0.196905	294	150	150	0.5	0.5
lneas	daner	0.362784	820	670	670	1	1
lneas	danlr	0.333469	820	470	470	1	1
lneas	danvik	0.198951	820	175	175	0.5	0.5
lneas	wgs	0.415266	87	950	950	1	1
lneas	boa	0.318621	279	200	200	0.5	0.5
lneas	bur	0.215656	276	100	150	0	0
lneas	mcia	0.354804	450	750	750	1	1
lneas	cir	0.134057	330	400	425	1	1
tdy	pbd	0.052742	369	50	50	0	0
tdy	mlm	0.215314	214.5	300	300	1	1
tdy	daner	0.24329	820	220	220	1	1
tdy	danlr	0.177728	820	20	20	1	1
tdy	danvik	0.183484	820	625	625	1	1
tdy	wgs	0.152557	36	500	500	1	1
tdy	boa	0.16012	201	250	250	1	1
tdy	bur	0.314359	195	350	300	1	1
tdy	mcia	0.338141	373.5	300	300	1	1
tdy	cir	0.147382	255	50	75	0	0

pbd	mlm	0.166454	192	250	250	1	1
pbd	daner	0.33534	880	270	270	1	1
pbd	danlr	0.265503	880	70	70	1	1
pbd	danvik	0.164934	880	575	575	1	1
pbd	wgs	0.272155	384	550	550	1	1
pbd	boa	0.198018	168	200	200	1	1
pbd	bur	0.185637	255	300	250	1	1
pbd	mcia	0.329087	3	350	350	1	1
pbd	cir	0.066178	115.5	0	25	0	0
mlm	daner	0.097487	880	520	520	1	1
mlm	danlr	0.121246	880	320	320	0.5	0.5
mlm	danvik	0.126812	880	325	325	0.5	0.5
mlm	wgs	0.270196	216	800	800	1	1
mlm	boa	0.123997	88.5	50	50	0	0
mlm	bur	0.11246	66	50	0	0.5	0.5
mlm	mcia	0.036746	198	600	600	1	1
mlm	cir	0.09656	99	250	225	1	1
daner	danlr	0	0	200	200	0.5	0.5
daner	danvik	0.055498	0	845	845	0.5	0.5
daner	wgs	0.061659	820	280	280	1	0.5
daner	boa	0.047051	880	470	470	1	1
daner	bur	0.196342	880	570	520	1	1
daner	mcia	0.104227	880	80	80	1	1
daner	cir	0.208389	880	280	305	1	1
danlr	danvik	0.047632	0	645	645	0.5	0.5
danlr	wgs	0.048168	820	480	480	1	1
danlr	boa	0.048913	880	270	270	0.5	0.5
danlr	bur	0.198862	880	370	320	0.5	0.5
danlr	mcia	0.181754	880	280	280	1	1
danlr	cir	0.184477	880	70	95	1	1
danvik	wgs	0.057618	820	1125	1125	1	1
danvik	boa	0.058803	880	375	375	0.5	0.5
danvik	bur	0.033446	880	275	325	0.5	0.5
danvik	mcia	0.138635	880	925	925	1	1
danvik	cir	0.038733	880	575	550	1	1
wgs	boa	0.082515	216	750	750	1	1
wgs	bur	0.249648	186	850	800	1	1
wgs	mcia	0.241263	387	200	200	0.5	0.5
wgs	cir	0.19907	270	550	575	1	1
boa	bur	0.153076	141	100	50	0.5	0.5
boa	mcia	0.159873	171	550	550	1	1
boa	cir	0.139385	54	200	175	1	1
bur	mcia	0.138633	261	650	600	1	1
bur	cir	0.04282	162	300	225	1	1
mcia	cir	0.187734	118.5	350	375	1	1

APPENDIX 2

NORTH-EAST ANGLO-SAXON DATA

A2.1 Introduction

In this appendix, descriptive statistics for Spofforth, Norton Bishopsmill School, Hartlepool Church Walk and Black Gate Newcastle are presented individually. Spofforth has never previously been studied or published, and thus forms 'new data', the report for Norton Bishopsmill School data and assessment is in the process of being compiled by Northern Archaeological Associates, and as such the data are not currently available in any published form, and the Hartlepool Church Walk and Black Gate data have similarly never been published. As such these samples represent previously unstudied or particularly inaccessible data, and thus warrant individual description here.

