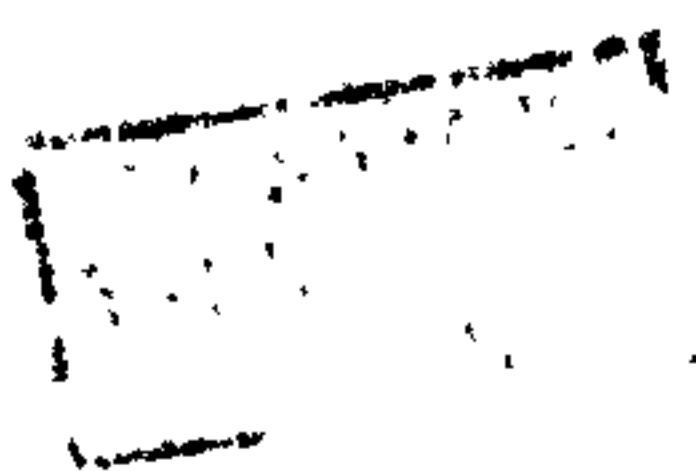


**The Biological Affinities of Several
Romano-British and Anglo-Saxon
Populations
as Shown by Dental Morphology**

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ABSTRACT

The aim of the research presented in this thesis is to test the applicability of some of the techniques of dental anthropology to begin to provide answers to certain questions facing British archaeology. The question directly confronted in this thesis is how the change in fifth century Britain, manifested by a change in cultural material from archaeological sites, came to pass.

The transition from the Romano-British period to the Anglo-Saxon period in the country now known as England is often assumed to have occurred as a result of invasions from people known as Angles, Saxons and Jutes. A common belief is that these Continental invaders wiped out the local population. The resultant replacement of the earlier culture with a 'Germanic' culture is due to these invasions. The competing hypothesis is that of biological continuity with cultural replacement. Either of these hypotheses can be supported when one examines only cultural aspects of the populations. Pottery, clothing, building and burial styles, as well as the history of the English language, have all been used to support versions of both hypotheses. It is at least theoretically possible for all of these cultural trappings to change without any biological contribution from an outside source. To ascertain which hypothesis more accurately describes the events of the fifth century in Britain, one must first know how the populations from the later period are related to those from the earlier period. To do that, one must assess the biological profiles of each population and compare them.

The remains of a total of 799 people from seven sites dated to the Romano-British and Anglo-Saxon periods are evaluated using the Arizona State University Dental Anthropology Scoring method. Six of the sites were chosen in pairs, one from the Romano-British period and one from the Anglo-Saxon period in each pair, in order to test for continuity or discontinuity across time. The site pairs were spread across Southern England to test for changes across geography. Several statistical methods are used to explore the data. The results of two different distance measures shows that people buried in Anglo-Saxon sites are closely related to people buried in nearby Romano-British sites. These results clearly support the hypothesis of biological continuity in the face of cultural change.

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Dedication

*To my parents, Jean and Richard
and my wife Kari*

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1 CHAPTER 1 INTRODUCTION

1.1 BACKGROUND

This research has been aimed at determining the feasibility of using dental non-metric traits to assess biological distances among Romano-British and Anglo-Saxon populations in Britain. Understanding these distances in quantifiable terms will allow us to shift the focus of research away from theories of whether a given cultural change was caused by biological replacement, or happened in spite of continuity, and toward other aspects of the transition from the earlier period to the later period. These other aspects include changes in the styles of clothing, housing and land exploitation as well as the development of language. The current lack of understanding concerning the biological relationships among these groups leaves us in a situation where the causes for these changes are, for lay people and many scholars, merely a matter for relatively uncontrolled speculation. By providing a clearer picture of the total biological contribution needed to affect cultural change it should be possible to construct new models that use biology as a constraint to speculation rather than as a speculative variable. This study also provides a chance to add to the body of information on dental morphology in Europe which is an area that is underrepresented in the dental anthropology literature (Scott and Turner, 1997:269).

The starting point for the development of hypotheses is to construct models that are simplified explanations for how change came about but are not necessarily specific to any one period or place. Two basic, commonly used models for the explanation of cultural change in Anglo-Saxon studies are the invasion model and the continuity model. In the most extreme and simplified version of the invasion model, the entire indigenous population is assumed to have been killed or driven out by an invading group. Under a similarly stripped-down version of the continuity model, one assumes that the local population found it expedient, for undeclared reasons, to adopt the culture of another population but continues to live in essentially the same area. By studying only the cultural trappings of the people involved, the imposition of a new culture, assuming it constitutes a complete overhaul, would have essentially the same appearance to an archaeologist if it were the result of an invasion or the more gentle process of cultural contact. The differences between the two processes would be seen only if the amount of time needed for the transition could be appreciated archaeologically.

Most of the evidence currently used to support the competing hypotheses of invasion and continuity comes from scanty historical accounts which were usually written long after the events took place, cultural material derived from archaeological settings, or a mixture of both. These hypotheses also include some implicit assumptions of the origins of the populations under study. The problem is that an accurate knowledge of the ancestry of the people involved – derived independently of the other sources -- is missing. Without this knowledge, the ascendancy of one of the hypotheses over the other is as likely to be due to social pressure as to careful evaluation of the evidence. The preference for the invasion hypothesis or the continuity hypothesis as an explanation for the transition from the Romano-British to the Anglo-Saxon period often depends on the political pressures or societal sensibilities of the day (Arnold, 1997:31-32).

The approach used in the current study focuses on the biological traits of the people found in cemeteries dated to these two periods at both the individual level and the population level. Through the use of statistical analysis of the recorded biological traits it should be possible to begin to unravel the question of who lived in Britain during these times, though not of their ultimate origins. In either case, the ultimate origins of the British populations are on the European Continent. If it can be established that the people who lived in Britain during the Anglo-Saxon period were substantially different from those in the Romano-British period, then the search for ultimate origins should probably turn to Continental sources from the fourth century. If the populations of the two periods are shown to be substantially the same, the Continental search should focus on earlier groups.

It cannot be emphasised strongly enough that a person's cultural identity is not determined by his or her biological lineage. Consider, for example, a situation where a child is born in China, to Chinese parents, and is then adopted by American parents of European origin. It is safe to assume that the child will display the physical attributes of his biological parents while displaying the cultural attributes of the adoptive parents. The cultural environment in which he is reared will determine his language, accent, choice of clothing, diet and all other cultural trappings. To assume that he would grow up speaking Chinese in an English-speaking household without special language instruction, would be resorting to biological determinism. This is equally true for the statements that classify a group of people as a "formidable race of pirates" (Green, 1916:6), who are "warriors born" (Robinson, 1927:27). An inclination toward militarism or general violence is not genetically inbred, merely culturally imposed.

It will be argued in this thesis that one must have a clear idea of the biological relationships of the populations under examination before one can begin to understand any perceived changes in culture found in archaeological settings before and after the cultural change took place. This does not require tracing the ultimate origins of the groups involved. It merely requires one to assess whether a biological change accompanies the perceived cultural change. It will be further argued that dental nonmetric traits can be an important tool in the armamentarium of anthropologists and archaeologists when trying to understand these changes.

This research assumes that a person's cultural identity and biological identity are separate issues and must be dealt with accordingly. The cultural material from the Romano-British and Anglo-Saxon periods, excavated at archaeological sites can be used only to make judgements on the cultural identity or 'ethnicity' of the people who lived in the area now known as England. Any statements concerning the biological origins of the people involved in these cultural changes should be based on an understanding of their biological relationships.

This study uses some of the techniques of physical anthropology to assess the biological affinities of three populations from the Romano-British period and four populations from the Anglo-Saxon period. To explain the biological evidence it will be necessary to delve into several areas of anthropology, developmental biology, dental research and statistics. To explain why the biological evidence is important to Anglo-Saxon studies, some discussion of several aspects of archaeology, history and sociology will be undertaken. It should also be pointed out that the terms 'Romano-British' and 'Anglo-Saxon' are used throughout this study to refer to people identified by cultural material. When used in reference to specific sites, the designation is that which was given by the excavator. The use of these labels should not be construed as a biological identification.

Obviously, this research was not conceived in a vacuum. The remaining sections of this introduction will outline some of the issues that led up to this project. Section 1.2 is titled The Invasion v. Continuity Debate in History and Archaeology. It serves as an introduction to the historical and archaeological arguments surrounding migration theories and some of the evidence used to support both points of view. Section 1.3 provides a discussion of the problems of understanding race and ethnicity and how these terms are used in this thesis. It also gives a brief history of physical anthropology and how it has been used and misused over the years. Chapter 2, Materials and Methods, is divided into nine sections. Section 2.1, Hypothesis Testing and Design of Research Models, describes the hypothesis to be tested in this thesis.

Subsequent sections of this chapter discuss genetics as it applies to dental anthropology, background and a discussion of the methodology of the Arizona State University Dental Anthropology Scoring Method. There is also discussion of some of the other applications of dental anthropology. A discussion of some of the problems of cemetery demographics and a description of the sites used in this study follow that. Another section (Data Recording and Archiving) describes the methods used in collecting and recording data, which includes the programming of a database system to archive the data. The last section of this chapter (Statistical Methods) is further subdivided into population level statistics and Individual Level Statistics. The section on population level statistics includes discussion of some of the statistical methods most commonly used in dental anthropology. The section on individual statistics takes the exploration of the data one step further than most studies by examining the individuals who make up the population.

Chapter three provides the results of the analyses discussed in chapter two. The sections are divided in the same order as the descriptions in chapter two. The conclusions derived from this study are presented in chapter four. Suggestions for further possible research that may help to clarify certain issues that could not be adequately addressed in this work are presented in chapter five.

1.2 THE INVASION V CONTINUITY DEBATE IN BRITISH HISTORY AND ARCHAEOLOGY

There are several models that have been developed in an attempt to explain the different types of change seen in different places in the world at different times in the past. The two models that are usually invoked to explain the changes that took place from the Romano-British period to the Anglo-Saxon period are often referred to as the 'Invasion Hypothesis' and the 'Continuity Hypothesis' (e.g., Higham, 1992; Higham, 1994; Welch, 1992). The extreme version of the invasion hypothesis, which may also be called the extirpation theory (Hodgkin, 1906:11), envisions total replacement of the indigenous population. This hypothesis would normally be presented as a bloody massacre where a warrior band kills or drives out most of the people who had been living in a given location. The result is a new gene pool, and probably a different culture and language. The continuity hypothesis posits a more gradual process where change may be attributed to a combination of biological and cultural evolutionary processes. The impetus for change may, or may not come from outside of the local group, but in either case, the links from the earlier time to the later time can be discovered if one looks closely enough. Often it is suggested that a

small band of outsiders dominated the locals by force, cunning or some other way and became their rulers. In the case of the Romano-British to Anglo-Saxon transition, this hypothesis may be envisioned as the simple application of “a superficial veneer” of language and other cultural trappings by a “conquering elite on a British population that remained basically in place” (Myres, 1986:22). The tone of this characterisation of the continuity hypothesis was probably meant to be pejorative, it is as good a way as any of summarising it.

The two hypotheses as they are presented above are stated as if they represent the only choices. The truth of the matter for the transition to Anglo-Saxon Britain is probably a combination of elements from both extremes with gradations, depending on the location and the time of transition (Arnold, 1997:31). Although there are probably no serious archaeologists working today who use the extreme versions of the two hypotheses to explain the changes that took place during the transition period, they can serve as starting points for analysis and be modified as information dictates.

Questions about the reliability of the evidence to support the complete elimination of the indigenous populations as portrayed in traditional accounts date back to at least the 1870's. This was when Lord Macaulay suggested that the logistics of moving enough people from the continent to repopulate what, by then, had become England after the original ‘invasions,’ were too cumbersome to be creditable (Macaulay, 1871). The debate continued in the 1880's with Seebohm's arguments about the English village community (Austin, 1990), in which Seebohm argues that the Anglo-Saxons inherited tribal and manorial systems already in place.

Historically, the archaeological understanding of human population movement has focused predominantly on cultural artefacts retrieved from archaeological sites rather than biological traits of the individuals involved in the movements. Archaeologists have tended to confuse affinities of material culture with affinities of a biological nature and assume that the artefacts truly reveal the biological origins of the people with whom the artefacts are buried. There is archaeological evidence that some settlements such as Feddersen Wierde and Wijster were abandoned in the fifth century (Laing and Laing, 1979; Myres, 1986). The traces of culture found at these sites correspond with materials found in British sites such as Mucking (Myres, 1986). On the other hand, the people who abandoned the villages did not necessarily go to live in Britain. Furthermore, those who did migrate to Britain were probably not confined to the neat, homogeneous groups implied by the presentation of evidence cited above. “Yet it remains a tacit assumption among most archaeologists and all

historians that the bulk of the dead in these cemeteries consisted of coherent groups of Germanic-speaking migrants, distinct from others” (Austin, 1990:17).

The popularity of one hypothesis over another has shifted as the political needs of society shift and will continue to do so until there is an objective test of an individual’s origins (Arnold, 1997:31-32). The increased popularity of the continuity hypothesis in Britain coincides with the conclusion of World War II (Arnold, 1997; Härke, 1998). This has been attributed to a desire to distance contemporary Britain from any relationship with Nazi Germany. Conversely, German archaeologists still prefer the explanations offered by the invasion hypothesis (Härke, 1998:19). Others have raised the possibility of reintegrating migration theory into explanations of change in various parts of the world (Anthony, 1990; Anthony, 1992; Härke and Wolfram, 1993).

Arguments have been made in favour of both positions, using historical accounts and archaeologically derived cultural material. The historical material is largely built upon sources that fall into three categories. The first is near contemporary sources from the Continent. These include Zosimus, Constantius and Prosper Tiro. The next category is that of the slightly later ‘British’ sources such as Gildas and Ninnius. The last category is ‘English’ historians who wrote at even greater remove from the events that they describe. This last group includes the Venerable Bede and the various authors of the Anglo-Saxon Chronicles.

Prosper Tiro gives the “only contemporary evidence” of the “Saxon invasions” (Hodgkin, 1906:82). He mentions a sickness that wasted the strength of the Romans, and later, about A.D. 441, that Britain had been “brought under the dominion of the Saxons” (Hodgkin, 1906:82). The Byzantine historian Zosimus, who was writing in the sixth-century (Myres, 1986:7), marks the collapse of Roman rule in Britain as a revolt of the natives (Hodgkin, 1906:83). The last of the early continental writers to be mentioned here is Constantius who wrote the Life of St. Germanus in about A.D. 480. Along with the story of the famous ‘Hallelujah’ battle, Hodgkin notes that this book describes the situation in Britain when Germanus came to Britain as a missionary. He states that there were natives who were still wealthy enough to have the time to learn about, and debate theological matters (Hodgkin, 1906:85; (Myres, 1986:8). The general impression of these writers given by Hodgkin is that everything they wrote should be only minimally trusted due to their physical distance from events, and a general lack of scholarship (Hodgkin, 1906:82).

The next group of historians were the “descendants of the conquered” (Hodgkin, 1906:82). Ninnius lived in South East Wales during the mid- to late-eighth

century. His book, *Historia Brittonum*, was completed in about 796. Much of this book seems to be a muddle of events and mythology that do not compare well with other histories or even with events described elsewhere in the book (Hodgkin, 1906:101). The British author whose work is taken much more seriously and has had much greater impact on Anglo-Saxon studies even up to the present day is Gildas. He was a monk who was probably born in Scottish Strathclyde during the early-sixth century. His book, *De Excidio et conquestia Britanniae*, was written in the middle of that century and was, therefore, more nearly contemporary with the events than was the work of Ninnius. *De Excidio* is essentially a long diatribe informing readers that the invasion by the Anglo-Saxons and the havoc they caused was brought about by the sins of the British people (Hollister, 1988:20; Stenton, 1947:31). He is given credit as the source for the dates of the appeal to Rome from the British for help against the Picts, and for the approximate date of the *Adventus Saxonum* in Britanniam (Myres, 1986:8).

The last group to be considered is that of the 'English' writers: Bede and the authors of the *Anglo-Saxon Chronicles*. Bede was an English monk, some say 'Saxon' (King, 1930:xx) who lived in Northumberland from 672 or 673 until about 735. He wrote many books, but his most famous was *Historia Ecclesiastica Gentis Anglorum*, which is perhaps better known as the *Ecclesiastical History of the English People*. The *Ecclesiastical History* was completed in about 731 (Marsden, 1996:25). As Bede was writing some 300 years after the events he was describing, he depended heavily on the work of Gildas, among others, even while decrying *De Excidio* as a "tearful discourse" (Hodgkin, 1906:95). He is credited with the first mention of the names of the British King, Vortigern and the names of Hengest and Horsa (Hodgkin, 1906:86).

The *Anglo-Saxon Chronicles* were first compiled in the late ninth century (Hollister, 1988: 20), probably under the direction of King Alfred (Myres, 1986:4). The *Chronicles* record 'important' events and the lives of 'important' people. This has the effect of placing great emphasis on the aspects of history that have very little to do with the majority of the population. To a certain extent, this complaint could be made of almost any history, but the format of the *Chronicles* seems to encourage the reader to accept the entries as the only events that happened during those years, even though other things obviously did happen. This may not be all bad however, as it does provide some insight as to how the elite viewed themselves. The episodic nature of the *Anglo-Saxon Chronicles* forced the authors to divide the entries somewhat arbitrarily into four-to-eight-year cycles (Hodgkin, 1906:87; Myres, 1986:4-5) which

has led some to discard all but the parts that are most readily verified by comparison to other documents.

The overall impression left by the reports of the authors cited so far in this discussion of historical accounts is that the early histories are not very reliable and should be used with great caution. For example, Prosper Tiro is called a “dull and second-rate writer” (Hodgkin, 1906:82), and Ninnius is described as being an “ill-informed and uncritical scribe” (Hodgkin, 1906:101). Given these feelings about the documentary evidence, it is almost surprising that they should play any part in modern explanations of the Romano-British to Anglo-Saxon transition. There are those, on the other hand, who argue that because these histories were written in much greater proximity to the events than the interpretations of archaeological material, they should not be discarded lightly (Welch, 1992:11).

Regardless of how one views the worth of historical accounts, the fact remains that they have been used to formulate many of the ideas that control how archaeologically derived information is interpreted. In many cases, archaeology is treated as being subservient to history (Austin, 1990; Austin and Thomas, 1990). Much of the work by early archaeologists seems to have been designed to fill in the gaps left by the historical record. Leeds (1913) states that we know that the human remains recovered from ‘Anglo-Saxon’ graves are, indeed ‘Anglo-Saxon’ because, in “the first place, the graves containing the relics usually known as Anglo-Saxon are only found within the limits of the districts which history designates as the scene of the early activities of that race” (Leeds, 1913:24). The theoretical basis for classifying sites as Anglo-Saxon is, as demonstrated by this statement, a self-fulfilling prophecy (Austin, 1990:16). Medieval archaeology, it seems, is still controlled by the “tyranny of the historical record” (Champion, 1990:91).

Such is the impact of the historical explanations of the transition period that if one were to conduct a survey of the general population today, a fairly high percentage of people would probably relate their understanding of the transition in much the way Birley stated the situation in 1979:

“Britain was now outside the empire, permanently as it transpired, because its inhabitants had thrown out the Roman officials – presumably those of the usurper- in AD 409. Roman rule effectively ended in that year. What followed was ‘sub-Roman,’ the age of Arthur, and the arrival of the peoples *who became the English.*” (Birley, 1979:11 emphasis added)

Implicit in the last sentence of this statement is the tacit support of Bede’s assertion that the invaders came to Britain and the indigenous population was forced

out of the country or was “killed in heaps” (King, 1930:75). In other words, Bede states that it was the people who arrived who became the English, not the natives, or a mix of native and invader. Another example of the opinion that the inhabitants of what is now England during the Romano-British period did not survive in great numbers is seen in Hodgkin (1906). He states that “we have dwelling close beside us and mingling their blood with ours a gallant little people who own no descent from the Anglo-Saxon invaders” (Hodgkin, 1906:1), thus showing that he clearly believed that most people in early twentieth-century England were descended from the Anglo-Saxons. “For much of the first half of the 20th century British archaeologists felt themselves under strong compulsion to ascribe every change, every development to overseas influences of one kind or another” (Clark, 1966:172).

The transition period is often dealt with very quickly in books that are concerned with the origins of Anglo-Saxon society. Green (1916) devotes ten pages (plus a map) to the years 449-577. It is a fairly poetic description of the invasion of Britain by the people from Angln. His description reaches an almost religious fervour when he claims that “no spot in Britain can be so sacred to Englishmen as that which first felt the tread of English feet” (Green, 1916:7). In some ways, the historical evidence can take on an almost mythic quality, which is appropriate as many of the stories are based on myth. Most authors seem to feel obliged to mention the name of Arthur in their historical accounts and give some justification as to why they do, or do not, consider him to be a real historical figure (e.g., Ashe, 1971; Green, 1916; Hollister, 1988; Stenton, 1947). The theme of invaders arriving in three long ships shows up in several places in relation to various leaders other than those referred to by Bede.

More recent writers have been more academic in their prose, but still maintain their support of Bede’s accounts of invasions. Welch (1992) devotes eight pages to the transition, Hollister (1988) and Blair (1984) give it four pages each. While each of these authors point out that there is debate over continuity or invasion, they all tend to return to invasion as the more creditable alternative. Hollister, for example, suggests that the evidence of continuation of Romano-British occupation of Verulamium throughout the sixth century may be due to the possibility that the Anglo-Saxon invasions had simply not reached that far until the seventh century (Hollister, 1988:27).

Written records of the transition period are scant. This lends support to the idea that the literate culture that had been present in the British Isles all but disappeared and a new, mostly illiterate culture replaced it (Myres, 1986:4). The lack

of written records may simply be due to a decrease in the size of the group who formed the literate core. The simple existence of *De Excidio* by Gildas suggests that Latin was still being used by some people 150 years after the invasion was said to have occurred (Hollister, 1988:20). By the end of the sixth century, the histories tell of a land in which the rulers lived "on the spoils of their neighbours" while their dependants and "the surviving remnants of the British population" were turning to subsistence agriculture (Myres, 1986:2). What we do not know is how that change came about. The time between the end of Roman governance of Britain and the beginning of the seventh century is the most obscure portion of British history. As Myres puts it, the time remains "a void of confusion" (Myres, 1986:1).

While it is reasonable to have a research paradigm (Kuhn, 1970; Smith and Harrold, 1997) it should be one that allows advancement of knowledge, not simply confirmation of what is assumed to be fact. It may be tempting to use documentary evidence to fill in details of the people who lived in the archaeological contexts that are uncovered (Binford, 1983), but archaeology must ask its own questions rather than simply respond to the needs of historians. The questions must be framed in such a way that the evidence from archaeological sites can answer them.

When basing a hypothesis on cultural material there is a danger of neglecting the fact that cultural change can follow a very different course from biological change. People can move from one place to another and take their ideas with them (demic migration) or, change may be due to cultural migration (sometimes called diffusion) where ideas and material goods spread without biological exchange taking place (Cavalli-Sforza and Feldman, 1981). Diffusion, in this sense, should not be confused with 'Diffusion-ism'. The Diffusionists, such as Grafton Elliot Smith, "argued that culture and technology were invented once and were later transmitted throughout the globe" (Barkan, 1992:39). The process of cultural diffusion is merely one of the ways that culture can be transmitted and can help explain some of the similarities seen in different parts of the world. Diffusionists particularised culture and technology, studying the development of each invention in its own right rather than as part of a whole process (Barkan, 1992:39-40).

These two types of migration (demic and cultural) reflect the types of transmission defined by Cavalli-Sforza and Feldman: Vertical, Horizontal and Oblique. Vertical transmission is seen when a trait is passed from a parent to child. Horizontal transmission is seen when the trait is passed from one person to another person of the same generation who may, or may not, be related. Oblique transmission refers to a trait being passed from one generation to the next as with

Vertical transmission, but to someone who is unrelated as with Horizontal transmission. Horizontal and Oblique transmission are similar in that neither form, as defined here, allows a genetic contribution from the donor to the recipient, the only real difference between Horizontal and Oblique transmission is that Oblique transmission crosses generations and Horizontal transmission does not. As the current analysis does not make a distinction between the generations of the individuals found in cemetery populations, the differences between the concepts of Horizontal and Oblique transmission do not matter and can be treated as if they are synonymous. Cultural change can be achieved by any of these three methods of transmission (Jones, 1992:399). Biological change is strictly vertical, i.e. from parent to offspring (Cavalli-Sforza and Feldman, 1981:54).