A2.2 Village Farm, Spofforth: craniofacial morphology

Table A2.1 Village Farm, Spofforth: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	9	67.90	85.51	74.52	5.267
CLH index	4	65.78	75.43	72.39	4.503
CBH index	4	96.88	103.79	98.99	3.223
FP index	8	63.39	77.24	70.16	4.440
TF index	1	86.16	86.16	86.16	.
UF index	3	47.06	55.75	52.08	4.503
N index	9	44.87	59.21	50.40	4.571
O index	8	76.16	92.79	83.69	5.839
MA index	8	102.44	127.12	118.11	8.317
P index	9	58.02	87.37	76.87	8.797
Valid N (listwise)	0				

Table A2.2 Village Farm, Spofforth: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	15	70.77	78.88	74.91	2.210
CLH index	13	61.93	77.37	70.22	4.053
CBH index	10	83.56	99.29	92.68	5.160
FP index	14	63.89	76.59	69.02	3.517
TF index	4	82.93	91.80	88.66	4.159
UF index	4	50.14	54.64	52.58	1.944
N index	11	44.46	55.08	49.28	3.568
O index	13	72.69	95.53	81.51	6.348
MA index	13	99.03	123.20	112.46	6.979
P index	12	59.32	82.61	71.73	6.948
Valid N (listwise)	2				

Later Anglo-Saxon females from Village Farm, Spofforth are long-medium headed, with medium height skulls relative to length, and high-medium skulls relative to breadth. The forehead is broad-medium relative to the maximum cranial breadth, and the breadth of the face both including and excluding the mandible and teeth is average. The nasal aperture is average and the orbit is average-wide. The maxilla is broad relative to length, but the palate is narrow.

Males are long-medium headed, with medium-low skulls relative to both length and breadth. The forehead is medium-broad relative to the maximum cranial breadth, and the breadth of the face both including and excluding the mandible and teeth is average. The nasal aperture is average and the orbit wide. The maxilla is average relative to length, but the palate is narrow.

Females and males are similar in craniofacial morphology, although the male skulls are lower relative to breadth than the females, and this difference is statistically significant (*p*=.044). The small number of individuals involved in the calculation of some of the indices may have impacted on the usefulness of analyses of female/male difference, and precludes any further discussion of female/male variability.

A2.3 Norton Bishopsmill School: craniofacial morphology

Table A2.3 Norton Bishopsmill School: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	2	73.56	79.65	76.61	4.305
CLH index	2	70.35	76.44	73.39	4.305
CBH index	2	88.32	103.91	96.11	11.020
FP index	2	67.88	73.44	70.66	3.927
TF index	0				
UF index	1	50.82	50.82	50.82	.
N index	3	46.00	58.14	50.27	6.824
O index	3	86.49	90.00	87.89	1.861
MA index	4	112.50	130.43	117.97	8.451
P index	0				
Valid N (listwise)	0				

Table A2.4 Norton Bishopsmill School: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	3	68.21	70.98	69.83	1.448
CLH index	3	68.72	73.06	70.32	2.380
CBH index	2	100.75	102.92	101.84	1.533
FP index	3	72.54	73.68	73.07	.578
TF index	0				
UF index	0				
N index	1	38.18	38.18	38.18	.
O index	0				
MA index	2	110.71	118.97	114.84	5.835
P index	0				
Valid N (listwise)	0				

Although this sample is very small, the description of craniofacial indices is as follows. Later Anglo-Saxon females from Norton Bishopsmill School are medium headed in both length relative to breadth, and height relative to length and breadth. The forehead is broad-medium relative to the maximum cranial breadth and the upper face average-broad. The nasal aperture and orbit are average, and the maxilla is broad relative to its length.

Males are very long headed, with medium-low skulls relative to length, and high skulls relative to breadth. The nasal aperture is narrow, and the maxilla average-broad relative to length.

No further analyses have been conducted on this sample due to the very small sample size for both females and males.

A2.4 Hartlepool Church Walk: craniofacial morphology

Table A2.5 Hartlepool Church Walk: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	5	71.20	80.85	75.96	3.525
CLH index	3	69.63	76.80	72.16	4.019
CBH index	3	91.61	100.00	96.47	4.350
FP index	4	65.03	71.32	68.32	2.791
TF index	2	91.68	93.22	92.45	1.090
UF index	3	52.79	55.70	53.96	1.537
N index	3	46.94	56.28	51.45	4.677
O index	3	76.34	78.57	77.58	1.139
MA index	4	100.00	128.30	110.86	12.375
P index	4	79.01	117.07	92.87	16.717
Valid N (listwise)	2				

Table A2.6 Hartlepool Church Walk: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	8	67.84	85.16	75.73	5.700
CLH index	5	68.88	80.22	74.22	5.029
CBH index	5	93.10	111.85	101.27	7.496
FP index	6	68.28	73.68	70.61	2.070
TF index	4	85.82	94.62	89.64	3.719
UF index	4	51.06	56.15	53.81	2.101
N index	5	44.04	59.18	48.95	5.964
O index	5	71.43	88.89	80.73	6.343
MA index	4	110.53	125.93	117.99	6.706
P index	3	77.55	97.30	85.09	10.666
Valid N (listwise)	2				

Later Anglo-Saxon females from Hartlepool Church Walk are medium-long headed, with medium height skulls relative to both length and breadth. The forehead is medium relative to the maximum cranial breadth, and the face is narrow including the mandible and teeth and average excluding it. The nasal aperture is average and the orbit wide. The maxilla is average-narrow relative to its length and the palate is broad.