It seems reasonable to assume that the precursor to Modern English had been introduced to Britain, and had begun the process of modification into the language spoken today by the middle of the fifth century (Laing and Laing, 1979; Myres, 1986). There is no way to know for certain that this was the time it was introduced, but there is no advantage to be gained for this study by arguing over whether it arrived shortly before or after this time. What is important is that the arrival of a new language is often taken as a sign of the arrival of a new gene pool (i.e., an invasion). The idea that 'race', language and culture are "different manifestations of...one inherent entity" (Barkan, 1992:19) has diminished over the years to the point where few, if any, researchers would be willing to assert that shared language is 'proof' of genetic relationship. The study of how languages spread is very interesting in its own right, and comparisons of linguistic, genetic and phenotypic data are useful in building pictures of how groups may have moved and interacted over time, but linguistic change should never be equated with genetic change. With this warning in mind, it can be useful to explore the models used to explain linguistic change. These models are quite similar to models of genetic change and can be used at least as analogies for the process of biological change.

Renfrew (1988) provides several examples of reasonable models for linguistic change. These models reflect those of cultural change rather than biological change. They are identified as Initial Colonisation, Replacement and Continuous Development. The first two models (Initial Colonisation and Replacement) have similarities to the model of invasion used in the current study. The last model, Continuous Development, is most similar to the continuity model and may also be explained as Evolution in situ.

Renfrew's Initial Colonisation model is used to explain situations where the linguistic evidence suggests that the population being studied was the first group to appear in a region. A study of the languages of Native American groups would, in most cases support Initial Colonisation. If one were to compare the results of studies of initial colonisation shown by language with studies of the biological traits of those same people, there is a high probability that there would be a high correlation between the level of differences in the cultural traits and the differences in the biological traits. Indeed, there have been studies of Native American groups that show reasonably high correlations between language, dental nonmetric traits and serological traits (Greenberg et al., 1986; Sofaer et al., 1972). This model does not apply to the current study, however, because we know without doubt that the Anglo-Saxons did not move into a virgin landscape.

The Replacement model is such that one group displaces another either physically, politically or both, allowing the new language to become dominant (Renfrew, 1988). We see examples of this type of linguistic change later in the history of the Americas, for instance, where English, French, Spanish and Portuguese have all but wiped out the indigenous languages. The Replacement model is similar to the most extreme version of the invasion hypothesis as defined in this thesis—mass destruction of an existing population, resulting in total replacement. Archaeologically it would be seen as an abrupt change in the cultural evidence, a discontinuity from one time period to the next indicated by substantial change in the cultural materials found. In a biological context, one would expect to find distinct differences in the morphological features of the skeletons found in that location.

Continuous Development is described by Renfrew as language change due, in part, to interactions between two groups. The groups gradually develop a common language, a pidgin or creole, to facilitate communication. Material culture and biological markers may change over time, but the commonalities from one time period to the next can be clearly identified. The Continuous Development model of language development is analogous to the continuity hypothesis as defined in this thesis.

The incidences of saucer brooches, chevron and dot patterns, and zoomorphic designs that are seen in both continental and British contexts argues for extensive contact, but it does not give proof of biological change. As Hills (1990) points out, "the Japanese television in many British homes does not prove we are Japanese" (Hills, 1990:51). Similarly, a Japanese cemetery filled with men wearing western-style clothing, known as sebiro, would not lead one to conclude that they

were actually English. This is true even if one had the linguistic evidence that *sebiro* was a corruption of Savile Row (Bryson, 1990:184). Esmond Cleary takes a different approach to interpreting the data. He sees the decline of Roman life-ways as being the factor that led to the abandonment of villas and cities, not an influx of invaders from the continent. The decline of the Roman systems and subsequent removal of centralised government and the ending of the money-based economy meant that the specialist crafts, such as pottery, weaving and metalworking, could no longer be supported (Esmonde Cleary, 1989; Hollister, 1988). Esmonde Cleary cites several examples of villas that showed evidence of lower-intensity use in the fourth century. These sites have often been referred to as showing evidence of 'squatter occupation,' in the fifth century, but he notes a lack of stratigraphic differentiation of these sites from the occupation of the fourth century.

The analysis of cultural material will never provide a satisfactory answer to the question of whether the transition from the Romano-British period to the Anglo-Saxon period was a matter of invasion or a matter of limited migration. As these arguments are based on disagreements over interpretations of the data, they have failed to give a definitive answer to the question of whether these changes were caused by a relatively large group of incomers or by groups so small that they cannot be seen in the biology of the bodies recovered from archaeological sites.

Cultural material can, however, provide evidence for the movement of the material and give insight into how the people expressed themselves, but it does not show any evidence of their biological relationships. To answer the questions of how the 'Anglo-Saxon' culture came to be so prominent in Britain and to decide between invasion or biological continuity one must examine the biological evidence. "Invasions and minor intrusions have undoubtedly occurred, even if for less often than other forms of culture contact, but their existence has to be demonstrated, not assumed" (Clark, 1966:188).

1.3 PHYSICAL ANTHROPOLOGY, RACE AND ETHNICITY

This section presents some of the issues that face all studies falling into the broad category of physical anthropology. It is necessary to give some of the history of the development of the field to round out the discussion in relation to the ideas of 'race' and 'ethnicity' and how they relate to our understanding of past populations are also discussed.

Physical anthropology has suffered from a problem similar to that of Anglo-Saxon archaeology in that much of the work, particularly the early work, was carried

out in order to support a preconceived notion of what the facts were. In archaeology, the purpose was to find evidence to support the historical record. In physical anthropology, it was to find evidence supporting the popular ideas about 'race' and 'racial' differences. Early workers in physical anthropology had a tendency to classify 'types' into which people could be categorised. This typological approach, which is similar to the use of typologies in pottery styles or metalwork, led many researchers to create racial groups that were static, unchanging entities. This reification of human groups started long before the field of physical anthropology existed, but anthropology became the avenue used to provide 'scientific' support for these classifications.

Race and ethnicity are two extremely contentious issues. The past three decades have seen much debate over the worth and proper use of these terms in anthropology, archaeology, sociology, medicine and everyday life. It is well beyond the scope of this thesis to resolve these issues. The best that can be done at this time is to present the definitions used here and provide some of the background that went into forming them.

1.3.1 PHYSICAL ANTHROPOLOGY

Physical anthropology is a relatively young science. The theoretical framework for much of its history has been divided between two general schools of thought; the monogenist and the polygenist. Both of these ideas actually predate anthropology and greatly predate Darwin (Wolpoff and Caspari, 1996:57). The adherents of these two schools of thought could also be classified as "Lumpers" and "Splitters" (Scott and Turner, 1997:168; Gould, 1981:350; Cavalli-Sforza et al., 1994:19; Lewin, 1997:91). Monogenists lump all members of the human race into one group whereas the polygenists split humans into many races. The boundaries for these racial divisions are set at points where differences are seen in a number of traits. The number of different traits, and just how much variability in those traits is needed to make a 'racial' division is fairly arbitrary.

Monogenism was originally based on Platonic Essentialism (Wolpoff and Caspari, 1996: 61) and the idea that the range of human variation is an indicator of how far certain groups have deviated from one, ideal (usually European) form. One early monogenist was Johann Blumenbach (1752-1840). He is sometimes credited as being the 'father of physical anthropology' (Wolpoff and Caspari, 1996:60; Brace, 1982). It may be more appropriate, however, to call him the 'father of the German School of physical anthropology.' Although Linnaeus developed a racial classification

system that predates Blumenbach's, Blumenbach often gets credit as the first person to develop a modern racial classification (Wolpoff and Caspari, 1996:61). Blumenbach's scheme was based on his studies of crania from different regions of the world. It was a system of five races in which Caucasoids were seen as having deviated least from the 'ideal' form. Asians and Ethiopians (Africans) deviated most from the Caucasoid. Malays were the intermediate race between Caucasians and Africans and Aboriginal Indigenous Americans (AIA) were intermediate between the Caucasoid and the Asians.

While this taxonomic system is now interpreted as having been meant to show distinct divisions, Blumenbach himself thought that it proved the continuity of the human race (Wolpoff and Caspari, 1996:62). The differences between 'major' (Caucasoid, African and Asian) and 'minor' (AIA and Malay) were depicted in a linear arrangement with Caucasians at the centre of the line. He hypothesised that the gradations between the races were due to different climates rather than genetics (Wolpoff and Caspari, 1996:63). Blumenbach explained the deviation from ideal form as the race having become 'degenerate'. Caucasoids were the least degenerate whereas Asians and Africans were the most degenerate. It is important to recognise what Blumenbach meant by 'degenerate.' "During the 19th century, racism as a derogatory term did not exist. From a later 20th century hindsight, the beliefs of most Europeans in the racial superiority could be labelled racist" (Barkan, 1992:18-19). The degenerate skull shapes described by Blumenbach may have deviated from the ideal form but this does not mean that the race itself was considered to be inferior. Blumenbach saw his classifications as just that — classifications. The social problem arising from the use of these classifications came when others turned the linear nature of Blumenbach's system to a hierarchical tree.

The other major school of thought is polygenism. Polygenism holds that "the human races are separate, *really* separate" (Wolpoff and Caspari, 1996: 57 original emphasis). Polygenists claim that races have different characteristics, histories and origins. It has even been taken so far as to claim that the races are different species. A famous proponent of this idea was Paul Broca (1824-1880) who, as the founder of the Société d'Anthropologie de Paris, may as well be called the father of the French School of physical anthropology. Some have remarked on Broca's brilliance as a surgeon, his compassion as an abolitionist, and his early support of Darwinism (Sagan, 1979). While not wanting to call into question the first two points, there is some debate about the last. The idea of polygenism to which Broca subscribed

required that species be fixed. Early on, Broca rejected Darwin's ideas out-of-hand. By the 1870's he had apparently decided that species could change, but the Darwinian mechanism (natural selection) was a "shining mirage" (Broca 1870, quoted in Brace, 1982).

The thinking of many of the early physical anthropologists was not as rigorous as one might expect from scientists whose contributions were great enough to have had schools of thought attributed to them. Unlike scientists such as Darwin and Lyell whose intellectual styles were shaped by the Scottish Enlightenment (Brace, 1982; Brace, 1997), Blumenbach and Broca, as well as Sir Arthur Keith, Earnest Hooton and Ales Hrdlicka could be included among those whose thinking was more in line with the Romantic School (Brace, 1982), although Barkan (1992:15) states that Blumenbach was actually a product of the Enlightenment. The thinking of the Romantic School was shaped more by 'common sense' than by empirical data. This is not to say that these workers did not collect good data, simply that their conclusions were often based on dubious assumptions (i.e., preconceived notions).

1.3.2 RACE

Defining the term 'race' has proven to be a difficult endeavour in the history of physical anthropology. In fact, "there is no proper technical definition of race in anthropology" (Harpending and Relethford, 1997:362). This is not due to a lack of trying. 'Race' was originally a zoological term to designate all members of a single species (Barkan, 1992:15). The Oxford English Dictionary gives several definitions of race: They range from "a genus, species, kind of animal" and "a great division of living creatures" to "a tribe, nation or peoples regarded as of common stock" and "the offspring or posterity of a person" (OED, 1971). Molnar (1983) gives seven different definitions of race published between 1944 and 1977. These range from "...races are populations which can be readily distinguished from one another on genetic grounds alone" (Hulse 1963: 262, quoted in Molnar, 1983:17), to "...race may be defined operationally as a rough measure of genetic distance in human populations and as such may function as an informational construct in the multidisciplinary area of research in human biology" (Baker 1967:21 quoted in Molnar, 1983:17). These definitions are strictly biological, but others (e.g. Montegu, 1964) incorporate other factors as well, thereby adding to the confusion.

By the early twentieth century the term covered a range of human divisions — religious, geographic, class and colour (Barkan, 1992:5). These definitions have not

held up “because concepts of race have often been based on composites of biological, social and ethnic criteria used in a typological fashion” (White, 1991:328). Typologies require that there be clear divisions between the groups. Because superficial traits like skin colour, hair and facial characteristics are clinal, even the traits that have been considered to be diagnostic of one group are present in other groups (Weiss and Maruyama, 1976:45). Also, Brues notes that attempts to find a “global set of measurements which would automatically pick out significant differences between *any* two races” (Brues, 1990:5 original emphasis), have led to problems of understanding what ‘race’ means.

Classification of individuals into ‘races’ is a long-standing tradition which predates genetics and evolutionary theory. Eighteenth-century workers assumed that taxonomic groups were fixed and unchanging (Molnar, 1983). For many years there have been questions about whether race is even useful as a concept. “The lack of correlation, when more than a single trait is used as a criterion, has been recognized again and again and renders any search for racial purity a futile and, often silly exercise” (Molnar, 1983:10). Popular ideas about what ‘race’ means are based on scientific formulations from the nineteenth and early twentieth centuries (American Association of Physical Anthropologists, 1996). Skin colour, head shape, certain facial features and several other traits have been used to categorise individuals. Often these differences are used to construct theories of how one group is superior to another. Broca, like Blumenbach, believed that the races could be ranked on a linear scale (Gould, 1981). It was not an unusual position to take at that time, and it was usually asserted (at least by Broca and Blumenbach) that the classifications were not hierarchical, even if their studies were not always used as if this were the case. Much of the work carried out by physical anthropologists up to the middle of the twentieth century involved finding differences among groups in order to show the ‘superiority’ of one group, usually the group to which the researcher belonged. Broca and some of his French colleagues waged a long-standing battle with their German counterparts over whether the French or the Germans had the larger brains. This was important to them as brain size was thought to be directly correlated with intelligence and, therefore, superiority. The only advantage arising from the interest in finding ways to show superiority with physical characteristics is that the research produced huge amounts of data for present day researcher to use. Many of the early researchers used contradictory paradigms of what makes a trait a sign of superiority which left many people very confused. “The confusion from these difficulties has

persuaded some anthropologists to conclude that the very use of the term race is counterproductive” (White, 1991:328).

Part of the problem stems from not clearly defining the level of differentiation the term ‘race’ is meant to describe. How one assesses the usefulness of the term can depend on whether the level is that of worldwide differentiation or more localised variation. Harpending and Relethford (1997) use the term “race in the sense of subspecific variability” (pp.362) which, in their case, means essentially the same as ‘major races’ with clinal variation. “All populations or population clusters overlap when single genes are considered and in almost all populations, all alleles are present but in different frequencies. No single gene is therefore sufficient for classifying human populations into systematic categories.” (Cavalli-Sforza et al., 1994:19). Some 90% of the variability in humans is left unexplained by findings of studies using ‘major races’ (Weiss and Maruyama, 1976:44). This is due to the fact that most “of the variability to be contained within the local group rather than between the races” (Weiss and Maruyama, 1976:44). Attempts to create a more scientific definition of race using blood groups have failed. The data from such attempts “were largely the basis for the development of human population genetics in the late 1930's and 1940's which redefined humans into gene pools instead of races” (Schneider, 1995:87).

In general, race is a term that has been used to describe groups based on a shared genealogy. Race “is a sociological construct that is poorly correlated with any measurable biological or cultural phenomenon other than the amount of melanin in an individual's skin” (Crews and Bindon, 1991:42). Recent arguments over the utility of ‘race’ in forensic science have led to the conclusion that there are some physical differences that can be seen between groups of different geographical origins, otherwise, forensic scientists would not be able to identify the differences so readily (Brace, 1995; Sauer, 1992). The ability to identify these differences is due to societal classifications rather than the biological realities (Brace, 1995). White (1991) asserts that there are “no human skeletal markers that correspond perfectly to geographic origin” (pp. 328). There may be some functional meaning of anthropometric differences. Their susceptibility to environmental modification, however, means that these differences should not be assumed to be essential or inborn (Lasker, 1994:4).

The period of transition from Romano-British to Anglo-Saxon also marks a modification in the “physical character of the people” (Myres, 1986:1). The nature of this physical change is stated by Myres, but not detailed. The use of the cranial or cephalic index is one of the few examples of the use of physical anthropology in early

British archaeology. The first publication of the index is attributed to Anders Retzuis in 1860 (Lasker, 1994). This Swedish anatomist devised a measurement of the ratio of the width to length of the skull. Those with short, round skulls (cephalic index >0.8) were called brachycephalic, those with long, thin skull (< 0.7) were referred to as dolichocephalic, and those in between as mesocephalic. Leeds (1913) states that the "examination of the skull-types has shown that the people who buried their dead with such relics belonged to a type never found in England in Roman or pre-Roman times, but, on the other hand, to one which is of common occurrence in North Germany; in short, to the districts from which tradition brought the ancestors of the English race" (Leeds, 1913:24-25). Contrary to Leeds' assertion, Hodgkin (1906:7) states that skulls from Neolithic Britain were uniformly dolichocephalic (long narrow skull), whereas the skulls of the Bronze Age were brachycephalic (relatively round). The dolichocephalic skulls are found again in the late Celtic barrows of the Iron Age.

Of course, neither assertion about the shapes of peoples' heads matters much, as was shown by Franz Boas. Boas published his 1899 work showing that the cephalic index can vary within groups, even during the lifetime of an individual (Gould, 1981). In 1911 Boas found that American-born children differed significantly from their immigrant parents (Gould, 1981). This plasticity of cranial shape is further shown in a comparison of Japanese immigrants to Hawaii and people of Japanese ancestry born in Hawaii (Shapiro, 1939). While there is a certain genetic component to the shape of the head there is a complex interaction with the environment.

Part of the reason for the shift in cephalic indices can be explained by allometry. Allometry is the term used to describe the proportional relationship between a variable and the overall body size of an individual. For example, the size of a person's feet is usually related to the overall size of the body. If a man who is 6'4" tall had feet the same size as a 5'1" woman his feet would not be considered normal. In the case of the cephalic index, taller individuals have longer (dolichocephalic) skulls (Molnar, 1983:64). The index may still be of interest when used in studies of overall growth and development (Molnar, 1983:64), but it must be used with extreme caution, if at all, as an indicator of ancestral origin.

For all of the racism that seems to have been present in the early days of physical anthropology, most people now working in this field would agree with the sentiments expressed by the American Association of Physical Anthropologists in their statement on race prepared for UNESCO. In it they state that it is "meaningless from the biological point of view to attribute a general inferiority or superiority to this or to that race" (American Association of Physical Anthropologists, 1996).

For whatever general worth the term 'race' may or may not have, it is not particularly useful for this study as all of the individuals examined would fall into the same 'major race' classification. What is of interest here is how one can assess the microevolutionary differences that came about primarily due to genetic drift and isolation. Some might ascribe these differences to 'micro-races', but it is probably more useful to describe them in terms of local gene pools as described by Schneider (1995).

1.3.3 ETHNICITY

As with 'race', there is also a wide range of possibilities for a definition of the term 'ethnicity' and its cognates. The OED defines 'ethnicity' as an obsolete, rare word referring to "Heathendom, heathen superstition." Ethnic pertains either to "nations that are not Christian or Jewish" or "to race" (OED, 1971). The 7th edition of the Concise Oxford Dictionary defines ethnicity as "gentile, heathen, of a specified racial, linguistic, etc. group (1982). Things are not made much clearer by 1992 when, according to the OED2 on CDROM, ethnicity pertains "to race" or is "peculiar to a race or nation" (1992). The terms 'race' and 'ethnicity' are often used synonymously to describe human groups, regardless of whether members of these groups consciously assert any sort of 'ethnic' or 'racial' identity. Montagu (1964) is often cited as the first to argue explicitly for the replacement of the term 'race' with "Ethnic Group" (Gill, 1990: viii). Members of the general public, as well as researchers involved in relevant areas of study, have in the past, and continue today, to confuse the two issues of biology and culture. The isolation of one breeding group from another that allows physical differences to evolve also allows cultural differences to arise. Indeed, one commonly held belief from the early days of genetic research was that "race, culture and language were manifestations of...one inherent entity" which allowed researchers to delineate a racial taxonomy (Barkan, 1992:19). Even though modern researchers have moved away from such blatant errors in concept, many times they will still make the mistake of linking the putative physical identity of 'race' with 'ethnicity' because of the tendency for cultural differences to become stronger, as the isolation of breeding groups becomes greater (e.g., Konigsberg, 1988; Konigsberg, 1990a; Eller, 1999; Rudan et al., 1988).

As cultural identity is often a strong contributing factor in mating, it is easy to see how a term which applies to the manifestations of culture ('ethnicity') would come

to be conflated with a term ('race') that is meant to apply to a biological relationship. Because of this confusion, it may not be self evident to everyone that 'ethnicity' does, in fact, refer solely to cultural identity.

'Ethnicity' is constructed out of language, religion, culture and ancestry (Nagel, 1998: 237), among other things. 'Ethnicity' is a mutable notion that involves the labelling of individuals as part of a group either by oneself or others (Barth, 1969). Crews and Bindon (1991) agree and state that 'ethnicity' is made up of "language, style of dress and adornment, religion, patterns of social interaction and food habits" (Crews and Bindon, 1991: 42). Jones defines 'ethnic identity' as "that aspect of a person's self-conceptualization which results from identification with a broader group in opposition to others on the basis of perceived cultural differentiation and/or common descent" (Jones, 1997: xiii). The problem with this definition is in the last phrase "common descent." This opens the door to confusion between biological and cultural matters in much the same way Gill (1990) complains that the description given by Montagu (1964) does.

If 'ethnicity' is meant to describe common descent as perceived by the individual rather than an actual genealogical relationship, then all of the identifiers of ethnicity are dependent on the individual's concept of him or herself. With this definition, where 'ethnicity' is based solely on the basis of self-perception, archaeologists will never be able to know the ethnicity of a person excavated from a cemetery. A person who is long dead cannot make an assertion of group membership. Even the grave goods may not represent the individual's self-concept. The grave goods were placed there by members of the community in which the dead person had lived so the grave goods represent how those people perceived the dead person, or how they perceived the dead person to have perceived himself or herself. One may present a definition of 'archaeological ethnicity' as the cultural identity of a person defined by the way in which that person was perceived by the community who buried him or her as shown by the cultural trappings in the graveyard.

Culture and history are part of a "toolkit" (Swindler, 1986) people use to create their own ethnic identity or 'ethnicity'. One's 'ethnicity' can change depending on the audience (Nagel, 1998). A person born in Aberdeen, for example, may claim to be Aberdonian to another Scot, Scottish to someone from England, and British to an American. Each identification denotes membership in a slightly different group.

"Many examples can be found of people sharing similar material cultures yet having different social, political, or linguistic affiliations" (Trigger, 1978:116). Cultural similarities can be shown among people who have no biological relationships and

biological similarities can be found among groups that have different cultures. Trigger (1978) gives examples of these situations from Early Dynastic Egypt and Five Nations Iroquois (also see Moral et al., 1994). The relevance of this 'layering' of identity to the current study is that the individuals of whom the indigenous population of fifth century Britain was composed could well have chosen to assume Anglo-Saxon 'ethnicity' in order to facilitate co-operation with the members of a newly installed ruling elite, but may have maintained, or even asserted their distinctiveness in ways that cannot be detected archaeologically.

The consideration that race is meant to indicate biological affinity, and that 'ethnicity' is meant to indicate a cultural identity, suggests that it is a mistake to use the two terms interchangeably. Unfortunately, it is the case that many people do make indiscriminate use of both terms. Ahdieh and Hahn (1996) reviewed 914 articles which studied human populations and were published in the American Journal of Public Health between 1980 and 1989. Of the 461 (50.4%) that used classifications of 'race,' 'ethnicity' and 'national origin,' 1.3% used the terms race and 'ethnicity' interchangeably. In 5.6% of the articles, they were used as combined categories (e.g., race/'ethnicity'). They further state that very few of the articles included a definition of the categories that were used (8.4%). They conclude that if there is to be an improvement in how the medical professions assess differences in health status among the different groups there must be more research into how to define these groups and how to assess the validity of the classifications. Crews and Bindon (1991) conclude that it is these factors, more than any biological differences that may be present among groups, which are useful in understanding the health differences among those groups (Crews and Bindon, 1991: 42).