Males are medium-long headed with medium skulls relative to length and high skulls relative to breadth. The forehead is broad-medium relative to the maximum cranial breadth and the face is average-narrow including the mandible and teeth and average excluding it. The nasal aperture is average-narrow and the orbit wide. The maxilla is broad relative to its length, and the palate broad-average.

There are no statistically significant differences between females and males, which again may be partially due to the effects of small sex-specific samples. Additionally, although the standard deviations for the indices calculated indicate more male than female variability, the sample sizes for some of the indices are too small for this difference to warrant further consideration.

A2.5 Black Gate, Newcastle: craniofacial morphology

Table A2.7 Black Gate: females

	N	Minimum	Maximum	Mean	Std. Deviation
C index	4	71.98	76.67	74.5957	2.32556
CLH index	2	68.06	72.22	70.1425	2.94114
CBH index	2	89.04	94.20	91.6220	3.64995
FP index	4	63.04	73.57	69.2356	4.82909
TF index	0				
UF index	1	58.62	58.62	58.6207	.
N index	2	48.94	50.00	49.4681	.75224
O index	2	92.31	92.31	92.3077	.00000
MA index	0				
P index	4	67.39	85.71	78.3875	8.50460
Valid N (listwise)	0				

Table A2.8 Black Gate: males

	N	Minimum	Maximum	Mean	Std. Deviation
C index	14	68.72	84.41	73.9223	4.66908
CLH index	8	67.31	74.87	70.5962	2.81138
CBH index	7	84.08	106.72	93.8124	7.08767
FP index	13	63.06	75.18	69.6140	3.73799
TF index	0				
UF index	3	55.68	57.25	56.4541	.78536
N index	7	44.25	50.94	47.2791	2.42610
O index	6	81.25	100.00	88.4689	7.60728
MA index	0				
P index	10	59.62	97.47	79.1990	12.10379
Valid N (listwise)	0				

Later Anglo-Saxon females from Black Gate, Newcastle are long-medium headed, with medium-low skulls relative to length and low-medium skulls relative to breadth. The forehead is medium-broad relative to the maximum cranial breadth and the face is narrow excluding the mandible and teeth. The nasal aperture is medium in breadth and the orbit narrow. The palate is narrow relative to its length.

Males are long headed, with medium-low skulls relative to length and medium skulls relative to breadth. The forehead is medium-broad relative to the maximum cranial breadth and the face is narrow excluding the mandible and teeth. The nasal aperture is narrow-medium in breadth and the orbit medium. The palate is narrow-medium relative to its length.

There are no statistically significant differences between females and males, possibly partially due to the effects of small sex-specific samples, particularly for females. Additionally, although the standard deviations for some male craniofacial indices are rather high, the differences in sex-specific sample sizes mean there is no justification for considering sex-differences further.

APPENDIX 3

VARIABLE-SET COMPARISONS

A3.1 Introduction

In this appendix, variable-set comparisons based on a limited (by virtue of the range of measurements existing for them) set of samples and individuals are presented. The same individuals and samples are used in each test, so as to provide a controlled test of the effect of using different sets of variables. For each comparison, the d^2 matrix, HCA dendrogram and PCO plot(s) are presented. Mantel tests comparing the four d^2 matrices are also presented, to test the magnitude, and significance level, of the associations between them.

Test 1 is based on the eight standard craniofacial variables used throughout this work, comprising GOL, XCB, BBH, BNL, OBH, OBB, NLH and NLB. Test 2 is based on these eight variables, with the addition of one more facial variable, and three more cranial variables, comprising GOL, XCB, BBH, BNL, OBH, OBB, NLH, NLB, ZMB, FRC, PAC and OCC. Test 3 is based on seven cranial (i.e. excluding facial) variables, comprising GOL, XCB, BBH, BNL, FRC, PAC and OCC. Test 4 is based solely on five facial variables, comprising OBH, OBB, NLH, NLB and ZMB.

A3.2 Test 1: Eight standard craniofacial variables

Table A3.1 Biological distance (d^2) matrix derived from the unbiased R matrix

Population	ukeas	uklas	pbd	daner	danlr	danvik	wgs
uklas	0.141912						
pbd	0.214296	0.119069					
daner	0.033304	0.104916	0.283919				
danlr	0.030598	0.178928	0.325113	0.000000			
danvik	0.159469	0.094657	0.131301	0.121115	0.133377		
wgs	0.094950	0.240705	0.273769	0.115767	0.041527	0.043258	
mcia	0.219379	0.177436	0.361498	0.043610	0.159936	0.187221	0.293665