The fact that many medical researchers routinely use the terms 'race' and 'ethnicity' as descriptors of their research subjects does not mean that they have a better, more scientific definition for either term. Nor is the subject of how to define the terms any less contentious for them than it is for archaeologists and anthropologists. Cooper (1984) states that anthropologists have abandoned the term 'race' as a biologic concept (though this is an overstatement of the situation, (c.f. Brace, 1982; Sauer, 1992). Cooper further states that, although its use is widespread in epidemiological research, 'race' is a scientific anachronism. Cooper's definition of 'race' is slightly ambiguous. He states that "racial definitions should be seen as primarily social in origin" (Cooper, 1984: 715). If one reads this quote as meaning that the definitions are social constructs, as Crews and Bindon (1991: 42) argue, then there is little to argue with. If, on the other hand, this is meant to define 'race' in the

same way that 'ethnicity' has been used here, this would only add to the level of confusion already found in discussions of these issues.

1.3.4 THE NEED FOR BIOLOGICAL STUDIES

To bring an end to the circular arguments caused by looking for signs of biological affinity in the historical accounts and the cultural material we need to examine the biological material directly. It is no longer considered acceptable to equate the movement of artifacts with that of populations (Hemphill, 1998). "Dental morphological traits do not vary without reason across the landscape...Tooth morphology is part of the biological heritage" of people (Scott and Turner, 1997:12). When people migrate from one place to another they carry these traits with them "much like their blood group genes, fingerprint patterns, PTC taste reactions and other biological traits" (Scott and Turner, 1997: 12). On the other hand, when people stay in one place and are isolated from other groups "for a period of time, their crown and root trait frequencies diverge to varying degrees, depending on population size and the extent and temporal duration of isolation" (Scott and Turner, 1997: 12).

One of the ancillary objectives of this research is to stress the importance of moving beyond this confusion and give appropriate attention to biology and culture as separate issues. Trigger (1978) states that it is "possible to learn something about the racial, linguistic, and cultural changes..." but each field "must be investigated independently, using the data that are appropriate to it. Only when this has been done, is it possible to combine these different categories of data in order to investigate what happened to specific groups..." (Trigger, 1978: 131). It is the premise of this thesis that if one is to assess the extent of an influx of people into an area and what impact those people have on native populations, one must start from a knowledge of the numbers of in-comers involved. In other words, one must first define the biological history of the populations involved before one can assess the method by which changes in cultural trappings took place. The reason for attempting to assess biological distances in this study is to help reconstruct the population history (Smith, 1977: 463).

The methods used to arrive at such numbers for the Anglo-Saxon period have normally involved interpretation of historical documents and cultural material. As has been stated above, this method is inadequate. The only way to understand the biology is to study the remains of the populations from the time. Calls to avoid such

studies out of a fear that such material would be used to fuel racist sentiment are misguided in part because those who wish to make racist statements do make them without evidence or by twisting what evidence there is. There are those who will claim that attempts to define the transition in terms of biological continuity in order to deny German influence in Britain on political grounds and deny the 'real' history of the transition in Britain (Arnold, 1997: 22).

Biological studies may even help to stop some individuals from spreading their racist ideas because there would be evidence which contradicts their stories of what happened in Britain in the fifth and sixth centuries. As things stand now, anyone can make interpretations of the historical and archaeological evidence that fit with their own preconceived ideas of how they want history to have happened. In short, it is the ignorance of the biology that gives us the most to worry about.

2 CHAPTER 2 MATERIALS AND METHODS

2.1 HYPOTHESIS TESTING AND DESIGN OF RESEARCH MODELS

To test the two models of invasion and continuity, one must first state a hypothesis in a testable form. An experiment must then be designed in such a way that the hypothesis is actually tested. The hypothesis for the invasion model could be stated as: 'The population of Anglo Saxon Britain was composed of an immigrant population that replaced the indigenous population.' The alternative hypothesis for the continuity model might be stated as: 'In spite of cultural change, the actual genetic component of the population remained largely unchanged.'

To test these hypotheses one must choose a tool that measures the biological relationships among populations. As has been argued throughout this thesis, these relationships must be tested using the human remains, not the cultural material associated with them. The cultural material represents the cultural identity or ethnicity of the individual, not the biology. The ASU Dental Anthropology scoring system is used here because the traits defined for this system have been shown to be under strong genetic control and are easily observable (Scott and Turner, 1988; Turner et al., 1991).

It may seem that archaeological samples are inherently random because the archaeologist does not have a bias in choosing to excavate one grave rather than a different grave or because there is no prior selection of which bodies will have been preserved. The term 'random' may be correct in that sense, but it is not the sense used when discussing research design. Randomising is a technique used in experimental studies where the investigator can manipulate the groups being studied. Randomising a sample involves the investigator assigning subjects to groups, one of which will receive a certain type of treatment while the other gets a different treatment (Spector, 1993:10-11).

The nature of archaeological investigation is non-experimental. That is, the groups being tested are not randomised, but are selected to meet certain criteria (Spector, 1993:2). The selection criteria can be any group of variables for which information is available. For example, if one wanted to test for the status of an individual based on the variation in the number of beads found in graves, one might chose to separate graves by sex and by age, thus controlling for differences that may be attributable to those factors.

The term control refers to holding all variables, except the variable in question, constant. This allows the researcher to test the hypothesis that variance is due a change in the specified variable. In this case, which sites are used as the controls, depends on the question being asked. The basic question being asked in this study is; 'are populations excavated from sites dated to the Romano-British period biologically different from populations found at sites of the Anglo-Saxon period?' To test this, one must first examine sites from both periods. As the variation between these periods is unknown, this test would require a minimum of three sites—one from the first period and two from the second. This would hold the time variable constant for two sites while testing for change across time in the third. The problem is that if biological differences are found, they could be explained by geographical distance rather than an influx of new genetic material. The important, confounding variable of geographic distance has been left unaccounted for.

To control for geographic distance one must use sites that are geographically similar for two of the sites and the third must be geographically distant. This second design exhibits the same problem as the test in the first design, because it again confounds the variables of time and distance. The way around this is to geographically pair sites from different time periods. In this third design, which is the design used in this research, sites are paired by period, one Romano-British and one Anglo-Saxon in each particular region. In this study, three pairs of sites are located in different regions across England (see Sites section below). The more geographically similar the sites are, the more likely it is that any differences between them could be attributed to an actual biological change in the population. Conversely, an inability to distinguish between any two sites may not show that the people are truly biologically similar. The similarity may be accounted for by a failing of the ASU system to be able to distinguish between groups.

This design provides a good test for differences between the time periods, as well as providing a start on an assessment of the biological variation across southern England. As this study is concerned with variation within Britain rather than finding the ultimate origins of those people, there is no need for a control group from the Continent. If the results were to show support for the invasion hypothesis, it would be sensible to then compare these and other sites to Continental sites in search of the Anglo-Saxon origins.

2.2 THE ROLE OF PHYSICAL ANTHROPOLOGY

What does physical anthropology have to offer in the way of information about the transition from the Romano-British period to the Anglo-Saxon period? The answer to that question depends on how the question is asked. As stated above, Austin (1990) challenges the role of History in dictating the way sites are classified as being 'Anglo-Saxon.' He notes that the migrating groups are often portrayed as being heterogeneous, and that this idea would bring in to question the validity of assertions that their origins would be homogeneous. To test these origins "we must separate material culture from genetic lineage" (Austin, 1990:16).

Hills (1990) states that studying the "human bones offers the greatest hope of achieving certainty as to stability or change among the population" (Hills, 1990:50). Arnold also asserts that there is some promise in results obtained from physical anthropology. He quite rightly points out that there are dangers in trying to understand ethnicity as a biological concept (Arnold, 1997:21). As discussed above, the cultural identity of an individual is quite separate from the biological identity. Using the definition of ethnicity stated above, physical anthropology cannot determine the ethnicity, only the biological identity. Using this definition, Austin quite rightly states that "physical anthropology has nothing to offer" in terms of understanding ethnicity (Austin, 1990:16).

There are literally hundreds of studies comparing populations using skeletal and/or dental traits. Many of these compare populations from differing times and geographical regions (e.g., Greenberg et al., 1986). Some studies include comparisons of the results from skeletal or dental traits with blood or linguistic evidence (e.g., Sofaer et al., 1972; Greenberg et al., 1986; Moral et al., 1994). Some of the studies that include aspects of physical anthropology of particular relevance to this study are outlined below.

Phyllis Jackson came to physical anthropology after a career as a chiropodist in the Cotswolds (Jackson, 1992; Jackson, 1995). During that time, she noticed familial patterns in the feet of her patients. At one point she noticed an anomaly that she had seen in the feet of another family from a nearby village who happened to share the same surname. The families denied a relationship, but Jackson found a co-ancestor by searching the parish records (Jackson, 1992).

She felt that there were morphological differences in the bones of the feet that could be used to show difference among the people who had been interred in ancient cemeteries. Indeed, the development of the round bones of the feet and hands are

known to be under considerable genetic control, though not to as great an extent as the genetic control of dental development (Garn, 1977: 82). After evaluating several cemeteries, she came to the conclusion that the feet she had examined did show differences. Based on the observed differences, she divided the remains from Lechlade into those with local, "Celtic" feet and those with foreign, "Saxon" feet.

Her study is not without problems. The descriptions of the traits examined are limited to fairly vague distinctions of bigger and longer. This in itself would not be a big problem if there were some sort of reference to which the samples could be compared, but there is not mention of them in the article. The assignment of a foot belonging to one group or another is dependent on an overall impression on the part of the observer. This is not an unusual situation for a method in early stages of development and Jackson has made public appeals for more samples as a way to address this problem.

Another similar problem is the lack of quantification. There seems to be no way to assess how much difference is needed to make a foot belong to one group rather than the other group. This is, again, the problem with using overall impressions for diagnosis. The lack of quantification also makes it impossible to know if there is a significant difference between the two groups. Two of the questions that cannot be answered by examination of the data presented in the article are 1) how closely are the various cemetery populations related and 2) what portion of each cemetery belongs to which group?

The last problem to be taken up here is with the designation of "Saxon Foot." There are two problems to this approach. Firstly, it has the flavour of the classic typological style of physical anthropology that has caused so many problems in understanding human evolution as was discussed above. This problem might be avoided if she was to describe it as a foot exhibiting traits that are commonly associated with those of Germanic origins, or some other way that did not denote categorisation into a fixed group. Secondly, Jackson gives the explanation that this type of foot belongs to the aliens that history tells us came to live in that area at about the right time to have built up a sizeable portion of the population (i.e., the Saxons). Unfortunately, this violates one of the rules of scientific method in that, as Feder (1996: 27) points out, the last hypothesis on your own list of possibilities is not necessarily the right one. The better solution would be to designate this foot type as being simply "non-local." This would have allowed the investigator to point out the differences found and state that they belong to two groups without making an untested statement about the origins of the second group. The question of the

origins of the second group could be explored in an extended study that included information about the total range of variation within Britain and on the Continent for several different time periods. Again, to her credit, Jackson seems to be taking steps to do just that.

Härke (1990) includes the cemetery at Berinsfield in his study of "Warrior Graves". In this study he makes some assumptions that are dependent on preconceived notions of biological makeup of the populations he examines. The opening sentence of this article explicitly states the assumption that at least some of the people who lived in England could be classified as belonging to "Germanic tribes" (Härke, 1990: 22). He notes that there is variation from one cemetery to another which he describes as surprising "even taking into account the heterogeneous social and ethnic make-up of the Germanic immigrants and their descendants" (Härke, 1990: 26). With this assumption made, Härke proceeds to define the differences between Romano-British and Anglo-Saxons in terms of the weapons found in the graves. He then compares them with several anthropometric measures. One of the measures he uses is stature.

He dismisses the possibility of differential height being due to better food supply of the group he identifies as Anglo-Saxon because the rates of enamel hypoplasia are similar between the two groups. This is an invalid assumption because hypoplasia can be caused by any systemic insult, not just starvation (Goodman et al., 1984; Goodman and Rose, 1990; Rose et al., 1978; Goodman and Rose, 1991). Furthermore, even if starvation is the cause of the hypoplasia, the body can recover if there is a return to improved nutrition during the developmental period (e.g. Seow, 1992). This means that social status alone may account for the differences in stature, not the differences in origin as this study proposes.

When Huber (1968), studied remains from a Alemannic row-grave cemetery at Weingarten in Southern Germany, he concluded that the calculations based on the Trotter and Gleser formulae may not apply to the Alemann population, as the formulae were based on studies of American soldiers. Another problem with these formulae is that Trotter and Gleser took the live measurements before the soldiers had reached their full height (Huber, 1968: 77) so the bones at death (2 years later on average) may have been longer than they were when the live height was calculated. There is also no way to assess the possible differences in 'trunk length' on the material in Härke's study. Trunk length may change the proportions enough that the short limbed individuals were more nearly the same height as the long limbed. It is

also interesting to note that Huber, similar to Härke, found that the more heavily armed men were taller than the more lightly armed or unarmed men were. There was no history of biological invasion for the Weingarten cemetery, and Huber attributed the differences to statistical artefact related to the sample size of each group (Huber, 1968: 76).

There also exist questions as to whether the differences in height found in this study are actually significant. Estimates of stature are based on regression equations which include standard errors that can be as much as 4.72 cm (using the formulae of Trotter and Gleser (1952), calculated on the ulna of white males, cited in (Bass, 1987: 171). This means that there is about a 68% probability that the actual stature of the individual is within 4.59 cm of the calculated height (White, 1991: 328). According to Härke, the “Anglo-Saxon immigrants were on average 4 centimetres (1½ inches) taller than the native Romano-British men” (Härke, 1990: 40) which means that they are probably within one standard deviation, and certainly within two standard deviations which would make his results statistically insignificant. The other problem with these calculations is how they were derived. By examining table 4 of his article (pp 39), one finds that the range of the differences between those with weapons and those without is from -3.7 to +4.8 for the whole sample and from +0.2 to +4.7 for the five early cemeteries. This gives a mean of the different heights of 1.72 cm for the whole sample and 2.66 cm for the early cemeteries or a median of 2.3 cm for the whole sample and 2.4cm for the early sample. Either way, this is far less than the 4 cm he reports. Unless the averages for these differences in height were calculated from some other, unidentified data, this would put his results in an even worse light.

When he then shows the differentiation between those with weapons and those without weapons at Berinsfield, he notes that the “individuals buried with weapons have some traits which do not appear among individuals without weapons” (pp41). By examining table 5 (pp41), one sees that the already small sample of 23 cases has been further depleted to just over half as many (14) individuals who were identified as males with epigenetic traits. While the table seems to show clear differences, caution should be shown when making conclusions based on such small sub-samples and when one does not know what other traits may have been present in those individuals who were eliminated from consideration.

Tyrrell (1993) conducted a study that is probably most similar to the current study of any of those outlined here. He used six sites from England dated to the Romano-British and Anglo-Saxon periods plus a ‘control’ group from Yugoslavia. He

included six dental traits, but the main focus of his study was the relationships shown by osseous traits. The results of his study failed to show a clear pattern of division among the sites. The fact that a modern continental population showed little divergence from the British populations was an unexpected result.

Tyrrell proposed several theories as to why this happened. First is that the traits were all scored as either present or absent. This is a necessary condition for the statistic used, the Mean Measure of Divergence (MMD) (see population statistics below) but a great deal of information is lost, at least when the dental traits scored with the ASU system are considered. Another possibility is that the results show statistical artefact. Artefact could have been caused by following the advice of Finnegan and Coopridier (1978) who state that a large number of traits must be studied (pp 43). It may have been better to follow the example of Sofaer et al. (1972) who found that by removing the traits that were considered to be the least useful (i.e., traits that cause 'statistical noise') their comparisons of Zuni, Pima and Papago Indians made much more sense (pp. 364). There is also the matter that the sample from Yugoslavia was scored by another researcher and the selection of traits differed from his own list.

Sokal et al (1987a) conducted a study of cranial measurements on skulls from three time periods in Europe. They used 428 individuals and 10 cranial traits to identify the relationships among these individuals from "the Early Middle Ages, the Late Middle Ages and the Recent Period" (Sokal et al., 1987a:1). Their analysis included comparisons of these biological traits to geographic distances and language groups. Overall, the results showed that an increase in geographic distance was a contributing factor to an increase in biological distance. Comparisons of affiliation with language groups did not match as well with either the biological or geographic information. They concluded that the "racial classifications along traditional lines...cannot be upheld" (Sokal et al., 1987a:16)

In a study of the inhabitants of Sardinia by Moral et al. (1994) the genetic profiles (as shown by 20 polymorphisms in the blood) of several groups were compared. The focus of the study was to ascertain if the Catalan-speaking population from the town of Alghero, on the north-western coast of the island was more closely related to other Sardinian Islanders, to Spanish or to Italian groups. The cultural distinctiveness of this city from the rest of the island prompted the question of whether the genetic makeup was also distinct. The statistical analysis suggested that, of all the Sardinians, the Algherans were most closely related to the Catalonian groups, which was expected due to the history of Alghero as an occupied city and the

fact that Catalan is their language. On the other hand, they found that the Algheran population was more closely related to other Sardinian Islanders than to the Spanish. This suggests that there is no biological support for the hypothesis that linguistic affinities between the Algherans and Catalonians are indicative of biological kinship (Moral et al., 1994:452).

These last two studies highlight some of the problems associated with equating historically defined groups with biologically defined groups. The fact that two groups of people share a language and where historical accounts seem to show a relationship does not mean that the groups are genetically related (Saunders, 1989). While it is true that people who share a language often share genes, there are situations where a language can be replaced through colonialism with very little direct genetic influence (Moral et al., 1994: 452).

2.3 WHY TEETH?

Teeth are probably the most frequently found human material in archaeological contexts, in some cases they are the only remaining evidence of a burial (Scott and Turner, 1997; White, 1991; Butler, 1963; Hillson, 1996). This is due in part to the fact that the crowns are composed of enamel, a highly inorganic substance (approximately 97% mineral salts primarily Calcium Hydroxyapatite $\text{Ca}_{10}(\text{PO}_4)_6(\text{OH})_2$) (Ten Cate, 1985; Robinson et al., 1986; Larsen and Kelley, 1991; Cruwys and Foley, 1986; Scott and Turner, 1988). There is evidence that the early stages of decomposition affect the collagen content of the decaying structures (e.g. bone or dentine). Mineral deterioration does not begin until the last stages of the process of disintegration (Beeley and Lunt, 1980). Because the enamel is composed of mostly mineral, they do not decompose as readily as bone or soft tissues. The roots, too, while more like bone in composition, are often preserved because they are encased in cementum and the bone of the jaw. These extra layers of protection also delay decomposition.

The abundance of teeth in archaeological contexts is not the only advantage of using them instead of skeletal features. Teeth are unique among hard tissues in that they are directly observable in living subjects. This allows comparisons between living groups and between living populations and archaeological samples. There is the added benefit that, because everyone has some teeth, even the researcher has a full set, and the teeth can function as a personal, portable reference set for the most basic comparisons (Hillson, 1996: 1).

The ideal way to assess affinity among archaeological populations is to use traits that are “directly and exclusively controlled by genes” (White, 1991: 370). This is not possible as all traits are, to some extent, influenced by the environment (i.e., phenotype = genotype + environment). The form of teeth has been shown to be under considerable genetic control (Turner, 1967; Scott and Turner, 1988; Hillson, 1996; Larsen and Kelley, 1991; Møller, 1967). The proof of genetic control takes many forms. Sometimes it involves technologically advanced analytical procedures, while sometimes it is straightforward.

The study of teeth begins with the ‘normal’ dentition. ‘Normal’ is identified first by the dental formula. In humans the dental formula for the permanent dentition is 2-1-2-3 (Hillson, 1986; Scott and Turner, 1997; Dean, 1992). This means that in each quadrant of the dental arch there are two incisors, one canine, two premolars and three molars, for a total of 32 teeth. All of the catarrhine primates (Humans, Old World monkeys and apes) share this formula (Scott and Turner, 1997). This is the first indication of genetic control. If there were no genetic control, it would not be possible to distinguish the dentitions of one class of animal from another, much less distinguish groups within a single species.

Practitioners and anatomists tend to concentrate on this basic pattern and the identifying morphology (e.g., Incisors are spatulate and molars are multicusped). For them, minor variations from the norm may be interesting, but not of any particular importance in practice because the variations do not have much impact on immediate dental care. In a busy practice, a dentist would be lucky to have time to notice anything beyond the obvious deviations from normal. The noticeable deviations would probably include hyperodontia (extra or supernumerary teeth) and hypodontia (missing teeth or agenesis). Hyperodontia is rare, affecting only about 5% of people worldwide (Scott and Turner, 1997). Hypodontia, on the other hand, is common enough that one can quantify the variation from one population to another. There are also studies that examine the relationship between tooth size and agenesis (e.g., Keene, 1968), between missing third molars and other missing teeth (e.g., Garn et al., 1963), and some studies have compared frequencies of third molar agenesis between populations (Pedersen, 1949). The ASU score sheets (see appendix I) incorporate congenital absence of upper lateral incisors, lower central incisors, upper and lower second premolars and upper and lower third molars as standard observations as well as a space to record extra teeth.

As well as being well preserved archaeologically, dental enamel is “nonvital” (Ten Cate, 1985: 212). That is to say that it holds a unique place as being the only

tissue that is not replaced nor remodelled once formed (Sarnat and Schour, 1941; King and Wei, 1992). This unchanging nature is one of the reasons that dental traits are often considered to be superior to osseous traits as there is less chance for environmental factors to complicate the issue (White, 1991: 334).

The formation of enamel begins in the embryo. The stages of tooth development are divided into six morphological stages: 1) dental lamina; 2) bud stage; 3) cap stage; 4) early bell stage; 5) late bell stage; and 6) enamel and dentine matrix formation. Ontogeny is similarly divided into 1) initiation; 2) proliferation; 3) histodifferentiation; 4) morphodifferentiation; 5) apposition 6) calcification; and 7) eruption (Scott and Turner, 1997:76).

The early signs of the mouth appear in about the second month in utero. Shortly thereafter, the dental lamina forms. By about the tenth week in utero there is evidence in each jaw of swelling of the epithelium of the dental lamina which corresponds to the individual deciduous teeth that are being formed (Hillson, 1996: 118). The permanent molars, which have no deciduous precursor, begin to form as the lamina extends posteriorly at about four months in utero.

The tooth germ is composed of the enamel organ, the dental papilla and the follicle. The papilla forms the dentine and the follicle becomes the cementum. During the late cap stage the enamel organ differentiates into the outer enamel epithelium, the stellate reticulum, the stratum intermedium and the inner enamel epithelium. Enamel forms from the stratum intermedium and the inner enamel epithelium. During the bell stage, the hollow portion of the enamel organ deepens and, due to differential rates of cell division, folds. These folds outline the basic form of the morphologic features of the crown.

As the cells of the enamel epithelium mature, they differentiate into the cells that form the actual enamel (ameloblasts). As the process of enamel production (amelogenesis) progresses the ameloblasts migrate from the tip of the cusp down the slope of the crown. Odontoblasts begin to produce the dentine from the opposite side of the basement membrane forming the roots. Calcification proceeds at a fairly constant, predictable rate (Goodman et al., 1984), although some have noted that there is some slowing toward the last stages of development (Liversidge et al., 1993). The deposition of enamel in this layer pattern leaves lines which are known as Striae of Retzius.

Because of this unchanging nature, the teeth provide a permanent record of development from about 3½ months in utero (when the first deciduous teeth begin to develop) to about 17 years (when the third molars complete mineralisation). It is

during this developmental period that environment plays its biggest role. Depending on the time of the disturbance, different changes can be observed. In an experiment using halved, 20-day rabbit molar tooth germs Glasstone (1952) showed that each half could develop an entire molar crown. When the procedure was repeated on day-22 germs, the tooth half had lost its ability to form the other half.