Figure A3.1 Hierarchical cluster analysis dendrogram

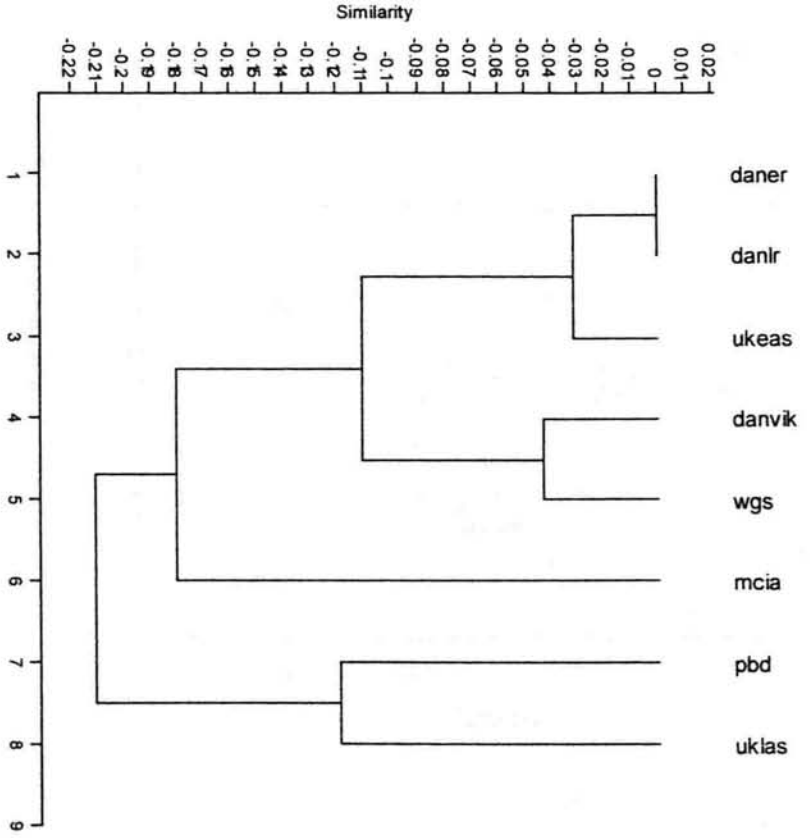


Figure A3.2 Principal coordinates plot: axes 1 (45.5%) and 2 (26.74%)

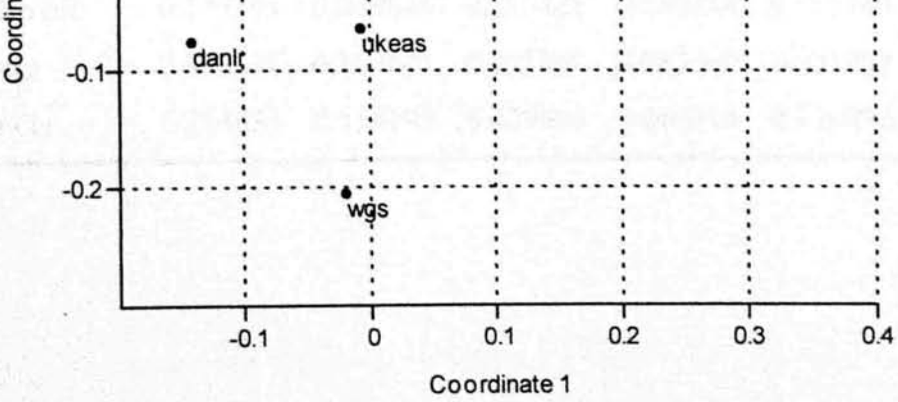
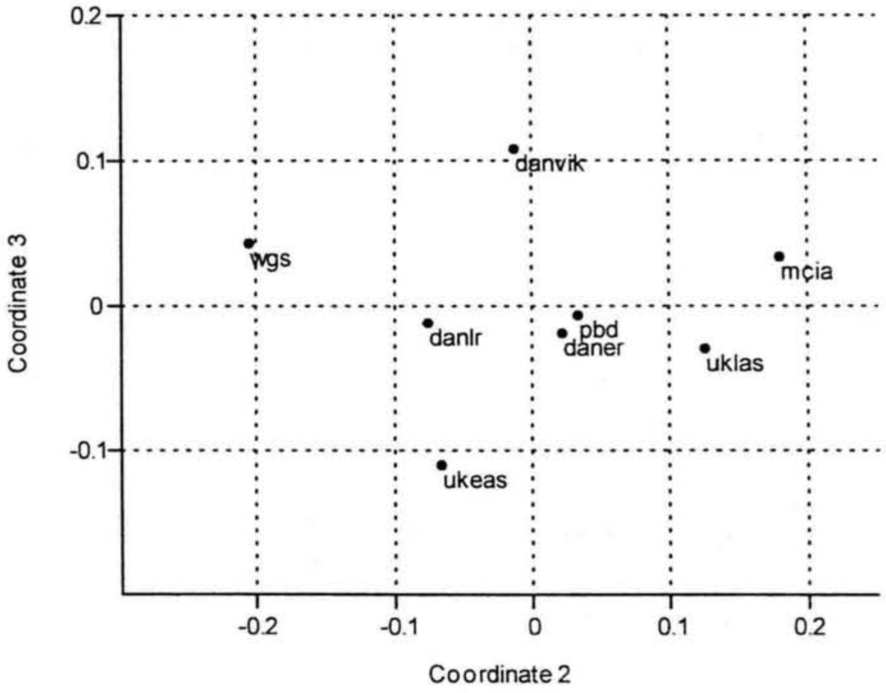


Figure A3.3 Principal coordinates plot: axes 2 (26.74%) and 3 (7.33%)



A3.3 Test 2: Twelve craniofacial variables

Table A3.2 Biological distance (d^2) matrix derived from the unbiased R matrix

Population	ukeas	uklas	pbd	daner	danlr	danvik	wgs
uklas	0.116663						
pbd	0.185435	0.184605					
daner	0.023979	0.077132	0.242543				
danlr	0.062863	0.154061	0.338656	0.000000			
danvik	0.139343	0.049634	0.215421	0.089024	0.127263		
wgs	0.098631	0.162841	0.311867	0.082309	0.041793	0.020413	
mcia	0.244033	0.154193	0.429943	0.066911	0.110870	0.159263	0.218666

Figure A3.4 Hierarchical cluster analysis dendrogram

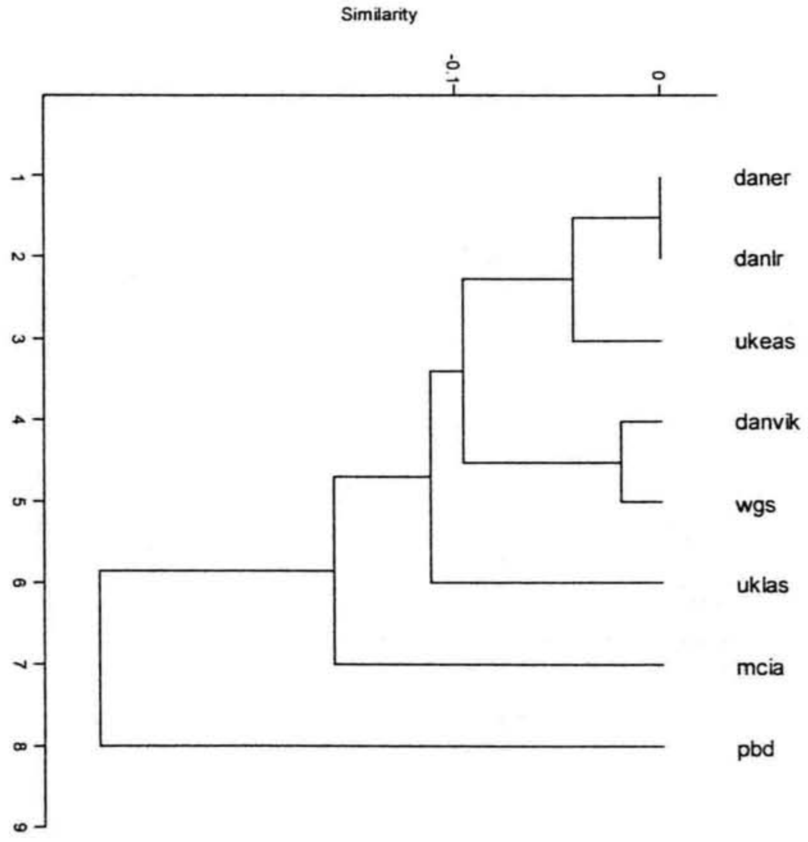


Figure A3.5 Principal coordinates plot: axes 1 (57.83%) and 2 (14.79%)