When examining human teeth that were allowed to develop in situ one can see evidence of disturbances in the layers of enamel. Disturbances to normal development are recorded both micro- and macro-scopically. One commonly studied defect is hypoplasia. Hypoplasia is usually seen as a horizontal line across the tooth surface resulting from the cessation of enamel production. Most often, the assumed cause of hypoplasia in studies of archaeological populations is a nutritional deficit of some sort. This deficit is usually attributed to either famine or weaning (Blakey et al., 1994; Goodman and Rose, 1991; Moggi-Cecchi et al., 1994; Rose et al., 1985; Mittler et al., 1992). While this may often be the case, virtually any systemic disturbance can cause the defect. Maternal fever, prolonged infection, and physical trauma have all been cited as causing hypoplasia (Bhat et al., 1992; Bhat and Nelson, 1989; Murray and Johnsen, 1985; Murray et al., 1987; Wood, 1996).

Many of these studies seek to differentiate between groups or individuals based on changes in the normal dental structure caused by the environment. The fact that so many factors can influence normal development does not mean that studies of hypoplasia are without merit. They do, in fact, provide valuable information about the populations being studied. Defects of the teeth are often used in studies of ancient populations. General assessments of health and analysis of biological stress are not uncommon in the literature of physical anthropology (Goodman et al., 1992; Hall and Bowman, 1992; Larsen and Hutchinson, 1992; Mittler et al., 1992; Skinner and Goodman, 1992). Dental defects are commonly used in modern forensic situations to assist in identifying bodies. Most frequently, dental restorations or visible anomalies are utilised, but stress indicators (such as hypoplasias) have also been correlated to the medical records of a missing person (Skinner and Anderson, 1991). There are also studies under way that examine the dental evidence for what role the timing of systemic events may have in the development of schizophrenia and posttraumatic stress disorder (Bracha and Lloyd-Jones, in progress), as a forensic tool in cases of "recovered memory" (Bracha et al., 1997).

Animals whose dentition is divided into different classes are called heterodonts. The different forms of teeth relate to the specialised tasks for which the teeth are needed, grasping, cutting or grinding. The more varied the diet, the more

generalised the form of these multipurpose teeth (Scott and Turner, 1997: 81). These varied forms do not appear randomly in the mouth, but are grouped into classes. The boundaries are distinct, but the teeth at the borders of these classes are more similar to their neighbours than they are to more distant teeth. In some cases the borders become slightly blurred and a crossover type may be seen, for example, as in cases of molarization of second premolars (Lunt, 1975). There are two ideas of how these classes are formed: The field theory originally devised by Butler in 1939 (Butler, 1982; Scott and Turner, 1997) suggests that teeth develop certain forms depending on their location in the jaw. As was seen above in the experiments of Glasstone (1952) the tooth can develop normally even when it is grown in a culture rather than in the mouth. An alternative theory is that of the clone model developed by Osborn (1978). In this theory the teeth develop from primordial forms that are then replicated along the dental arcade until the dental formula is complete (Scott and Turner, 1997). In both models, field theory and clone model, one tooth in each field serves as the 'polar' or 'key' tooth which is the most stable tooth of the class. Whichever theory is used, and regardless of which more accurately describes formation of teeth within a class, it should be remembered that the "expression of a particular trait on one member of a tooth district is not independent of trait expression on other members of the district" (Scott and Turner 1997: 110).

Dichotomous traits, those that are expressed as either present or absent, are usually considered to follow a simple Mendelian mode of inheritance. Continuous traits (such as height or skin colour) are assumed to follow more complex patterns of inheritance. The work of Grüneberg (1957) on mice which to a certain extent built on the experiments on guinea pigs by Wright (1934), showed that many traits actually fall between these two modes of inheritance. The term 'quasicontinuous' (Berry, 1968; Grüneberg, 1957) is now used to describe these intermediate traits. This means that a trait may be present or absent (like dichotomous traits), but when present the trait shows a range of variability (like continuous traits). It is possible for a person to have genes that code for the expression of a quasicontinuous trait and yet, not express that trait. The trait is expressed only when a person has 'enough' loci coding for expression of the trait to cross the 'threshold' of trait presence.

Another feature of the traits used in the ASU system is that the correlation between the variation of one trait and another is low (Scott and Turner, 1997: 110). Even such traits as cusp number and fissure pattern on lower molars, which many people think is a reflection of cusp number, are actually independent variables

(Mayhall, 1992: 70). On the other hand, there is some evidence for intra-class traits (e.g., Carabelli's cusp on UM1 and UM2) to vary together. This would have the effect of doubling the weight of the variable if both teeth are used. In this study that type of weighting is avoided by using only one tooth in a class per trait.

Environmental impact is much greater in bone than teeth, although both are genetically controlled. Once the dental enamel is completely mineralised, it can only be changed by wear (attrition), disease (caries) or modification due to human activity (e.g., intentional or accidental chipping). Bone on the other hand, can heal after injury and be modified with use or disuse. For example, muscle attachments and bone thickness increase in size as muscles are used more. This was shown by Washburn (1946, 1947) when he paralysed muscles in rats and rabbits and later observed the muscle attachments.

2.4 ASU METHOD

There have been more than 100 morphological traits of the dental root and crown identified in human dentitions over the years. About 30 to 40 of these traits have been well defined and extensively studied by anthropologists (Scott and Turner, 1997: 25). The ASU system defines 35 of these traits. Dental anthropology has a short history as an identified field within the larger discipline of general anthropology. It does, however have a lengthy history in terms of the amount of research that was conducted prior to being formally recognised as a sub-discipline of physical anthropology.

2.4.1 HISTORY OF THE METHOD

The history of dental anthropology goes back at least to 1842 when Georg von Carabelli described the trait of the upper molars that bears his name to this day, the Carabelli cusp (Scott and Turner, 1997). Scott and Turner (1988) state that the term 'dental anthropology' first appears in the title of an article by George Buschan in 1900. Other traits were described by anatomists and anthropologists over the next few decades, but it wasn't until 1920, when Ales Hrdlička described the range of variation of "shovel shaped" incisors, that dental anthropology moved significantly forward. In that article he described the frequency of expression of shovel shaping in several human populations and in several other hominoid species (Hrdlička, 1920). It was after and, indeed, because of this article that dental anthropology began to gain some degree of prominence. Many more papers were published over the following

thirty years describing several traits and the frequencies of those traits in various populations around the world. Some of these which could be considered cornerstones of the field include “The East Greenland Eskimo Dentition” (Pedersen, 1949), and “The Aleut Dentition” (Moorrees, 1957). More comprehensive reviews of this material can be found in (Scott and Turner, 1997; Cruwys and Foley, 1986).

The next major advance came in 1956 when Albert A. Dahlberg, a Chicago-area dentist turned anthropological researcher, released a set of reference plaques to help standardise the observations of dental traits see (Scott and Turner, 1997). These plaques became the basis of the Arizona State Dental Anthropology Scoring Method discussed in greater detail below.

A full description of dental anatomy is beyond the scope of this work. It would be impossible, however, to explain the subject fully without using a certain amount of dental terminology. There are some occasions where the dental anatomist, clinician, and anthropologist will use different terminology to describe traits and even directional terms in the mouth. The following glossary provides basic definitions for some of the common dental terms as they are used in this study.

Buccal: Cheek side, or away from the tongue.

Cervix (Cervical): Neck of the tooth, where the crown and root meet.

Cingulum (Cingular): Bulge around the cervical region.

Distal: Away from midline along the dental arch.

Incisal: Cutting or chewing surface (anterior teeth).

Labial: Toward the lips.

Lingual: Toward the tongue.

Mesial: Toward the midline along the dental arch.

Occlusal: Chewing or biting surface of the tooth (posterior teeth).

Palatal: Toward the upper arch.

Both labial and buccal are used to describe the outer surface of the tooth in the dental arcade (as opposed to the lingual surface). Labial is used for the anterior teeth (incisors and canines) while buccal is used for the posterior teeth (molars). Either term can be applied to the premolars. The posterior teeth are also sometimes referred to as the ‘cheek teeth’.

It is interesting to note that some of these terms are used to describe direction and position of skeletal traits in general medical contexts. Terms such as anterior/posterior, distal/medial/proximal, are used in the dental context as well, but

there are some curious additions. The term 'mesial' is similar to the term 'medial' but the former is specific to the dental arcade. The latter term is most often used when discussing matters of the tongue and palate. The dental arcade is shown in figure 1.

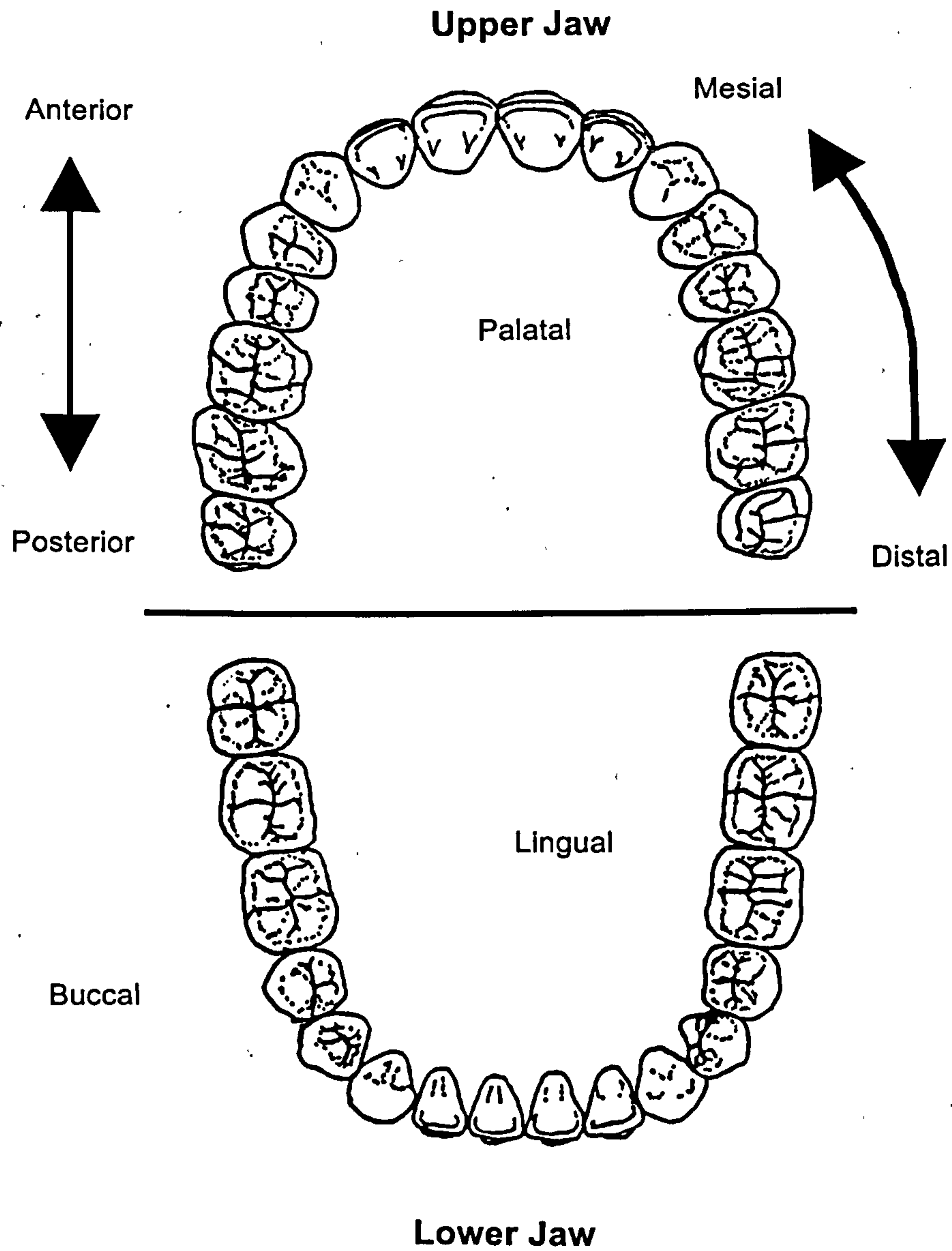


Figure 1. The dental arcade. Adapted from van Beek

2.4.2 TRAITS USED IN THIS STUDY

There are plaster reference plaques for 26 different morphological features in the version of the ASU system used in this study (a 27th plaque was recently added). Several other traits are recorded on a presence/absence basis. From this scope of traits, the number used in this study was pared down to only twelve on the basis of several statistical and heuristic methods such as paired T-tests of test/retest data and assessing overall abundance of the trait in the combined populations. These issues are further discussed in the Reliability and Validity section below. The descriptions of the traits used in this study are adapted from Turner et al. (1991). Only summaries are presented here. Full descriptions of these and the rest of the traits in the ASU system can be found in Turner et al. (1991). They include the name(s) for each person involved in describing each trait and development of its reference plaque, as well as the publication date, if any. These credits are also included here. In some cases, the plaque was developed by Turner and a co-worker (usually a graduate student) but the trait description was not published before 1991. In these cases the format for giving credit is “Turner and co-worker, date, (first published in Turner et al., 1991).”

There are several different systems used to identify which tooth is being recorded. One system that is commonly used by British physical anthropologists in the skeletal reports contained within site reports is the Szigmondy system. This system uses numbers for the permanent dentition (1-8) and lower case letters for the deciduous dentition (a-e) (Hillson, 1996: 8). The numbers increase relative to the position of the tooth away from midline for each quadrant, as shown in figure 2.

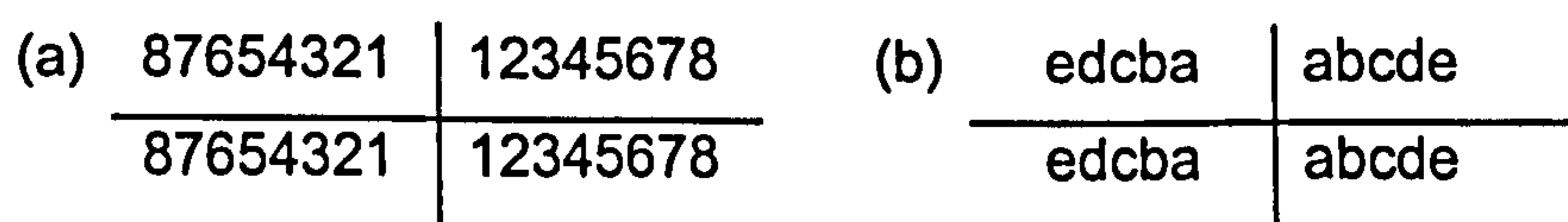


Figure 2. The Szigmondy recording system, for (a) permanent teeth and (b) deciduous teeth.

The method used here uses a set of abbreviations that are more nearly common language. The first letter in the identifier is either ‘U’ or ‘L’ signifying upper or lower, respectively. The next letter identifies the tooth; I = Incisor, C = Canine, P = Premolar, M = Molar. The next character is the number which indicates the place of the tooth in its class; for example, ‘UI1’ indicates Upper First (central) Incisor. This number is excluded from the identifiers of canines because there is only one tooth in the canine class. Premolars are identified as first and second (e.g., UP1, LP2). This method of classification for premolars is used because it is more immediately

recognisable when one is examining the human dental arcade. Physical anthropologists, whose training was based in palaeontology rather than anthropology or human dental anatomy, argue that human permanent premolars are evolutionarily analogous to the third and fourth premolars of other mammals (Hillson, 1996: 7-8).

Upper Second Incisor (UI2) Shovelling: Shovelling affects the lingual surfaces of the upper incisors, canines and lower incisors. It manifests as ridges at the margins of the lingual surface of the affected tooth. The scale for this trait was first developed by Hrdlička (1920). A plaque was developed by Dahlberg (1956), and that was, in turn, modified by Scott (1973). Figure 3 shows this plaque in its final form. The scale runs from a score of zero, where the lingual surface is flat, to a score of six where the mesial and distal ridges are in contact at the cingulum. There is a further grade of seven for the upper second incisor (the tooth used in this study) which describes the “barrel-shaped” incisor. The degree of shovelling appears to be correlated between the incisors and canines. To avoid inappropriately biasing the data for this variable, only one tooth, either the first or second incisor or the canine, should be used for population studies.

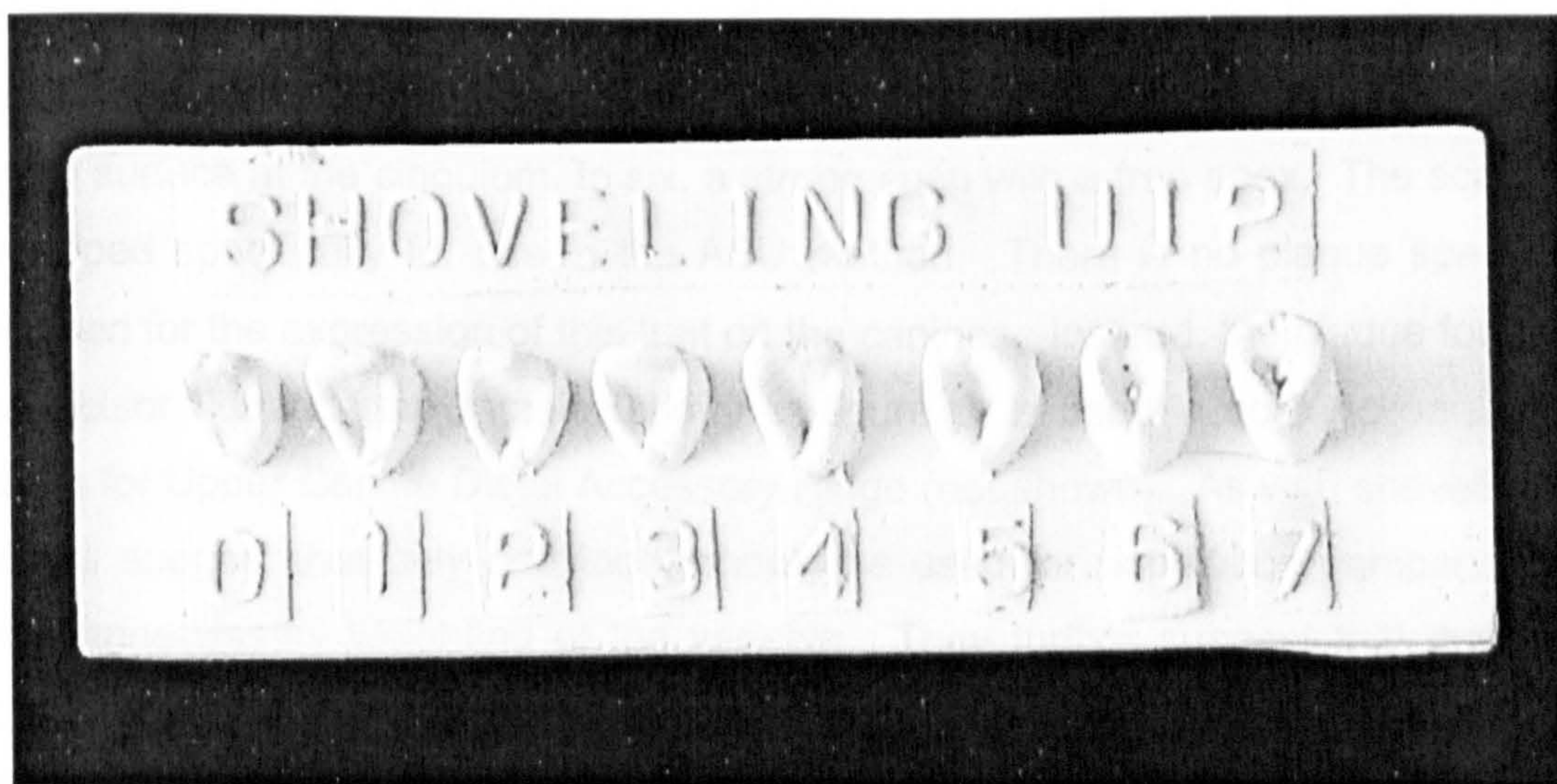


Figure 3. Upper Second Incisor (UI2) Shovelling. ASU plaque. Scores range from 0, no expression, to 7, barrel shaped.

Upper First Premolar (UP1) Double Shovel: Double shovelling affects the upper incisors, canines, first premolars and the lower incisors. This trait is similar to shovelling in that it is expressed as marginal ridges, but in this case the ridges are on the labial surface of the affected teeth. The scale runs from zero, a smooth labial surface, to six, extreme ridges. The reference plaque was originally developed by

Dahlberg (1956), and modified by Turner and Laidler Dowda in 1979 (first published in Turner et al., 1991). This plaque is shown in figure 4.



Figure 4. Upper First Premolar (UP1) Double Shovel. ASU plaque. The plaque for incisors, shown here, is also used for the premolars because the size of expression is the same on the premolars.

Upper Canine (UC) Tuberculum Dentale: This trait is expressed on the upper incisors and canines. It takes the form of a ridge or tubercle on the lingual surface of the cingular area of the affected tooth. The scale includes scores from zero, smooth lingual surface at the cingulum, to six, a strong cusp with a free apex. The scale was developed specifically for use in the ASU method. There is no plaque specifically designed for the expression of this trait on the canines. Instead, the plaque for Upper first Incisor Tuberculum Dentale (shown in figure 5) is used in conjunction with the plaque for Upper Canine Distal Accessory Ridge (not shown). As with shovelling the authors suggest that only one tooth should be used for population comparisons to avoid unnecessary weighting of the variable. They further suggest that the lateral incisor (I2) is the central tooth in this morphogenic field, however the canine is used here as it was shown to be more reliably scored by this researcher.

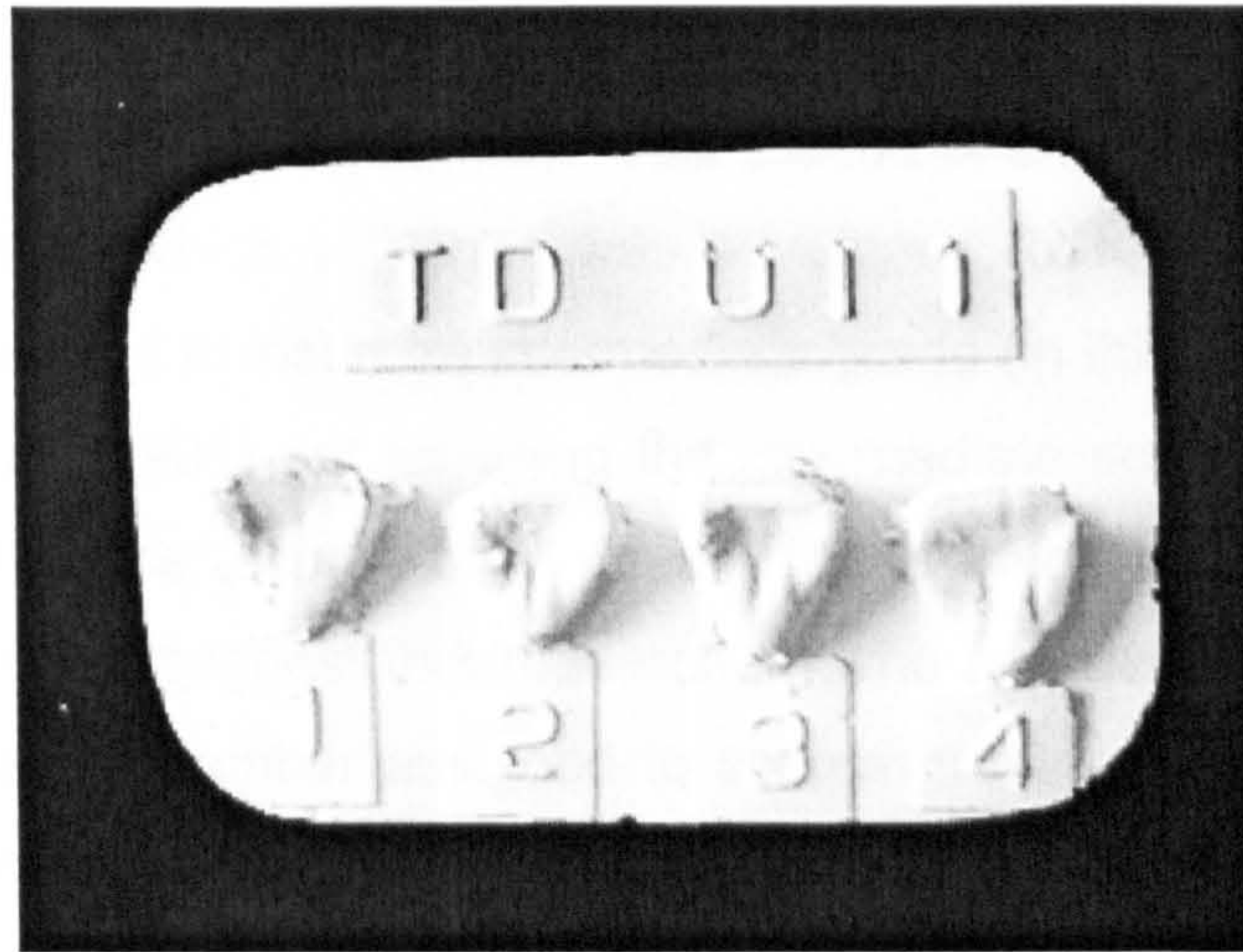


Figure 5. Upper First Incisor (UI1) Tuberculum Dentale. This plaque should be used in conjunction with the plaque for the Upper Canine Distal Accessory Ridge to score the Canines

Upper Canine (UC) Mesial Ridge: This trait affects only the upper canine. Its expression is an enlargement of the mesial ridge of the canine in comparison to the distal margin. The range of expression is from zero, mesial and distal ridges are the same size, to three, the mesiolingual ridge is much larger and incorporated into the tuberculum dentale. The largest grade of this trait is the form that was originally described by Morris and called the “Bushman Canine” (Morris, 1975). The scale was developed by Turner and Dale Klausner in 1979 (first published in Turner et al., 1991). This plaque is shown in figure 6.