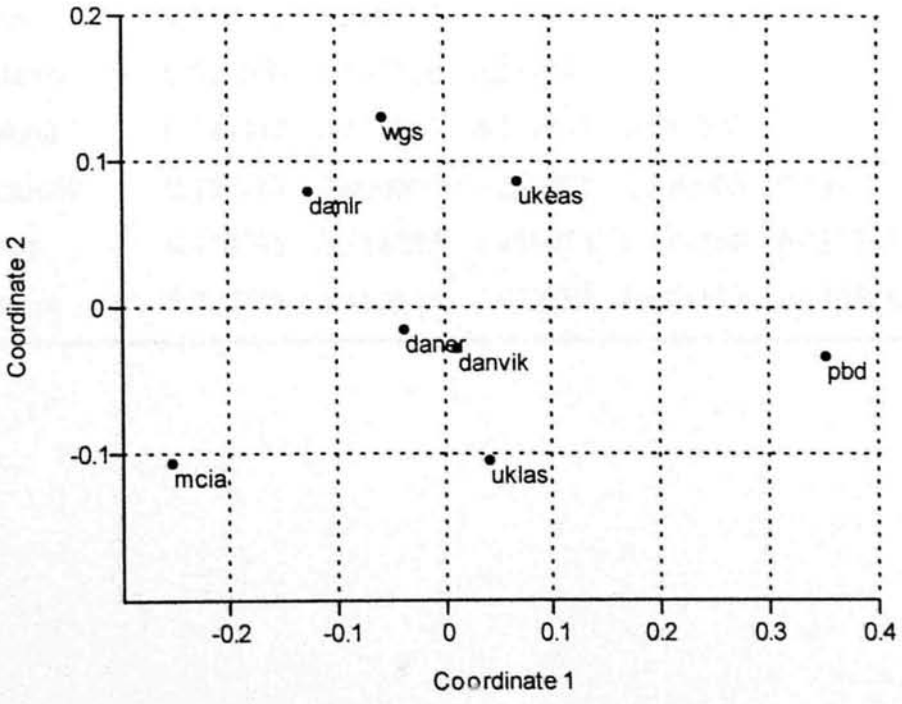
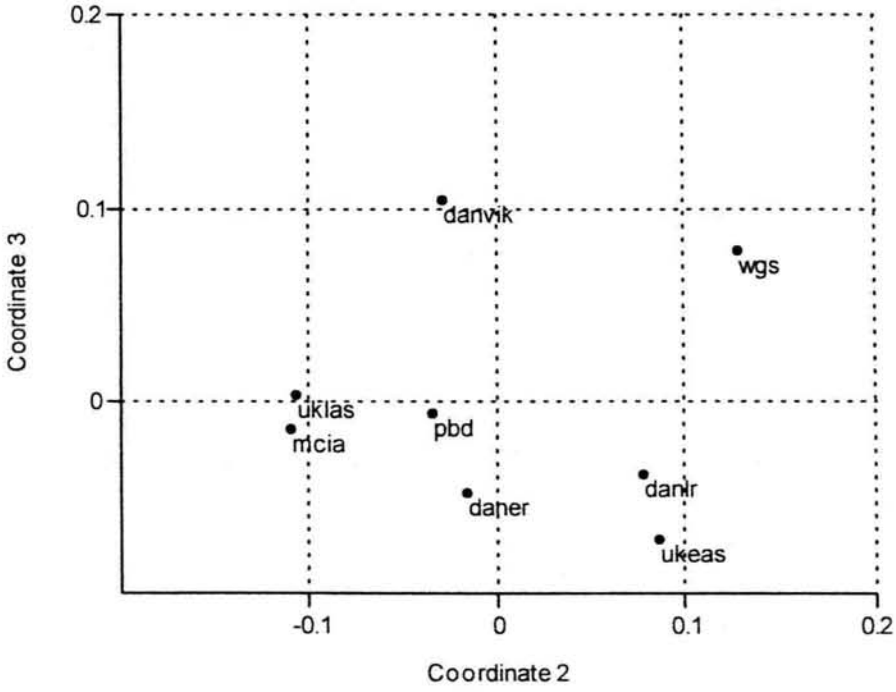


Figure A3.6 Principal coordinates plot: axes 2 (14.79%) and 3 (6.94%)



A3.4 Test 3: Seven cranial variables:

Table A3.3 Biological distance (d^2) matrix derived from the unbiased R matrix

Population	ukeas	uklas	pbd	daner	danlr	danvik	wgs
uklas	0.145557						
pbd	0.337141	0.200722					
daner	0.021650	0.137920	0.341291				
danlr	0.144344	0.255241	0.577472	0.000000			
danvik	0.181269	0.000000	0.256991	0.099005	0.184230		
wgs	0.128098	0.114557	0.456274	0.017238	0.031343	0.032443	
mcia	0.221888	0.153845	0.478183	0.074142	0.050588	0.062051	0.014222

Figure A3.7 Hierarchical cluster analysis dendrogram

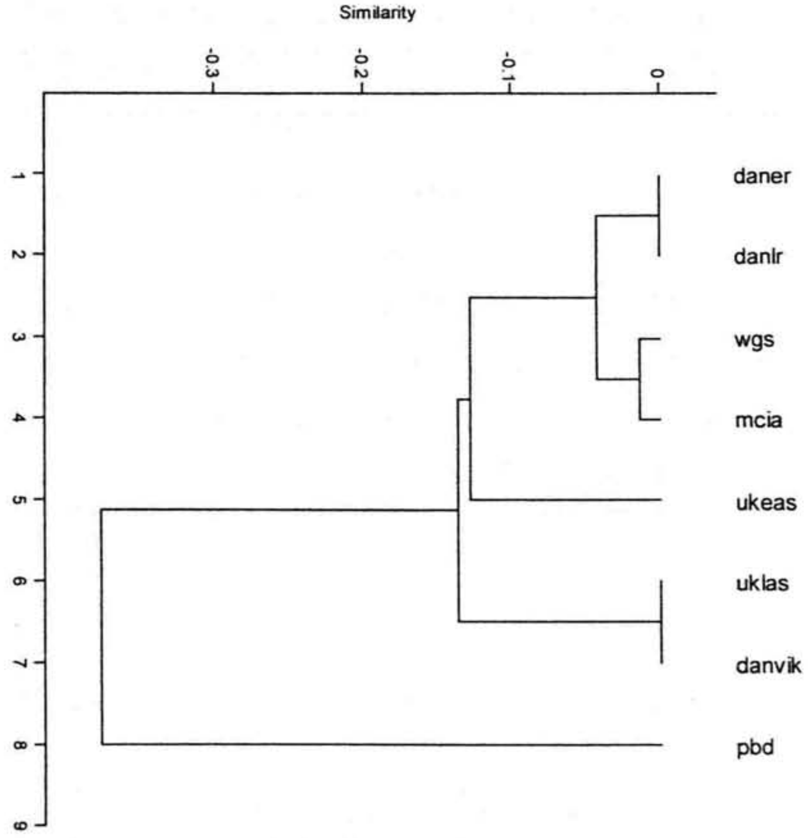
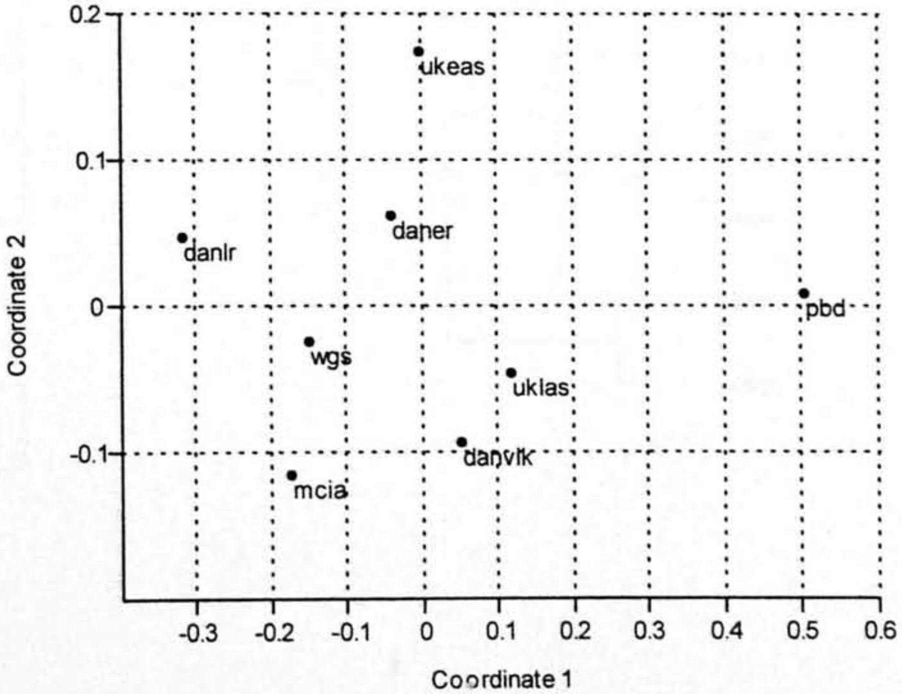


Figure A3.8 Principal coordinates plot: axes 1 (67.32%) and 2 (9.61%)



A3.5 Test 4: Five facial variables

Table A3.4 Biological distance (d^2) matrix derived from the unbiased R matrix

Population	ukeas	uklas	pbd	daner	danlr	danvik	wgs
uklas	0.093841						
pbd	0.011461	0.152493					
daner	0.037637	0.001404	0.149087				
danlr	0.012073	0.058858	0.072423	0.016371			
danvik	0.097227	0.148657	0.230113	0.079498	0.061548		
wgs	0.111568	0.242820	0.181564	0.190130	0.083271	0.000000	
mcia	0.208724	0.133678	0.379354	0.031159	0.168895	0.332929	0.489313