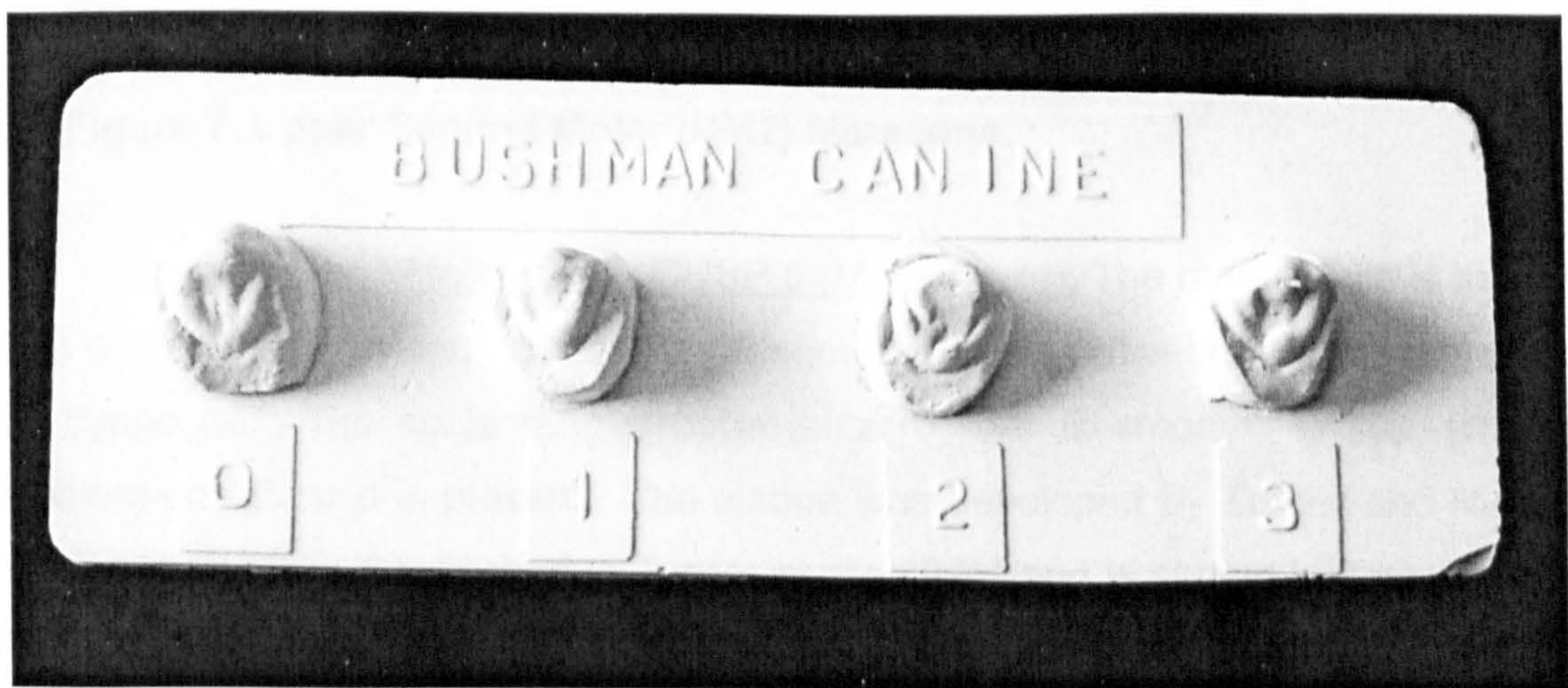


Figure 6. Upper Canine (UC) Mesial Ridge. This trait is also called the Bushman Canine.

Upper Second Molar (UM2) Metacone: The metacone is the third (distobuccal) cusp of the upper molars. The range of expression is from zero,

absence of the metacone (very rare), to six, very large cups equal in size to the hypocone (cusp four of the upper molars). This plaque is shown in figure 7. This is one of several traits for which a plaque was developed, but during field tests the developers found the need to insert an intermediate grade (in this case 3.5). In these situations Turner et al. (1991) opt for using the intermediate score. This is done to avoid having to change the records of all identifications made before the new score was added. They further suggest that researchers who are just beginning to collect data should increase the number assigned to scores greater than the intermediate score (i.e., 3.5 becomes 4, 4 becomes 5 etc.). The scoring range for this trait reflects that change. It should also be noted that need to avoid changing records is not as great as it was in the days before personal computers were readily available. It is fairly simple to write a computer routine to make the necessary changes in computer files, a fact to which this author can attest. The plaque was developed by Turner and Diane Kaschner in 1978 (first published in Turner et al., 1991).



Figure 7. Upper Second Molar (UM2) Metacone.

Upper Second Molar (UM2) CUSP 5 (Metaconule): The metaconule is the fifth cusp of the upper molars. When it is present it appears between the metacone and the hypocone. The scale ranges between zero, site is smooth, to five, when a “medium-sized” cusp is present. The plaque was developed by Turner and Richard Warner in 1977 (first published in Turner et al., 1991) and is shown in figure 8. The scale was based on that developed by Harris (Harris, 1977; Harris and Bailit, 1980).

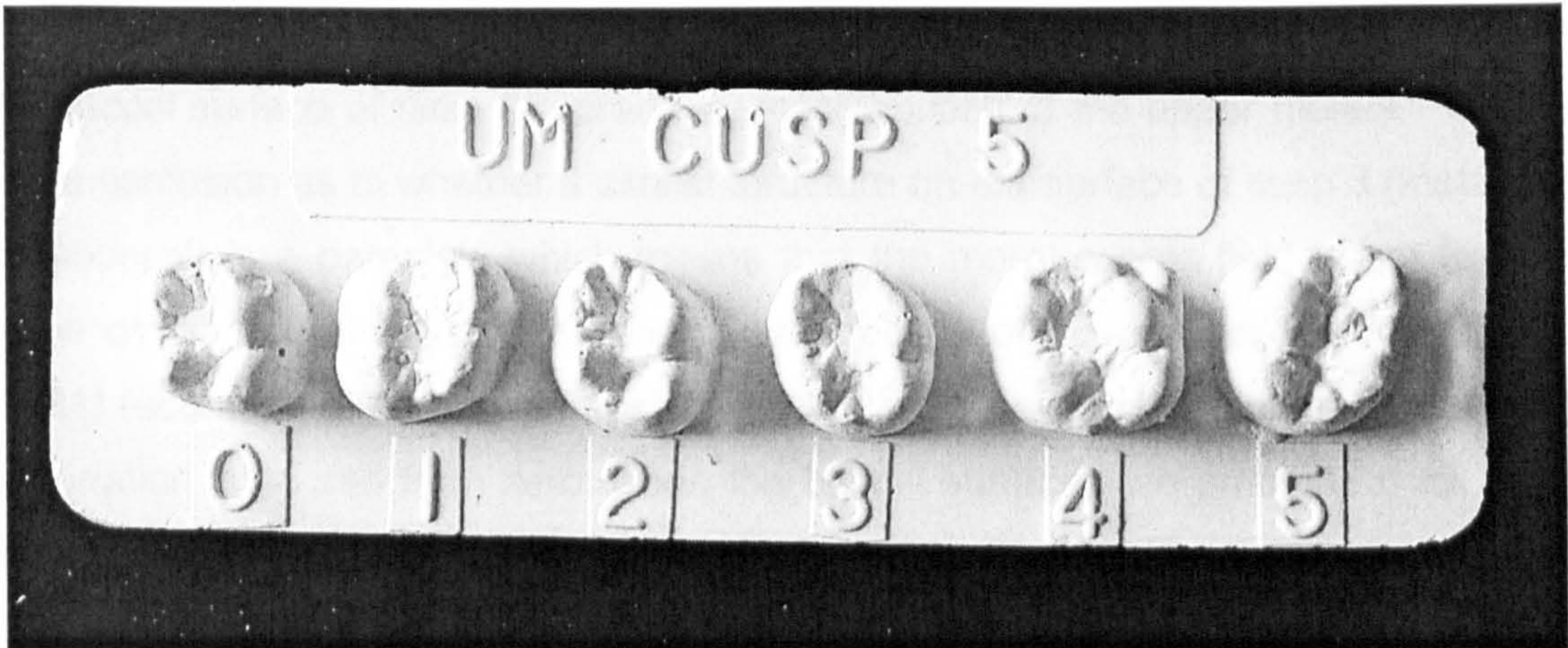


Figure 8. Upper Second Molar (UM2) CUSP 5 (Metaconule).

Upper Second Molar (UM2) Carabelli's Cusp: The Carabelli cusp occurs on the lingual surface of Cusp 1 (protocone, mesiolingual) of the upper molars. The range of expression is from zero, when the site of the trait is smooth, to seven, when there is a large cusp with a free apex. The variability of the expression of this trait is greater than most. The smallest expression (grade one [1]) is a groove, which gives way to a pit without a groove in grade two (2). Grades three (3) and four (4) are "Y-shaped" depressions, and scores five (5) through seven (7) are increasing sizes of cusps as shown in figure 9. This trait was originally described by Georg von Carabelli in 1842. The range of variability was described, and a plaque developed by Dahlberg (1956).

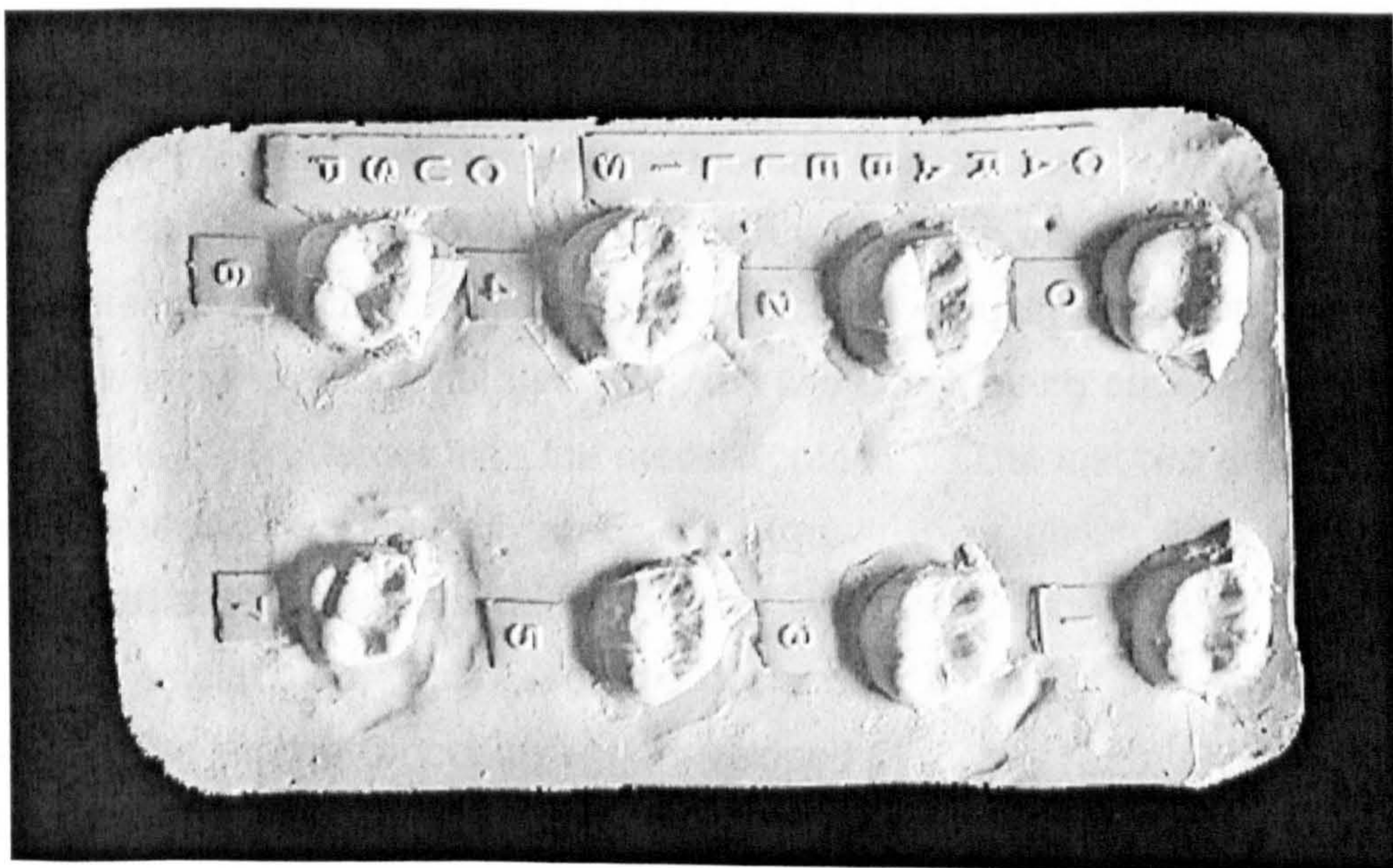


Figure 9. Upper Second Molar (UM2) Carabelli's Cusp.

Upper First Molar (UM1) Parastyle: This trait is an accessory cusp found on the buccal surface of cusp 2 (paracone, mesiobuccal) of the upper molars. There is some confusion as to whether a similar structure on the surface of cusp 3 (metacone, distobuccal) is a parastyle which means that the morphogenic field is not fixed, or some other, as yet unidentified, trait. Irrespective of this confusion, Turner et al. (1991) recommend that any expression on the buccal surface be scored. The range of variation is scored from zero, when the buccal surfaces are smooth, to six, when there is a peg-shaped crown attached to the root. The trait was first described by Bolk (1916). The plaque was developed by Turner and Joseph F. Kaitch in 1974 (first published in Turner et al., 1991) and is shown in figure 10.

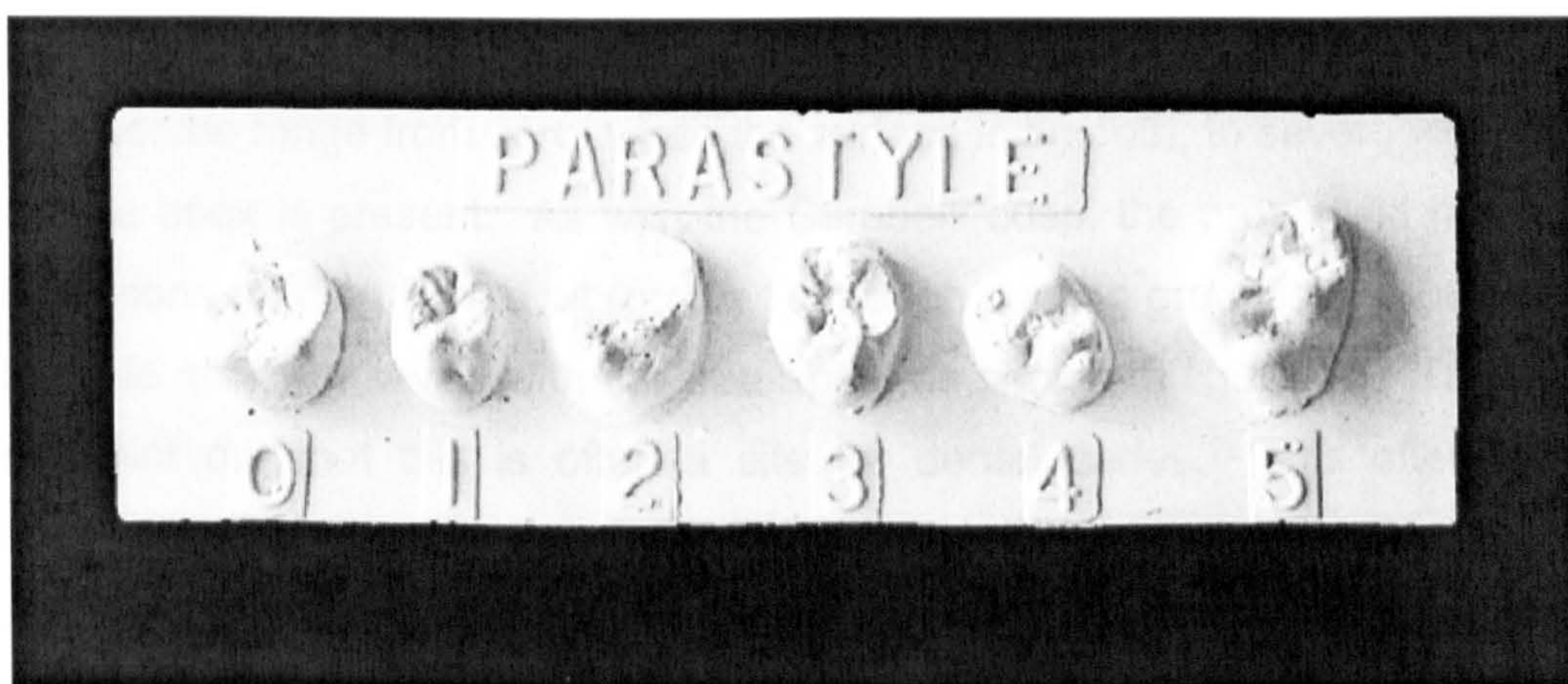


Figure 10. Upper First Molar (UM1) Parastyle.

Lower Second Premolar (LP2) Lingual Cusps: The ASU system scores only the variation in the size of lingual cusps on the lower premolars — not shape. The scores range from zero, where there is one lingual cusp, to nine, where there are three cusps and the mesial cusp is much larger than the medial and/or distal cusp. The intervening scores grade the size of cusps (usually two) from the mesial cusp being larger than the distal (grade 2), the two cusps being equal (grade 4), the distal cusp being much larger than the mesial (grade 7). The last two grades are for teeth with three cusps, either all three equal (grade 8) or grade 9 as described above. Turner et al. (1991) also added a grade of 'A' (absent) for teeth that show only a ridge and no actual cusp. This grade did not appear in any of the samples used in this study. The scoring procedure was developed by Scott (1973) and the plaque (figure 11) was developed specifically for the ASU system.



Figure 11. Lower Second Premolar (LP2)

Lower Second Molar (LM2) Protostylid: This is an accessory cusp found on the buccal surface of cusp 1 (protoconid, mesiobuccal) on the lower molars. The possible scores range from zero, when the surface is smooth, to seven, when a cusp with a free apex is present. As with the Carabelli cusp, the protostylid has several manifestations ranging from a pit (grade 1) through curving grooves and bulges up to the ultimate score of seven with the free apex, as shown in figure 12. Turner et al. (1991) point out that this is often a site for dental caries. This often leads to underreporting of the trait because the tooth is either destroyed or, in modern populations, filled. Either way, the site of the trait is destroyed. The reference plaque was developed by Dahlberg (1956).

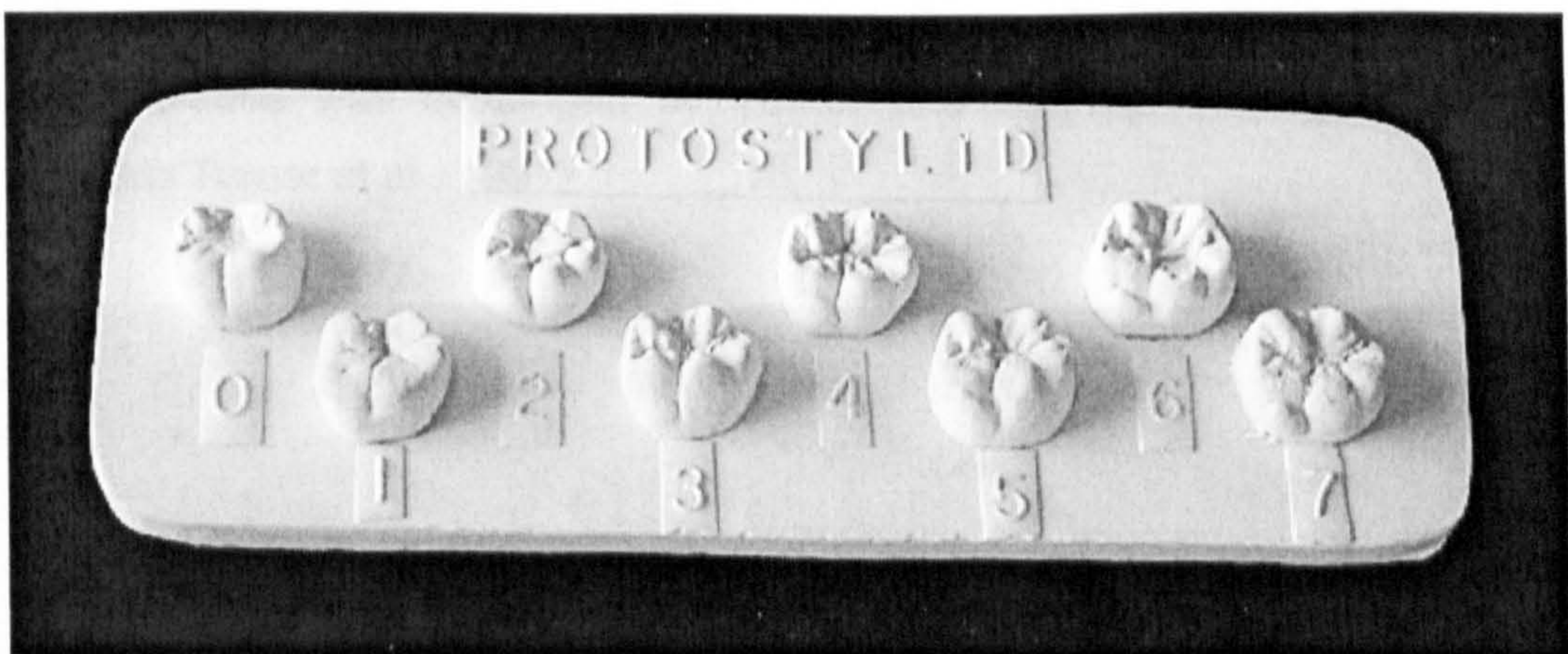


Figure 12. Lower Second Molar (LM2) Protostylid.

Lower Second Molar (LM2) Cusp 5: The hypoconulid (distal occlusal surface) is scored from zero, when there are only four cusps present, to five, when the cusp is very large. There is no way to be certain if, when five cusps are present, the fifth cusp is a cusp 5 or a cusp 6. In the ASU system, a single cusp in the distal position

is assumed to be cusp 5 and cusp 6 is a supernumerary cusp. The reference plaque, shown in figure 13 was developed by Turner and Richard Warner in 1977 (first published in Turner et al., 1991) and is shown in figure 13.



Figure 13. Lower Second Molar (LM2) Cusp 5.

Lower First Premolar (LP1) Tomes' Root: This is the only trait involving root form in this study. The anomaly is named for C. S. Tomes who first described it in 1923 (Turner et al., 1991). The current scoring procedure represents the recognition that the trait is actually a continuum of form from single to double root. The range of scores, as shown in figure 14, is from zero, when there is only one root with, perhaps, a slight developmental groove, to five, when there are two roots present. The reference plaque was developed by Turner and Stephan Herzog in 1979 (first published in Turner et al., 1991).