Figure A3.10 Hierarchical cluster analysis dendrogram

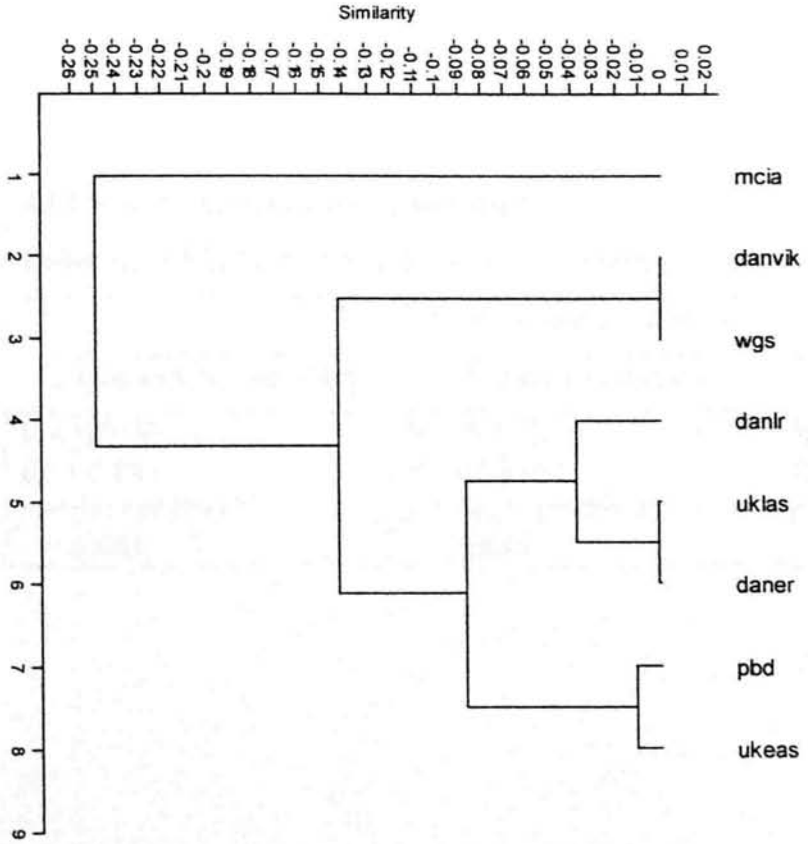
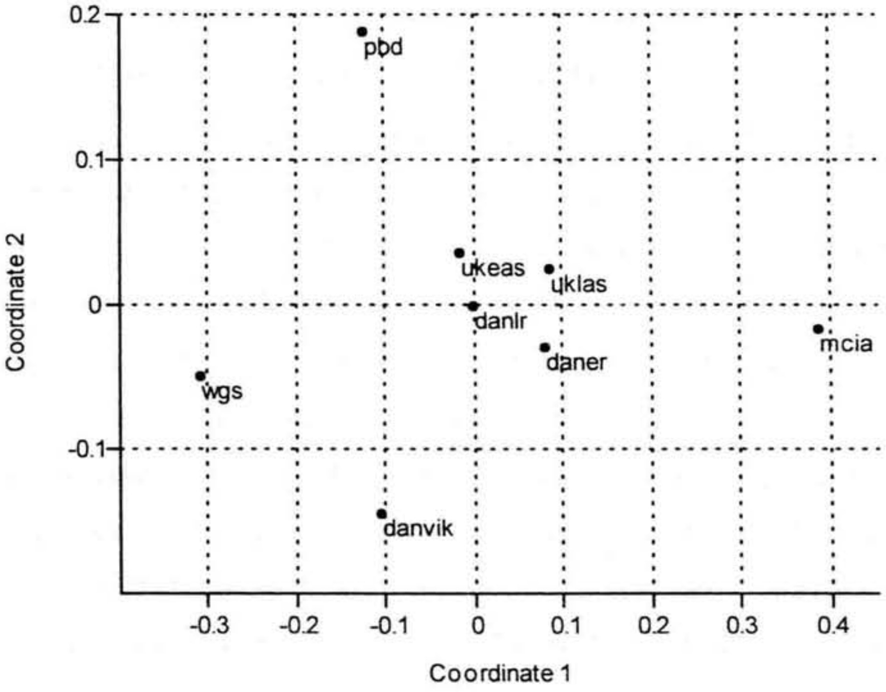


Figure A3.11 Principal coordinates plot: axes 1 (59.05%) and 2 (12.8%)



A3.6 Mantel matrix correlation tests

Table A3.5 Mantel test results: d^2 from alternative variable sets

8 craniofacial variables		
12 craniofacial variables	7 cranial variables	5 facial variables
$R = 0.9193$ $R^2 = 0.8451$ $p = (0+1)/(999+1)$ $=$ **0.001**	$R = 0.7171$ $R^2 = 0.5142$ $p = (42+1)/(999+1)$ $=$ **0.043**	$R = 0.6252$ $R^2 = 0.3909$ $p = (48+1)/(999+1)$ $=$ **0.049**

APPENDIX 4

DATA

The complete raw dataset collected for use in this research has been included in the back of this thesis on compact disk. It is hoped that the availability of these data will encourage further craniometric research to be done.

Data are included for all adult individuals of known sex (for the purpose of this research probable females and probable males were recoded as female and male respectively) for which data were collected in the course of this research, irrespective of whether they were included in the analyses conducted here. For some samples, data which may have originally been collected for sub-adults and for unsexed individuals have not been included, although they are available from the author.

Details not included in the dataset, including further data and details regarding each sample, may exist, and potential users of this dataset should refer to the sources referenced in Chapter 3 of this thesis.

Details regarding the provenance of individual samples are provided in Chapter 3, section 3.3.3 of this thesis, and details regarding the measurements are provided in Chapter 3, section 3.4.

The SPSS data document (*.sav) file included has been created in SPSS 11.0, using a Sony Vaio PCG-FX502 laptop, and Windows XP Home Edition. It can be accessed by inserting the CD into a CD drive, and double-clicking on the icon entitled **'Data'**.

Additionally a copy of this page, created in Microsoft Word (*.doc), has been included for reference. It can be accessed by double-clicking on the icon entitled **'Appendix 4 – data'**.