Figure 14. Lower First Premolar (LP1) Tome's Root.

Previous published analyses of these data (Lloyd-Jones, 1995; Lloyd-Jones, 1997) have included lower second molar cusp number. This trait was removed from this analysis because the discriminant analysis (discussed below) showed this trait to be highly correlated with lower second molar Cusp 5 in these populations. In theory the traits are not due to the same genetic factors, but at least in this case, it gave the appearance of causing double weighting for these variables. The resultant absolute values of the MMD scores did change slightly, but the relationships shown between sites did not.

2.5 THE PROBLEM OF CEMETERY DEMOGRAPHICS

The validity of any biologically based study of past populations depends on how closely the demographics of the death assemblage, or cemetery population, reflect the population that filled the cemetery. An accurate understanding of the sex and age distributions is the best way to assess whether the available sample truly reflects the populations that had been living around that cemetery (Chamberlain, 1994). Unfortunately it is not always possible to know whether the determinations of age and sex are correct (Jackes, 1992; Rhine, 1990), which makes detailed demographic analysis problematic. In most cases, the representative nature of archaeologically derived samples cannot be demonstrated (White, 1991: 374) so some degree of error is inevitable. The bone reports for the cemeteries used in this study, and this author's own assessments do not always concur on the diagnosis of sex and age. There does, however, seem to be broad agreement on the overall percentages of distribution for sex and age in these cemeteries. As this study is interested in the biological profile of individuals and the population as a whole found in a cemetery, the demographic profile, at the level of who is related to whom within the cemetery, is not as important as it may be for some other types of study. Therefore, each cemetery is treated as if it represents at least a reasonable portion of each of the populations who used them.

Furthermore, dental morphological traits show very little sexual dimorphism and the dimorphism that does exist is "usually inconsistent among samples and low-order in magnitude" (Scott and Turner, 1997: 108-109). Likewise, the size of traits is unaffected by age, except in the case of attrition or tooth loss. Both of these subjects will be discussed further in the materials and methods section below. Knowing the distribution of age and sex can provide important information about the inclusiveness

of the cemetery population and should be included when possible (see further research below).

Another problem for this type of study is that a cemetery provides only a sample of a population (White, 1991; Ubelaker, 1987), not the full population that lived in a certain area. Some of the factors that affect how the assemblage reflects the original population include social differentiation in burials, either by location or cemetery exclusion, taphonomy, and population movement.

In regards to social differentiation, there are several reasons why only a certain segment of the society would be interred in a given cemetery. There may be wealth and status issues, for example, where only the elite are buried inside a church or next to the church walls. The underclass or socially liminal individuals (e.g., suicides), on the other hand, may be buried along the periphery, or even outside of the cemetery boundaries. There may be religious segregation such as the designation of a Jewish cemetery (e.g., Sofaer et al., 1986). While these are relatively modern examples, countless examples of mortuary segregation by age and sex also exist in prehistory (e.g. Brown, 1981; Buikstra, 1981; Goldstein, 1981; O'Shea, 1981). "To assume that any single cemetery comprises a representative sample of prehistory mortuary behaviour or osseous materials is unwarranted until the inclusive nature of the cemetery is demonstrated" (Buikstra, 1981: 125). The second factor affecting population representation in burial samples is taphonomy. Taphonomy is the "science of the laws of embedding or burial" (Lyman, 1994: 1). Lyman names four main taphonomic effects: disarticulation, scattering/dispersal, fossilisation (diagenesis) and mechanical alteration. Disarticulation, or the removal of soft and connective tissues by animal scavenging, human butchery (e.g., beheading) or putrefaction starts the process. Dispersal, in its strictest form, begins immediately in the sense that a bone that is disarticulated is dispersed from its usual location. On a longer time scale, human or other animal transport and fluvial transport can disperse the skeletal elements over a larger area. Diagenesis is the change in chemical composition of bone. The results of diagenesis vary widely depending on the composition of the soil matrix, its pH, temperature and water content. The results of diagenesis that are probably most often mentioned in bone reports for sites from the periods of interest here are weathering and fragmentation. Mechanical alteration is often seen as the result from deep ploughing, fluvial activity and compression of the bone in deep soil. Another less often noted form of taphonomic loss is 'curation' (Adams, 1996: 3). This type of loss can include sampling strategies that disregard a

portion of the site, discarding of less well-preserved skeletons, poor curation techniques that destroy material, and things 'just getting lost' in the storage facility.

The movement of people from one location to another will also have an effect on the composition of a death assemblage. The loss of locals to exogamy and the inclusion of others from endogamy will cause slight deviations from the local birth cohort population. It is important to note, however, that 'outsiders' will be contributing their genes to the next population, and will become 'invisible' in subsequent generations. Traders coming or going would have the same type of effect, although in different ways depending on whether their genetic material left behind in the cemetery assemblage is in the form of a corpse or as offspring. Finally, the last people alive before a cemetery goes out of use are never included for the very simple fact that there is no one else left to bury them.

The problems of taphonomy and population movement are not so easily discarded. In theory, these problems could skew the results by reflecting only the non-representative subsets of the populations. The relationships among the various populations as revealed in this study would not be likely to have occurred by chance if the populations used were not related to the surrounding populations in some systematic way. These relationships suggest, therefore, that the populations are, at least to some extent, representative of those people living in those areas.

2.6 THE CEMETERIES

It should be noted again that the terms Romano-British and Anglo-Saxon are used in describing the cemeteries and the skeletons that come from those cemeteries, but they are used as a matter of convenience. Those terms describe the context in which the remains were found and ascribed to them by the excavators of the sites. The use of contextual identification, as defined by the geography or the cultural material, is standard practice, and is completely acceptable in terms of identifying the groups by their ethnicity as it can be seen archaeologically. That is, the ethnicity as placed on them by the archaeological interpretation. Unfortunately, it is often assumed that the biological identities of the skeletons found in these contexts are the same as the cultural identities, which, as has been stated before, is not necessarily the case.

The Romano-British populations examined were Icklingham in Suffolk, Lankhills in Winchester, Hampshire, and Queenford Mill in Dorchester on Thames, Oxfordshire. The Anglo-Saxon sites were Brandon, which is about twelve miles from Icklingham, Portway Down, Andover, Hampshire about fifteen miles from Lankhills,

Berinsfield about one mile from Queenford Mill, and Lechlade Butler's Field which is about thirty miles up the Thames from Queenford on the Gloucestershire-Oxfordshire border. The locations are shown on the map in figure 15.

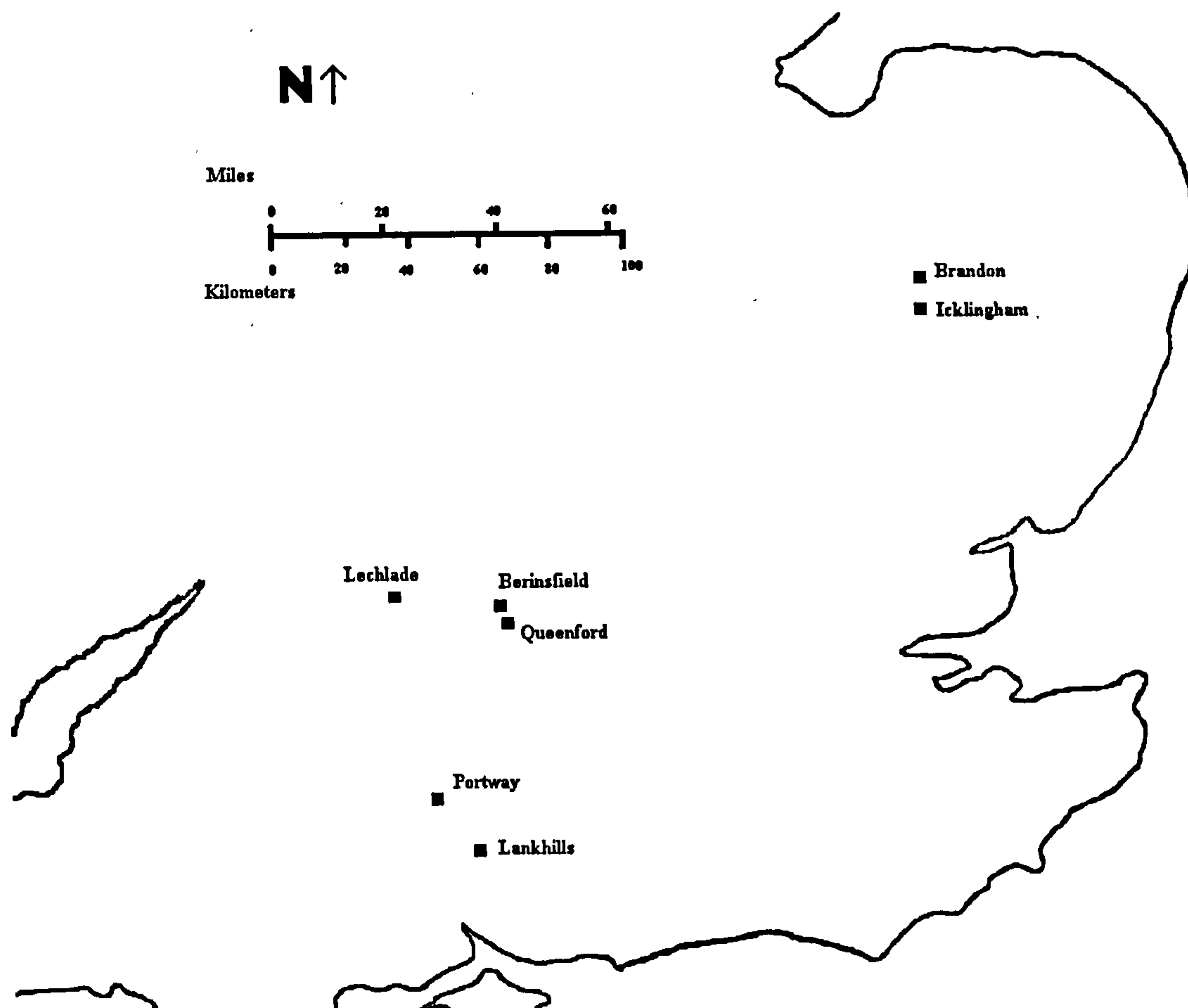


Figure 15 Map of the sites in this study.

2.6.1 SITES

The criteria for choosing the sites used in this study are as follows. First, a sufficient number of inhumations must be present. Second, that the site have a matching site from the other time period (i.e., a Romano-British site to compare with an Anglo-Saxon site and vice versa) preferably near by. Lastly, it should be possible to obtain permission from the excavator and/or curator of the material.

As was described in the Hypothesis testing section, the research model used in this study is designed to test for continuity or discontinuity across both time and space. To test across time, sites from the two periods of interest (i.e., Romano-British and Anglo-Saxon) which are fairly near one another are examined. A hypothesis of massive Anglo-Saxon invasion accompanied by massacre of the local population would predict a discontinuity across time, even where the sites are geographically close by one another. A hypothesis of assimilation of culture without

much in the way of biological contact would predict that the sites should be biologically very similar regardless of cultural material. A summary of the sites and the abbreviations used to identify them in tables and figures is given in table 1 following the site details.

In the following site summaries, there are several occasions where the number of bodies recovered from a site differs from the number of bodies examined at that site. In some instances, this was due to the portion of the body recovered did not include the head. On other occasions it was due to the individual having had no teeth left at the time of death. The one occasion when the number examined for this study is higher than the number examined by the specialist who wrote the report (Calvin Wells for Icklingham) it is probably due to the remains of two individuals having been given in the same context number.

Romano-British Sites

Icklingham: Suffolk (IKL). The site is located to the south east of the present day village of Icklingham above the floodplain of the river Lark. The excavation was directed by RJC Mowat of the Suffolk Archaeological Unit in 1974. Preservation of the bone was variable, some being nearly complete but most were very fragmentary. Perhaps because of the fragmentation, the site report is slightly confusing as to the number of bodies found. There is mention of forty-five, forty-one and, in Calvin Well's section, forty-seven burials and a total of fifty skeletons. Wells reports only twenty-five skeletons had teeth that could be examined, but the current study includes twenty-six. These relatively modest numbers make Icklingham the smallest site used in this study. The grave goods and other evidence suggest that the cemetery was in use from circa AD 350 through AD 400 or 420. The remains are housed in the Suffolk County Council warehouses in Bury St. Edmunds. The site report is published by West and Plouviez (1976).

Queenford Mill (Farm): Dorchester on Thames, Oxfordshire (QF). The main section of this site was discovered in 1972 when Amey Gravel Company reported finding human bones during preparation for gravel extraction. At this time, a two-week rescue excavation by Oxford City and County Museum and the Upper Thames Archaeological Committee revealed 188 graves. Eighty-two of those graves were then excavated (Chambers, 1987). Construction of the Dorchester Bypass in 1981 allowed for the examination and recording of the remaining graves to the South. During that excavation 102 graves were identified of which a further 82 were

excavated. The 164 excavated graves represent only a small portion of the 2,400 people estimated to have been buried in and around the cemetery (Chambers, 1987). Seventy individuals from the original excavation and another 33 from the Dorchester By-Pass were examined for this study. As the two sections of this site were scored almost two years apart, they were originally treated as separate sites. Statistical analysis revealed that there was no significant way to distinguish between them, so the scores were pooled. This brings the total number of individuals from Queenford included in this study to 103. The site is located 0.7 kilometres north of Dorchester on Thames and about 600 metres from the Berinsfield site. Radiocarbon dates suggest that the use of this cemetery began in the late fourth century and continued to mid-sixth century.

Lankhills: Winchester, Hampshire (LANK). The site was discovered in 1961 during building at Lankhills School. Excavations did not begin until 1967, but continued on for the next five years. The site was excavated by the students from an astounding array of local schools with additional help from Winchester College and the Hampshire County Council. The location of the site is some 500 metres from the north gate of Winchester and close to the main road leading to Cirencester. There is very little evidence for activity during the Bronze and Iron Ages, and only slightly more activity during the early Roman period. Most of the dating evidence is in the form of pots and coins found in graves, none of which predate AD 300. The excavators give a start date of c. AD 310 for the cemetery and an end date of c. AD 410. The end date is based on the absence of Quoit-brooch style metalwork (Clarke et al., 1979). A total of 439 inhumations are reported. Of these, 408 were at least partially excavated. The dental material from 197 of these are included in the current study. The materials are currently held by the Winchester City Museum Service.

Anglo-Saxon Sites

Berinsfield Wally Corner: Berinsfield, Oxfordshire (BER). This site has been observed as a cropmark complex since 1934. The site is 1.1 kilometres north of Dorchester near the river Thame, a tributary to the river Thames. The excavation was brought about by discoveries made during gravel extraction. It was excavated in 1974 over a three-week period by the Oxford Archaeological unit. The cropmarks showed evidence of three to four centuries of Romano-British occupation (Boyle et al., 1995). There is also some evidence of occupation that predate the Romano-British enclosures. The main focus of this excavation was the Saxon cemetery. Some features of the site are reminiscent of Saxon features found in SE England and

are very rare in the Thame valley. The only other known example is from Lechlade, Butler's Field (Boyle et al., 1995). It is reported that approximately two-thirds of the original Anglo-Saxon cemetery was excavated. One-hundred-fourteen inhumations were recovered from 100 graves with a further four cremations. Of these, 73 individuals had sufficient numbers of permanent teeth to be examined and included in this study. The grave goods recovered indicate that the cemetery was in use beginning in the mid-fifth century AD through the late sixth or early seventh century AD. The remains are stored in the Department of Archaeology and Prehistory at Sheffield University.

Brandon Staunch Meadow: Brandon, Suffolk (BRD). The site was excavated by the Archaeological Section of the Suffolk County Council as a rescue operation in 1980, with excavations continuing through 1987. It is located in the valley of the Little Ouse River. In normal times the site is a sand ridge surrounded by peat. In times of flood the area of occupation becomes an island. The site is a complete settlement with a church, two cemeteries and at least 25 post-built, rectangular buildings. Evidence of 220 inhumations was found. Of the total number of bodies excavated, 193 proved sufficiently complete for examination and inclusion in this study. Classified as Middle-Saxon, the evidence from radiocarbon dates, dendrochronology, pottery and coins suggest that the site was in use between AD 600 and 900 (Carr et al., 1988). The remains are housed in the Suffolk County Council warehouses in Bury St. Edmunds along with the remains from Icklingham.

Portway Down: Andover, Hampshire (PW). The excavations of the Saxon cemetery at Portway (East) began in January 1974 and were completed in July 1975 due to the efforts of the Test Valley Archaeological Committee (TVAC) and the Andover Archaeological Society (AAS). This portion of the site yielded 69 inhumations and as many as 87 cremations. In 1981 a further section of the site (Portway West) was excavated by TVAC and AAS. These excavations yielded another 14 individuals. In all, 53 individuals were examined for the current study. The site of Portway Down is situated overlooking the valley of the river Anton which is a tributary of the river Test. It is near the Roman track Harrow Way which intersects a Roman road from Winchester. The dates for use of the cemetery as shown by grave goods are placed as beginning in the late fifth century and ending around AD 600. The remains are held in the storehouse of the Hampshire County Museum Service. The excavation reports for the two sites are published by (Cook and Dacre, 1985) and (Scott and Powell, nd).

Lechlade, Butler's Field: Lechlade, Gloucestershire (LBF). This cemetery was excavated as part of a larger excavation of a site known to show activity from the Neolithic to the end of the Anglo-Saxon period. Examination of the grave goods led the excavators to suggest that the period of use for this cemetery was between the mid- or late-fifth century AD to the late seventh century AD. The excavations were carried out by the Oxford Archaeological Unit over a twelve-week period in 1985. It was done as a rescue excavation in advance of a housing development by the Cotswolds District Council. A total of 219 inhumations in 199 graves as well as 29 cremations were recovered (Boyle et al., 1998). Of these 154 were examined for this study. The inclusion of Lechlade in this study was due, in part, to the fact that permission to examine this cemetery was granted prior to scoring of Berinsfield. The simple solution would have been to eliminate this unpaired cemetery from this study. However, it was instead used a) to provide an extra site with which to test whether differences could be found using the ASU method and b) to provide a site relatively close to another pair. As it turned out, Lechlade also provided the impetus to refine the statistical methods to understand individual relationships within and between cemeteries. The remains were scored at, and are housed in, the Cotswold Countryside Collection in Northleach.

Site	Abbreviation	Period *	County	Total n
Icklingham	IKL	R-B	Suffolk	26
Queenford Mill	QF	R-B	Oxfordshire	103
Lankhills School	LANK	R-B	Hampshire	197
Brandon Staunch Meadow	BRD	A-S	Suffolk	193
Berinsfield Wally Corner	BER	A-S	Oxfordshire	73
Portway	PW	A-S	Hampshire	53
Lechlade	LBF	A-S	Oxfordshire/ Gloucestershire	154

Table 1. Summary of the sites used in this study. * R-B = Romano-British, A-S = Anglo-Saxon

2.7 RELIABILITY AND VALIDITY

A particular variable may do an exceptionally good job of measuring differences among populations, but if the scale of measurement is not reliable, the data will be of little use. On the other hand, the most reliable scale in the world does not necessarily measure a valid variable (Madrigal, 1998: 4). Once the reliability of a scale of measurement is shown to be reasonably good, the validity of the variable can be tested.

One of the acknowledged difficulties in using nonmetric traits is that the scoring of morphological characters is highly subjective (Hillson, 1996; Scott and Turner, 1988; Scott and Turner, 1997; Sofaer et al., 1972; Turner et al., 1991). One of the best ways to reduce subjectivity is to compare the item being assessed against a reference. The ASU method was designed just for this reason. The varying degrees of expression for twenty-six of the morphological features used in the ASU system are represented on plaster reference plaques. These plaques reduce the amount of error between observations making dental traits more reliable than most other nonmetric traits (Saunders, 1989)

Even with reference plaques, however, there is still the problem of diagnosis of the trait. Several decisions must be made with each assessment. First it must be determined if the tooth has been so affected by use, or disease that the location of the trait under consideration is still present. If the site is present, it must be determined if the trait is expressed. If there is some expression of some sort at the site of the trait, it must be diagnosed as being that trait or some anomaly. The researcher is faced with the problem of being overcautious and thereby reducing the sample size, or recklessly introducing erroneous data. The best advice is "if in doubt, don't guess" (Scott and Turner, 1997: 72).

To test the repeatability of observations, the traits from one of the cemeteries in this study (Queenford Mill) were scored twice. The two scoring sessions were separated by approximately two months to avoid familiarity with the sample, and thus avoiding unconsciously biasing the results. In the original analysis, scores from each session were compared by paired T-Tests following the example of several researchers (e.g. Sofaer et al., 1972; Scott, 1973; Nichol and Turner, 1986). With the critical value set at $\alpha=.05$ for a two tail test, the results showed significant differences in just 16 of the 336 variables tested. Selection of variables continued using the T-Tests as a guide. The least reliable traits (those which showed the least repeatability) were removed from further consideration. Selection from the remaining

variables was based on factors such as abundance in the population (i.e., there should be a reasonably large number of teeth on which that trait can be scored) and variability in the population. 'Variability in the population' does not mean variability between the cemeteries (that would have been purposely selecting the variables to give a desired result), but that the trait should have some variation of expression across the whole sample of all the individuals used in this study.

One problem with paired T-Tests is that they assume normal distribution of the differences (Ott, 1988: 197). These data are not normally distributed, so the results from T-Tests may not be statistically relevant. Fortunately, there are methods available that do not make assumptions of normality. Non-Parametric tests are sometimes referred to as being "distribution free" (Goodman et al., 1994; Welkowitz et al., 1982). Scott and Turner (1997) use the non-parametric Spearman correlation to assess test/re-test reliability. The scores for the Spearman correlations of the test/re-test scores for the traits used in this study are shown in table 2.

TRAIT	Right/Left	Correlation Coefficient
UI2SHOVEL	Left	0.879
	Right	0.897
UP1DSHOVE	Left	0.854
	Right	0.827
UCTDENT	Left	0.804
	Right	0.842
UCMESRIDG	Left	0.751
	Right	0.742
UM2METACO	Left	0.894
	Right	0.859
UM2CUSP5	Left	0.878
	Right	0.846
UM2CARABL	Left	0.817
	Right	0.779
UM1PARAST	Left	0.622
	Right	0.676
LP2LCUSPS	Left	0.901
	Right	0.784
LM2PSTYLD	Left	0.694
	Right	0.750
LM2CUSP5	Left	0.816
	Right	0.830
LP1TOMESR	Left	0.792
	Right	0.757

Table 2. Spearman correlations of test/retest scores; correlation coefficients signifying accuracy of initial data test.

The correlations range from 0.622 for the left upper first molar parastyle to 0.901 for the left lower second premolar lingual cusps. All of the correlations are significant at the 0.001 level for a two-tailed test. These scores are comparable to the scores reported by Scott and Turner (1997).

There are several areas where errors could occur. The first is by misclassification of the grade of the trait, or misidentifying the tooth (e.g., as a left premolar in the first session and as a right premolar in the second). The second is in recording the scores by hand (e.g., the score is written in the wrong space on the sheet). Transcription errors can also arise in the stage of computer data entry. Lastly, the trait may not be available in both sessions. If a fragile tooth breaks after the first session, it may be impossible to score it in the second. There are also difficulties in examining the roots of teeth. A tooth that comes out of the socket very easily in the first session may not yield in the second. This, in fact, did cause a difference in the T-Test for 4 different teeth, which were removed from consideration and further analysis. Every attempt is made to avoid these problems, but many do creep in.

2.8 DATA COLLECTION, RECORDING AND ARCHIVING

2.8.1 DATA COLLECTION

The remains from five of the cemeteries (Portway Down, Queenford Mill, Brandon, Icklingham, Lankhills) were brought to the Archaeology department at Glasgow University for analysis. The remains from Berinsfield and Lechlade could not, for various reasons, be taken from their respective storage places and, therefore, had to be analysed in Sheffield and North Leach, respectively. Material from Dorchester Bypass was scored at the Oxfordshire Museum Service's new location just outside of Oxford. It should have been included with the Portway material but was not because the material was separated from the collection during the move to new storage areas.

Photographic records of the material were not made due to financial and time constraints, and because the facilities for taking quality photographs were not uniformly available. Even though the specialised photographs were not taken for this

study, the archives for each site should contain photographs taken at the time of excavation or later by the specialists who prepared the bone reports.

Exact procedures for identification varied with each site because of the variety of storage and labelling methods used by the different excavators and curators. In essence, the tag or label on each box or bag (usually a context number) was used as the primary identifier. In several cases multiple individuals were found in a single container. In these cases a letter was arbitrarily assigned to each individual (e.g., LBF111-A, LBF111-B, etc.). As the analysis was done 'blind,' that is, without access to a bone report, these identifiers do not necessarily correspond to those in the site catalogue. While having the information from the catalogues would have been helpful in some respects, it was judged that remaining blind to other researchers conclusions was of greater benefit.

The teeth from each individual were arranged on the workbench by position in the mouth. Placement of loose teeth was verified by comparison to the empty sockets in the jaw whenever possible. In cases where the teeth were found in place in the jaw, an attempt was made to remove them gently so root form and number could be assessed. The removal attempt was abandoned if it appeared that damage would result from the removal. It is interesting to note that on the re-test of Queenford Mill, some of the teeth that had slipped easily out of the jaw on the first scoring session could not be removed on the second, and vice versa. In most cases where the teeth had been glued into place, no attempt was made to remove them even though a small amount of acetone would have dissolved the glue. The few cases where glued teeth were removed were those in which the tooth was glued in the wrong position. For example if the tooth was in the proper location but rotated 180 degrees, or the wrong location such as a lower left third molar glued in the rather unlikely position of upper right fourth molar (occasional examples of fourth molars are known to exist, but are very rare (see Suzuki et al., 1995) and never occur outside of normal alveolar bone as was the tooth alluded to in this case).

Observations were made by naked eye in the best available light with ASU reference plaques close at hand. Traits of finer detail (e.g., lower molar groove pattern) were assisted by the use of a hand-held 10X magnifying glass. Data were recorded by hand on copies of the ASU scoring sheets (appendix I) with slight modifications made for this study.

The data were entered into a computer using dBase IV. As dBase IV has a limit of 256 fields per database (Simpson, 1989; Townsend, 1989), and the ASU system has approximately 360 potential observations per individual adult dentition

(not counting metrics) plus about 300 per deciduous dentition, a fairly complex database system was required. As it is important that each observation (including the fact that an observation was not possible) be recorded, and that each missing observation be noted, and that each observation can only have one state, a database with a one-to-one relationship was needed. Due to the field limitations of dBase a series of six separate databases, one each for the permanent upper jaw, permanent lower jaw, deciduous upper jaw, deciduous lower jaw, permanent metrics and deciduous metrics, was designed. This study was designed to use only non-metric traits of the permanent dentition, so in practice, only information found in the first two databases was used. The data in the other databases are available for use in other studies should they be needed.

To facilitate data entry, forms that mimic the ASU scoring sheets were created. These computer forms include an error-checking facility that does not allow characters outside the allowable range for each trait to be entered, thus eliminating one potential source of data entry error. Other features of the system include an interface that allows a researcher to set up a complete set of database files for each new site by simply entering the name of the site and a unique identifier (usually an abbreviation of the site name). There are also modules for tabulation of scores by site or by trait and for calculating MMD (See statistics section below) using different combinations of sites and traits.

Data were collected from the dental material of the seven sites described above. The material from Brandon, Icklingham, Lankhills, Portway and Queenford were gathered from their respective storage locations and brought to Glasgow University Archaeology department. The material from Berinsfield was scored at the University of Sheffield. The Lechlade material was scored at the Museum of Country Living in North Leach, Gloucester. All observations were made in best available light and in accordance with the ASU scoring method, also described above. All scores were written by hand onto ASU score sheets (appendix I), and then entered into a computer using the data management program described below.

2.8.2 THE DENTAL DATABASE MANAGEMENT SYSTEM (COMPUTER PROGRAM)

A database management system was devised to keep track of the information generated by using the ASU system. A database is a file that holds an array of information in such a way that a user can retrieve the information with a minimum of effort. A database management system is a complex file system, a collection of databases, and the programs that integrate them and make them work together.

Databases are composed of fields and records. Fields are data units and contain the information about a specific variable. Records contain the information about each person as that information relates to the individual. Visualise a spreadsheet. In a database, fields correspond to the columns of a spreadsheet and records are like the rows of a spreadsheet. Databases and database management systems can be used to store data and manipulate the information they contain to calculate statistics in order to formulate models and more fully analyse the data.

In the database system for the ASU system, the number of variables scored for each individual (totals 426 variables for adults) and includes the morphological traits for each tooth, length and breadth measurements, sex and age, as well as information about the burial site. The parameters governing the format of this database are 1) only one possible score is allowed for a given trait within each field (a one-to-one relationship), and 2) the score of zero is possible for most of the traits; therefore, it is important to differentiate between missing data and the score of zero by assigning a unique value to fill in for missing data.

The simplest way to store this information would have been to use one large database file. However, since dBase IV restricts the number of available fields, or variables allowed, to 256 per file, it should be self-evident that it is not possible to store the 426 variables used in this study in a single file. To accommodate all of the available information, a rather complex database management system of separate database files, with each record linked by a unique identifier, was needed. The most logical method for dividing the data files was to place the scores for the upper jaw in one file, the lower jaw in a second file and the metric data in a third. An additional modification was required in that adolescents often have a mixed dentition (some deciduous and some permanent teeth in the mouth at the same time) which necessitates separate files for deciduous dentitions and permanent dentitions. To separate the data sufficiently, a total of seven files are used to hold all of the possible raw data for any given individual—one for upper permanent teeth, one for lower permanent teeth, one for measurements of permanent teeth, one for upper deciduous teeth, one for lower deciduous teeth, one for measurements of deciduous teeth and one for results of counting traits. As most of the data in these files were not used beyond the initial exploration phase, the bulk will be used in later studies (see further research). To facilitate file management and organisation, a program called 'Dental' (appendix II), as well as several subroutines used by this program, was written within dBase IV. The opening screen of the dental program presents the user with three menu options. They are Data, Statistics, and Exit (figure 16, flowchart I).

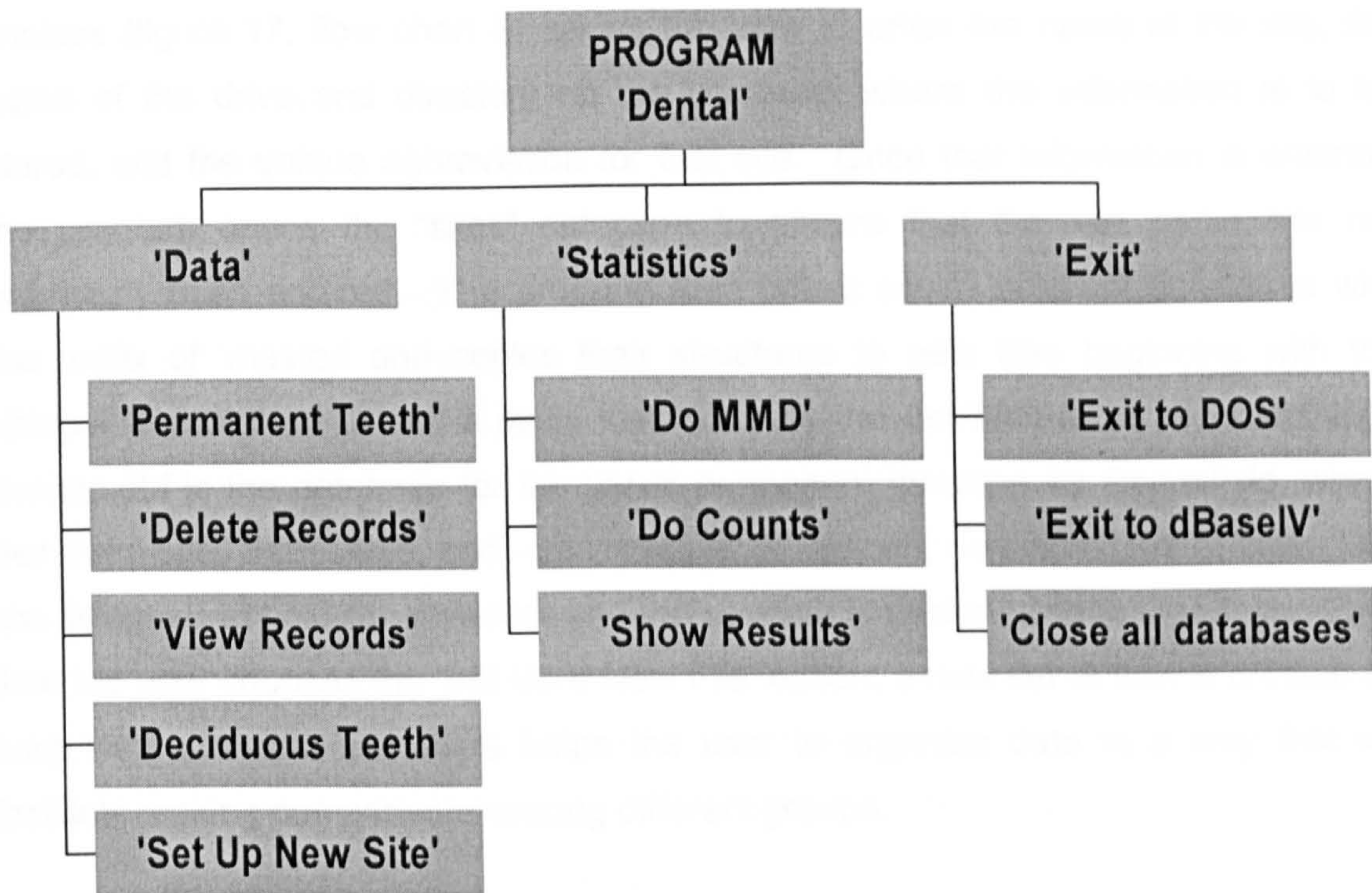


Figure 16. Flowchart I. The 'Dental' program

The 'Data' menu is the program used to contain and manage the raw data. Options within the Data menu are 'Set Up a New Site,' 'Permanent Teeth,' 'Deciduous Teeth,' 'View Records,' 'Delete Records,' 'Edit Records,' and 'Change Sites.' 'Set Up a New Site' allows the user to create a new set of files for a site, complete with all traits. The 'Permanent Teeth' and 'Deciduous Teeth' options both allow the user to add individuals (records) to their respective databases. The separation of these two types of dentition isolates the data within them in order that the appropriate files are updated. To avoid recording individuals with a mixed dentition twice within the same database, the individual is added to both the permanent and deciduous databases. The same individual's name is used in both. The scores of traits are entered into the corresponding record within the permanent or deciduous database. As long as the analysis is restricted to either permanent or deciduous teeth, there will not be an inappropriate duplication of scores for an individual. 'View Records,' 'Edit Records' and 'Delete Records' are self-explanatory. They allow the user to do just what the option names imply. The option, 'Change Sites,' gives the user the tool to 'move around' between sites. The mechanism first closes the databases which are currently active and then opens the databases associated with the next site.

The "Set Up a New Site" option takes the user through a series of menu choices (figure 17, flow chart II) asking the user to enter the name of the site, the name of the drive and directory on the computer where the information is to be stored, and the unique abbreviation for that site. Once that information is entered, the program opens the "sites" database to ensure that the site name has not previously been entered. The program then opens seven different databases with the prefix of 'master' and copies their structures to new files beginning with the abbreviation of the site and a suffix that identifies the dentition to be recorded; e.g., Berupa.dbf is the database for the upper permanent dentition for Berinsfield, where Ber = the site, Berinsfield, and -upa = upper permanent dentition. Six of these files are designed to hold the raw data and the seventh is designed to hold results. Each time the user chooses the 'Set Up a New File' option, a new set of files is created for each new site entered. This helps the user to organise data in a way that will facilitate making comparisons among different groups.



Figure 17. Flow chart II, 'Set up a New Site'

The 'Data' menu also includes options called 'Permanent Teeth' and 'Deciduous Teeth.' These options are used for adding new records (individuals, each with a complete set of traits) into the databases for permanent and deciduous dentitions. To ease data entry, dbase format (*.fmt) files were programmed and included as a standard feature. These format files act to show an on-screen form which approximates the ASU scoring sheets. Error checking capability was included in the format files by allowing only a specific range of scores for each trait (see appendices IV and V format code for the upper and lower jaws)

The 'Permanent Teeth' and 'Deciduous Teeth' selections for adding new records use the above mentioned format files beginning with the filename. The filename is the unique identifier for an individual, normally the "find" or "context" number assigned by the excavator. Before data entry is allowed to continue, the program scans the database for that filename in order to prevent duplicate entries of individuals within a set of database files ('Permanent Teeth' and 'Deciduous Teeth' are two separate sets of database files). The subroutine controlling data entry for the permanent dentition data is called "Adulproc". This program opens the three databases for the permanent dentition data of the active site. It then opens the format files (*.fmt) allowing the user to enter data in approximately the same order as the data are found on the ASU score sheets. At the end of each record the user is asked if more records are to be entered. If the answer is yes, a blank record is appended to the database and data entry proceeds as before. If the answer is no, the program closes the databases and returns to the opening screen, giving menu options Data, Statistics, or Exit. The program for data entry for deciduous teeth is controlled by a procedure called "Kidsproc" which is virtually identical to "Adulproc" with the exception being that the traits listed in the databases and format files are altered to reflect the lesser number of teeth in the deciduous dentition.

The selections 'View Records,' 'Edit Records' and 'Delete Records' simply open the databases and then use the standard dBase browse and delete commands. Any changes made to the number of records in one database will be reflected in the others.

The last selection on the Data menu is called 'Change Sites.' This option opens the 'Sites' database and displays the names of all the available sites. The 'Getinfo' window shows the full name of the site, the abbreviation of the site, data storage drive and directory for the chosen site, and confirms, through a Y/N inquiry, that this is the site needed by the user. If it is the intended site, the program then sets the path to the files associated with the site requested. The contents of the

variables that control the opening of databases are replaced with the appropriate information which corresponds to the site name. For example, the value of the variable 'uppera,' which controls the selection of the database for the upper adult dentition (upa), is changed from BERupa to IKLupa when moving from the site Berinsfield (BER) to the site Icklingham (IKL).

The second selection on the main menu, 'Statistics,' involves several functions for tallying occurrence of traits, calculating of MMD, and viewing of results. The first selection, 'Do Counts,' opens the 'upa' (upper adult) and 'loa' (lower adult) databases of the active site. The subroutine 'indvcoun' then compares the scores of the left and right antimeres for each of 128 traits in turn. The scores are counted in accordance with the individual count method which is described below in population level statistics, in the Arriving at n subsection. In the case where the scores of left and right are equal, the score of the right antimere is recorded; if the scores of left and right are unequal, the greater of the two scores is recorded. The frequency of the occurrence of each score is tallied and then recorded in the database for Results, which has a suffix 'res.'

The selection for 'Do MMD' (see flowchart III figure 18) takes the user through several dialogue boxes which ask questions about the number of sites to be used and the number of traits to be used in the calculation of the Mean Measure of Divergence. The next pop-up menu allows the user to select what sites to use from those available in the 'Sites' database and subsequently opens the appropriate files. The following pop-up menus prompt the user to select the tooth; e.g., upper first incisor or upper second molar. The next pop-up dialogue box asks which trait will be used; e.g., shovelling or double shovelling. The program then scans the database 'Nameabbr' to ensure that the desired trait exists for that tooth. If, for example, one were to choose the lower first premolar in response to 'select tooth' option and Carabelli cusp as the trait, the program would display an error message as the Carabelli cusp occurs only on upper molars, not premolars. The final question for each tooth and trait combination is "what breakpoint would you like to use for this trait?" The breakpoint is a number above which the trait is deemed to be present. A score less than or equal to the breakpoint indicates that the trait is absent. One would normally expect the breakpoint to be zero because any value greater than zero would indicate the presence of a trait. However, when assessing differences among very similar populations, the point at which differences between populations can be detected, may be as high as the penultimate possible score. The user is then prompted to enter a number within the range of possible scores for that trait to

designate the breakpoint. The selection is then stored in the database 'list.dbf.' Once all of the desired sites and traits have been selected, the program searches the Results files of each site for the chosen traits. It then sums the values of the frequencies which are above the breakpoint corresponding to the traits selected. The program then calculates the theta values (see formula in statistics section)

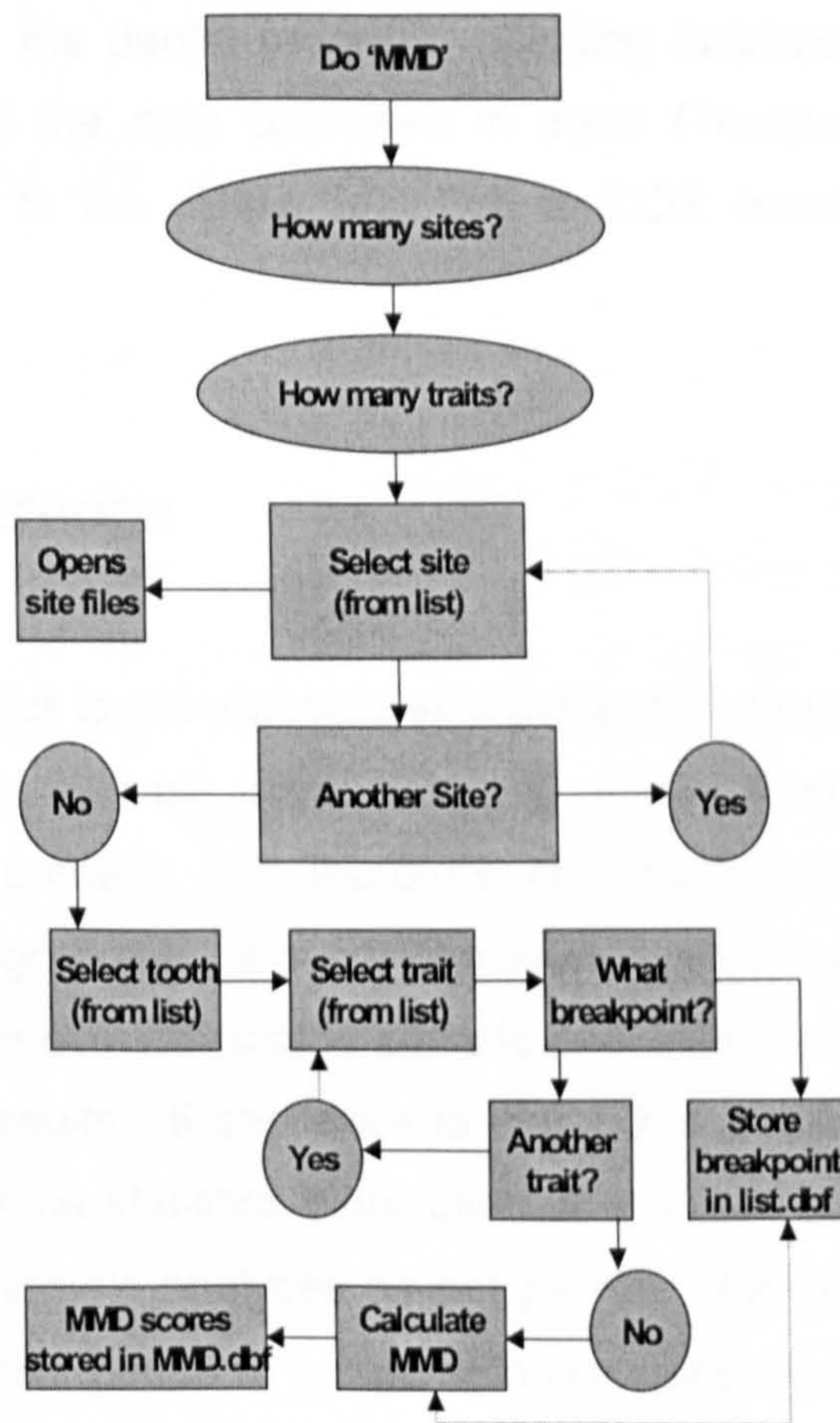


Figure 18. Flowchart III, 'Do MMD'

and stores them in a memory array. The dimensions of the memory array are calculated using the number of sites and traits used in the MMD calculation. These scores are also stored in the 'mmd.dbf' database which provides a storage location from which results can be taken for presentation later. Storing the theta values in the MMD database also provides a mechanism to check the accuracy of the calculations of the final MMD result. Each of the components for the rest of the MMD calculation, including variance, standard deviation, and significance are then derived from the information stored in the 'mmd.dbf' using dBase IV 'do...while' routines for the summations. The exact calculations are described in greater detail in the population level statistics Section. The final step of the MMD program is to create a file

'mmds.dat' which contains the abbreviations of the sites, the raw MMD score, the standard deviation, and a table containing the standardised MMD scores.

The final option in the Dental program is the 'Exit' menu. It has three functions—close all databases, exit to dBase, and exit to DOS. The 'close all databases' function removes all memory variables that are not needed to run the program and closes all of the open databases while allowing the user continued access to the menus in the dental program. Closing databases is used to avoid inadvertent corruption of the data contained in them (Townsend, 1989). Exit to dBase returns the user to the dBase IV. Exit to DOS terminates the dBase IV program.

2.9 STATISTICAL METHODS

The use of statistics is not always a straightforward proposition. Statistics are open to misuse. Data can be manipulated to show almost anything a given researcher may want to present. It is, therefore, important to choose the appropriate tools and to use them rigorously. It is not considered proper simply to throw all the data into a computer, run every available statistic and then choose the statistical tool that gives the desired results. If one were to claim that a study is purely objective simply because multivariate statistics were used, the results should be viewed with extreme caution. "Multivariate analyses do not provide objectivity, and just like any other analysis, special care needs to be taken to recognize intrinsic biases" (Wolpoff and Caspari, 1996: 355). This study utilises several statistical tools to explore data. Each tool has its own benefits and drawbacks, each of which is discussed below.

Interpretation of the data is another issue to confront. Just the simple fact that there may be a correlation between two variables does not mean that one caused the other or that there is any relationship beyond coincidence. One must be careful in choosing variables that will actually test the hypothesis in question. It is this very point that is the impetus for this study: In order to explain the biological relationships among the people of the Romano-British period and those of the Anglo-Saxon period one must study the biological material. Studying pottery or other cultural evidence will only tell how the cultural material moved from one area to another. Current models allow researchers to assume different numbers of people affecting the change depending on how they happen to feel about the continuity/invasion theories. Once the biological relationships are understood, models can be formulated to

explain how so much of the Romano-British culture came to be replaced by the Anglo-Saxon culture. A requirement of these new models would be that they use the incoming population as a constraint rather than a variable.

Along with the hurdles discussed above, one must confront several other problems such as the scale of measurement, how one counts individuals, and how to handle missing data. These matters are discussed in greater detail in the subsections below.

2.9.1 POPULATION LEVEL STATISTICS

2.9.1.1 Scale of measurement

The traits measured by the ASU system are rather complex in their biology. This can cause some problems when trying to decide which category of scales of measurement they fall into. Biologically, traits can be continuous, discontinuous or quasi-continuous. Continuous traits are those without natural divisions such as height, weight or skin colour. Discontinuous variables are those which are either present or absent. An example of this might be the Rh antigen on red blood cells. One is either Rh+ or Rh-, there is no in between state. Quasicontinuous traits are either absent or present and, when present, they exhibit a range of expression (Grüneberg, 1957). Most of the dental traits used in this study fall into this category.

Statisticians have different classes of variables. These divisions are nominal, ordinal, interval and ratio. Nominal variables are simply identifiers that have no real numerical significance. The numbers used in nominal scales are arbitrarily assigned although in the case of presence and absence, the numbers zero and one are conventionally used to designate absence and presence respectively. Ordinal scale is used when the variables can be placed in some sort of order, such as by size from smallest to largest. The interval scale is similar to ordinal as they both place objects in order. The difference is that the interval scale requires that the distance between two categories be fixed and equal. The ratio scale, like the interval scale, uses equally spaced units, but also requires that the zero of the scale be naturally defined (Shennan, 1988: 12). In a sense, the scores derived by the ASU method could fit any of these scales. They can be treated as nominal when calculating the MMD by converting them to present or absent (Scott and Turner, 1997). This is done at the cost of arbitrarily defining present at whatever point the researcher feels best represents the population. The scores can be treated as ordinal when considering the range of expression. Since the categories are designed to show equal

differences between scores (Scott and Turner, 1997; Turner et al., 1991) they could be considered to be interval scale. The zero is naturally defined (absent) so they could be used as ratio scores. The problem with using the ASU scores on the last two scales is that the differences may not always be equal units even though they are designed to be equal. The best approach in this situation is to be conservative and stay with the nominal scale for the MMD and with the ordinal scale for other tests that allow multi-state scores.

2.9.1.2 Arriving at *n*

Skeletons are basically symmetrical. Most of the bones of the human body are paired: left and right. Even bones that are unpaired tend to be symmetrically mirrored across the midline. This fact provides an opportunity and a problem. The opportunity presented is that since archaeological samples are often incomplete, one has the chance to observe a trait even if half of the bones are missing or destroyed. The problem that may arise is that counting every appearance of a trait will have the effect of over representation of a specific trait in more complete individuals. However, if the traits are distributed randomly through all populations, over representation will cause minimal skewing of the data, but it would still violate the rules of statistical sampling.

There is also a problem in that while the skeleton is essentially symmetrical, there is often some variation between sides. Therefore, relying on symmetry may misrepresent the frequency of occurrence of the trait in the actual population. A decision must be made as to how one deals with antimeres (same structure on the opposite side of the body). There are several methods available to dental researchers, most of which are very similar to the methods used by osteologists. Three of these methods are the total tooth count method, the unilateral count method, and the individual count method. Each of these is outlined below.

Humans are essentially bilaterally symmetrical. There can, however, be a certain amount of asymmetry (Van Valen, 1962; Staley and Green, 1974; Trinkaus, 1978; Scott, 1980). Because of asymmetry, one must choose a method of counting traits that best characterises the appearance of any one trait within a population. Scott (1980) provides descriptions of three methods commonly used in studies of dental morphology.

- 1) Total tooth count: all antimeres are counted and the total of affected teeth is then divided by the total number of teeth.

2) Unilateral count: a) score only the right or left antimere; when observations are not possible, due to incomplete skeletal sample, the trait is skipped for that individual or b) consistently score only the right side but substitute the left antimere when the right side cannot be observed

3) Individual Count: either antimere is used once per individual; in cases of asymmetry, the highest grade is used.

A fourth method of randomising the choice of side is to flip a coin when presented with a choice of left or right antimere is not considered by Scott, but has been used in other studies (e.g. Tyrrell, 1993). This method will also be discussed briefly below.

The underlying assumption of many dental studies is that an individual is composed of a single genotype which controls the development of both sides of the body. It also assumes that asymmetry is due to environmental suppression of the potential of the genotype which will have an effect on only one side. Therefore, the higher score is a better reflection of the genotype (Turner, 1967; Scott and Turner, 1997; Scott, 1973; Scott and Dhalberg, 1982; Turner and Scott, 1977). This is because, as was mentioned above, an individual's phenotype is an interaction of the genotype and the developmental environment (phenotype = genotype + environment), the lower score would reflect a higher environmental component in the phenotype.

The total tooth count method (1) essentially averages expression of a trait in the mouth. This can lead to an understating of the genetic background of the individual. In some studies, the sample size is reported as the total number of teeth observed. However, because symmetry is the most common state, this method would inflate the value of n.

The unilateral count method (2a) will underestimate n by discarding so many potential observations when only the 'other' side is present. Method (2b) is very similar to the individual count method but suffers the same problem of underestimating the genetic potential as found in method (1) by ignoring asymmetry when it does exist. The individual count method (3) is favoured by Scott (1980) and is used in the present study. This method maximises the sample size by not discarding data but does not overstate n by counting traits twice as with method (1). Nor does it ignore traits on the basis of appearing on the 'wrong' side as with method (2a). It also provides the best reflection of the genotype in cases of asymmetry under the assumption that the smaller expression of a trait is due to environmental interference.

The coin-toss method assumes that asymmetry is randomly distributed, that is, there is no directional influence from genetic or environmental factors for enlarged or diminished expression of a trait. This would be the method of choice for an investigator who feels that the assumption of environmental interference causing a decrease in trait size is invalid. In theory, this method would not dramatically reduce the frequency of the larger expression of traits, but it may cause one to miss larger expressions particularly in small populations.

2.9.1.3 MMD and the History of the Formula

Many methods for calculating biological distance have been devised over the years. Biological distance' is a general term that is meant to encompass both genetic and phenetic distance or dissimilarity. The concept is to "express by a single number how much difference there is..." biologically "...between two populations" (Smith, 1977:463). Literally hundreds of studies have been undertaken in all parts of the world. One widely used distance measure in studies using non-metric traits is the Grewal-Smith statistic (Grewal, 1962) or some variant (e.g., Kellock and Parsons, 1970b; Berry and Berry, 1967; Berry, 1974; Corruccini, 1974; Haeussler and Turner, 1992; Hanihara, 1977; Hanihara, 1996; Kellock and Parsons, 1970a; Lloyd-Jones, 1995; Lloyd-Jones, 1997; Rightmire, 1972; Johnson and Lovell, 1994; Johnson and Lovell, 1995; Prowes and Lovell, 1995; Prowes and Lovell, 1996). This statistic was first used in this type of study by Berry and Berry (1967) with the name of Mean Measure of Divergence (MMD). While it is important to choose a statistical tool based on how that well that statistic does the job of giving information about the population under study, it is worth noting that distances "calculated by different formulas are always highly correlated" (Cavalli-Sforza et al., 1994: 30) also see (Scott and Turner, 1997: 257; Jorde, 1985: 345). As so many distance measures provide essentially identical results, "the choice between these measures is one of taste and convenience" (Smith, 1977: 471).

The basic idea of the Grewal-Smith statistic is to make the "part of the variance which is due to errors of sampling independent of the incidence of the character" (Grewal, 1962: 229). In other words, the equation provides a measure that shows the true relationship between two populations with minimal interference by sampling error. The finding of a large biological distance between two populations could be interpreted as either a long period of isolation following a split from a parent population or a replacement of one population by a later group. A small genetic

distance, on the other hand, could be interpreted as an example of two groups who have a more recent common history (Smith, 1977: 464).

The basic equation used by Berry and Berry has been subjected to numerous refinements since its introduction. Finnegan and Coopriider (1978) give ten examples of refinements to the transformation equation and their corresponding equations for variance. The different equations have been used by many researchers in various studies over the years and, it is not always explicitly stated in the studies which of the equations was used. As any of these formulae can be incorporated in the MMD statistic, there is a danger of using different statistics under the same name. However, in their analysis of the ten different versions of the transformation equation, Finnegan and Coopriider show that the different permutations of the Grewal-Smith statistic all yield similar results when applied to the same dataset. They further point out that the method used to standardise variance does not matter much when the populations analysed are of similar size to those used in their study (Finnegan and Coopriider, 1978: 43).

In contrast to Finnegan and Coopriider who concluded that the transformation developed by Constandse-Westermann (1972) provides the best results, Green and Suchey (1976) concluded that, while all the transformations considered worked well on 'sufficiently large' samples, the angular transformation devised by Freeman and Tukey (1950) is preferred when dealing with small samples. One population in this study (Icklingham) would be considered to be very small ($n=26$), the Freeman-Tukey transformation is the equation for the MMD calculation here.

Testing for significance is as simple as taking the square root of the variance (i.e., the standard deviation or MMD_{sd}) and multiplying by two. If the value for the MMD is greater than this number (i.e., $MMD > 2 * [MMD_{sd}]$) the null hypothesis (H_0 = the samples come from the same population) is rejected.

The final refinement in the method was proposed by Green and Suchey (1976). They found that the Grewal-Smith transformation yielded values for the variance of θ (the proportion of the population expressing the trait within the population; represented as an angle measured in radians) that were greater than the expected value of $1/n$ (n = the population sample). This would increase the likelihood of falsely rejecting the null hypothesis to much greater than the predicted 3% (Green and Suchey, 1976: 67). To cure this fault, they suggest that $1/2$ be added to the n for each population in both the equation for MMD and the equation for variance.

The equation for the Mean Measure of Divergence, with all of the refinements as suggested by Green and Suchey is shown in equation 1. The angular

transformation proposed by Freeman and Tukey is shown in equation 2. The equation for variance, with Green and Suchey's corrections is shown in equation 3.

$$MMD = \frac{1}{r} \sum_{i=1}^r \left([\theta_{1i} - \theta_{2i}]^2 - \left[\frac{1}{n_{1i} + \frac{1}{2}} + \frac{1}{n_{2i} + \frac{1}{2}} \right] \right) \quad \text{equation 1}$$

$$\theta = \frac{1}{2} \sin^{-1} \left(1 - \frac{2k}{n+1} \right) + \frac{1}{2} \sin^{-1} \left(1 - \frac{2(k+1)}{n+1} \right) \quad \text{equation 2}$$

$$\text{var} = \frac{2}{r^2} \sum_{i=1}^r \left(\left[\frac{1}{n_{1i} + \frac{1}{2}} \right] + \left[\frac{1}{n_{2i} + \frac{1}{2}} \right] \right)^2 \quad \text{equation 3}$$

(adapted from Green and Suchey 1976)

Where:

r = Number of traits considered;

n_{1i} and n_{2i} = number of dentitions examined for trait i in populations 1 and 2 respectively;

k = the number of individuals expressing the trait out of n observable individuals in a sample (k/n = observed trait frequency);

Trait frequencies are transformed to the angle θ (measured in radians) through inverse sine; and,

θ_{1i} and θ_{2i} = transformed frequency of trait i in populations 1 and 2 respectively.

Sofaer et al (1986) suggest calculating a standardised MMD by dividing the raw MMD score by its standard deviation ($MMD_{\text{stan}} = MMD / MMD_{\text{sd}}$). This simplifies comparisons by integrating the standard deviation into the value of each MMD to be compared and eliminating the need to calculate a separate 'plus/minus' range for each MMD score.

While the MMD is a robust statistic, it is not without disadvantages. First, the scores collected using the ASU system are not used to their fullest advantage. By collapsing the multi-state scores into a single Present/Absent score, the within group and between group variation at intermediate levels of expression is lost. In studies of groups that are closely related, this could mean a failure to recognise differences that provide information about population movements or other demographic information. Another consequence of collapsing observations to a few categories is that most published data do not adequately explain at which point the researcher decides to make the transition from absent to present (the breakpoint). That is to say that the breakpoint is the score above which a trait is deemed to be present. Collapsing the scores of the traits without explicitly stating the breakpoint creates a situation where direct comparison to published data is not always possible (Mayhall, 1992: 73). It should also be noted that comparisons to published data are also dangerous when the data were not collected by the same individual, or at least by someone with whom tests of inter-observer concordance have been performed. Table 3, below, shows the values of n, k and the breakpoint for each trait by site.

SITES >	BP	BER		BRD		IKL		LANK		LBF		PW		QF	
		N	K	N	K	N	K	N	K	N	K	N	K	N	K
UI2SHOVEL	1	36	24	50	20	13	8	96	46	96	20	27	13	40	27
UP1DSHOVE	1	42	21	72	27	18	10	118	82	118	4	42	19	27	24
UCTDENT	2	41	38	59	53	14	13	99	114	99	47	36	33	51	48
UCMESRIDG	0	40	5	55	18	13	4	88	28	88	28	33	2	42	17
UM2METACO	4	43	15	86	4	16	0	107	17	107	0	42	1	59	17
UM2CUSP5	2	40	3	82	7	15	4	104	3	104	10	41	3	41	2
UM2CARABL	1	30	16	42	18	9	4	83	22	83	15	26	13	31	15
UM1PARAST	0	46	17	71	41	12	7	101	39	105	31	27	3	38	19
LP2LCUSPS	3	44	15	83	35	19	7	147	44	104	35	46	24	56	25
LM2PSTYLD	0	41	27	77	51	14	7	100	66	100	47	34	22	46	31
LM2CUSP5	1	47	12	96	24	18	4	107	25	107	19	43	9	50	23
LP1TOMESR	2	34	7	86	18	13	2	111	23	111	14	41	10	50	11

Table 3 Presence of traits in the test populations. Abbreviations for traits and site names are described in the text. BP= Breakpoint N= Total number of individuals examined for a given trait K= number of individuals expressing the trait.

2.9.2 METHODS FOR VISUALISATION OF RESULTS

It is difficult to make sense of a distance matrix with more than just a few comparisons. Commercially available statistics packages offer many options for creating graphs based on the analyses they can perform. In order to facilitate graphical visualisation of the results in this study, three methods, hierarchical cluster analysis, Multidimensional Scaling (MDS) and a simple scatter plot geographic distances against biological distances. Each method has advantages and disadvantages depending on what information one is trying to gain from the statistics.

2.9.2.1 Cluster Analysis

One of the most commonly employed ways to visualise the results from biological distance calculations is to use hierarchical cluster analysis (e.g. (Hanihara, 1996; Brace et al., 1993; Lukacs and Hemphill, 1991; Friedlaender et al., 1971; Relethford and Harpending, 1994; Turner, 1985). Hierarchical cluster analysis is actually a class of procedure rather than a single statistical tool (Baxter, 1994:140). There are many ways in which it can be used. Of the several goals of hierarchical cluster analysis defined by Aldenderfer and Blashfield (1984), the goal in this research is the “investigation of useful conceptual schemes for grouping entities” (Aldenderfer and Blashfield, 1984: 9). Hierarchical cluster analysis is used in this study is to classify the members of a large group (all of the populations examined) into sub-groups so that the members of one sub-group are more similar to one another than they are to the members of a different group (Baxter, 1994: 141). In this analysis, the ‘entities’ are the cemeteries, that is, the proximity of one cemetery to another is determined by the scores for the whole cemetery derived by the MMD statistic rather than the individuals in the cemeteries. How these groups cluster together is the point of interest. Do they combine in groups by time period (Romano-British cemeteries in one group and Anglo-Saxon cemeteries in another)? Alternatively, do they group by geographic similarity (the cemeteries from Oxfordshire in one group, the cemeteries from Suffolk in another, etc.)? A third possibility is a scenario where the groupings appear to be distributed randomly and have no interpretative power at all.

One of the problems with hierarchical cluster analysis is that, by definition, the procedure will create groups even where none exist. Hierarchical cluster analysis can impose two or more ‘clusters’ on to a randomly scattered dataset that has a normal distribution (Baxter, 1994: 161). It is easy to fall into the trap of assuming that

the statistically derived clusters are 'real' simply because the computer output shows them. It is important to keep in mind that "even though the strategy is structure-seeking, the operation is structure-imposing" (Aldenderfer and Blashfield, 1984: 16).

Another problem with hierarchical cluster analysis is that there are several different methods for calculating clusters. These methods include 'single linkage' (nearest neighbour), 'complete linkage' (furthest neighbour), 'average linkage' (unweighted pair groups method) and 'Ward's method' (error sum of squares) (Baxter, 1994: 141-142). For discussions of the technical differences among these different techniques, the reader should refer to one of the many statistical books available (e.g. (Aldenderfer and Wish, 1984; Baxter, 1994; Shennan, 1988). These methods "can, and do generate different solutions to the same dataset" (Aldenderfer and Blashfield, 1984: 15). Baxter (1994: 182) concludes that the single linkage method is of little practical use in archaeology and that the average linkage and Ward's method have more useful potential as hierarchical techniques.

Because different methods yield different results, Baxter (1994) suggests examining the results generated by "competing methods" (165). The greater the similarity in the output from one method to the next, the greater the likelihood that the results are 'stable'. "Stability is an important property of any classification in that stable groups are more likely to represent 'natural' groups in the data" (Aldenderfer and Blashfield, 1984: 37-38).

For the hierarchical cluster analysis used in this study, the distance matrix generated by the MMD statistic was entered in S-Plus. The procedure "hclust" (Data Analysis Products Division, 1997) with was performed single linkage, complete linkage, average linkage and Ward's method. The results are presented below in section 3.1.1.3.

2.9.2.2 *Multidimensional Scaling (MDS)*

Dendrograms restrict analysis of the results calculated by distance measures to one dimension (Relethford and Lees, 1982: 123). The clustering methods from which the dendrograms are derived also impose a hierarchical structure on data where none actually exists (Lalouel, 1980: 245; Jorde, 1985: 349). For this reason, tree diagrams are not always appropriate in studies of human populations (Jorde, 1985: 349). They can be useful if one is in the early stages of developing a hypothesis but further exploration of the data is called for (Lalouel, 1980). Therefore, in addition to dendrograms, the mapping method of Multidimensional Scaling (MDS) is used here.

Multidimensional scaling attempts to replicate the rank-order relationships of a distance matrix in the fewest possible dimensions while optimising the goodness of fit (Kruskal and Wish, 1978: 23). As Jorde points out, it can also “be performed on either metric or non-metric data. It has the advantage of statistical robustness” (Jorde 1985: 347). The distance matrix which results from the MMD statistic is entered in S-Plus was used in the ‘cmdscale’ procedure (Data Analysis Products Division, 1997).

2.9.2.3 *Geo-Distance vs. Bio-Distance*

As a general rule, populations that are not under some sort of external pressure, such as invasion or drought, will gradually fill the available local landscape, although some minor alteration in the breeding population may, theoretically create a marked deviance from the original population. As the population spreads, slight differences from the parent population will develop (assuming that the population spread is wide enough to cause some isolation of the groups). The greater the geographic distance, the greater the number of differences that will creep into the gene pool. When biological differences increase as a function of geographical distance a situation known as autocorrelation exists (Fix, 1994; Key and Jantz, 1990; Konigsberg, 1990b; Sokal Uytterschaut, 1987b).

There are statistical tools available for calculating the spatial autocorrelation among groups of people. These tools require the transformation of the data into time series for evaluation. These sites are not distributed regularly in time of space, so rather than imposing a structure that does not exist on the data just for the sake of one statistical procedure, a simple plotting method will be used. This is not a traditional statistical tool, but a way to visualise the two sets of data in the hope of making sense of the relationship between biological distance and geographical distance.

This is a simple plotting procedure performed in Excel. One column of the spreadsheet contains the biological distances from the MMD for each site-pair and the other column contains the geographical distance between each site-pair (in kilometres). The biological distances are plotted on the X-axis and the geographic distances are plotted on the Y-axis. While this procedure is not a statistical tool in the classical sense, it is a good way to gain a feel for the relationship between the biological distance and the geographical distance.

2.9.3 INDIVIDUAL LEVEL STATISTICS

Falconer points out that when one is studying the biological history of a population, that population "is not just a group of individuals, but a breeding group" (Falconer, 1989: 5). The point being that a population is not simply a random assemblage, but a group of individuals with many shared characteristics, be they cultural or biological characteristics. One of the problems with the statistics at the population level is that there is a danger of imagining the groups as fixed entities, in other words reifying them, which is the same problem encountered with the use of typologies as noted above in the discussion of race.

As will be seen later, the results of the MMD are interesting in their own right, but they do not tell the whole story. A population is made up of individuals who share some characteristics but it cannot be assumed that these individuals lived in complete isolation from individuals from other groups. In this study, the extreme difference of Lechlade compared to the other six sites begs for closer examination. Calculating distances among individuals should make it possible to assess whether Lechlade is different because the population as a whole is distinct from the other populations or if the difference is due to a relatively small number of outliers. To get a more complete picture of how the individuals from these sites interacted, a slightly different statistic must be used.

One of the benefits of this approach is that several multivariate distance measures are available in commercial statistics packages such as SPSS, SYSTAT and S-PLUS. Another benefit is that these packages can calculate distances based on the multi-state scores obtained by the ASU method. This avoids one of the problems of the MMD statistic, in that it requires that scores be transformed to be either present or absent. Making use of the full range of scores obtained by using the ASU method would allow for finer comparisons.

Interpretations based on individual statistics must be made with even greater caution than population level statistics. This is because the sample size is effectively reduced to one (i.e. $n=1$) for each population. This problem is further compounded by the removal of individuals who do not have complete data. Most packages have options for dealing with missing data which will be explained below.

2.9.3.1 Preparation of the data

One of the most important problems with analysing archaeological samples is incomplete data. In population level statistics, one simply counts each available

datum, which results in a frequency of that trait for that population. The frequency of occurrence for two or more populations is then compared. At the individual level, there are several possible ways to handle missing data. These include removal of missing values, replacement with trended or interpolated values or replacement with mean scores. Some version of each of these methods is available in commercially available statistical packages (e.g., SPSS and SYSTAT).

Data removal can be accomplished in two ways. The first is list-wise deletion where the individuals who do not have data for all of the traits under consideration are removed from the analysis. Of the 799 individuals in the current study, only 110 (about 14%) have information for all the traits. The size of this sample is much too small to be valid, considering the number of cemeteries being examined. The second alternative is to use pair-wise deletion where any one pair of individuals is compared on the basis of the traits available for both individuals. This method can result in making comparisons based on different variables for many individuals.

Linear interpolation replaces the missing value with a value calculated from the last valid value before the missing value and the first valid value after the missing value (SPSS Inc., 1993). The value of the replacement could change depending on how the data are ordered. The 'Linear Trend at Point' method calculates a value from the whole series of valid values based on an indexed variable.

As a compromise between these choices, another method is used in this analysis. The method is to replace missing values with mean scores (Ensor and Irish, 1995). To avoid unjustifiable weighting of the totals toward the mean scores, individuals with fewer than 80% of the true scores missing are eliminated. This procedure helps to keep the sample size large enough for more meaningful comparisons without inordinately skewing the data. The first step in this procedure is to calculate the mean scores for each trait within each population. These mean scores can be found in table 4. The individuals with more than 20% missing values are eliminated. The total sample of 799 is thus reduced to 304 (about 38%). While this sample is much smaller than one would like for statistical inference, it is better than the 14% mentioned above. Next, the missing values still present in the sample are replaced with the means for appropriate trait and site. A list of those individuals can be found in appendix 10.

SITES➤ TRAITS▼	BER	BRD	IKL	LANK	LBF	PW	QF
UI2SHOVEL	2.25	1.40	2.31	1.61	1.09	1.78	2.02
UP1DSHOVEL	1.41	1.41	1.61	1.53	.047	1.43	1.08
UCTDENT	3.36	3.72	3.54	3.10	2.17	4.12	3.60
UCMESRIDG	4.02	3.90	3.86	3.70	2.38	4.06	3.08
UM2METACO	4.28	3.84	3.81	3.95	3.49	3.79	4.10
UM2CUSP5	0.61	0.43	1.34	0.21	0.62	0.47	0.43
UM2CARABL	1.94	1.93	1.67	0.90	0.66	2.12	1.26
UM1PARAST	0.62	0.89	0.84	0.63	0.36	0.12	0.50
LP2LCUSPS	3.75	3.52	0.56	3.17	3.15	4.39	3.74
LM2PSTYLD	1.17	1.32	1.22	0.98	0.53	0.83	0.99
LM2CUSP5	0.79	0.81	0.56	0.54	0.55	0.80	3.74
LP1TOMESR	1.15	1.06	0.93	1.01	0.90	1.27	0.99

Table 4. Mean scores of traits by site.

2.9.3.2 Discriminant Analysis

Discriminant analysis is based on the assumption that members of a sample population belong to one of two or more groups. This is not an exploratory method in the classical sense, but in certain archaeological situations it can be considered as such (Baxter, 1994: 185). Discriminant analysis calculates the maximal distances between groups and within groups. One of the reasons for using it is to discover which variables have the greatest impact in showing statistical differences. In this study, the discovery that lower second molar cusp number and the size of lower second molar fifth cusp were strongly correlated in these samples, led to the decision to discard cusp number so as not to unjustifiably weight these traits. Aside from that variable, it had already been decided which variables were to be used based on the results from T-Tests and Spearman correlations. In this analysis, therefore, another function of discriminant analysis is used here. That being, to investigate how well the variables will predict group membership.

To do this one must first assign dummy variables to the groups to work as dependent variables to be compared to the independent variables (the dental trait scores). In the first analysis, the dependent variable is the period of the site; whether the site is dated to the Romano-British or the Anglo-Saxon period. The number '1' is

assigned to all sites from the Romano-British period and the number '2' is assigned to the Anglo-Saxon sites. In the second analysis, the dummy variable is 'site.' The sites were arranged in alphabetical order and a number was assigned to each site in order; Berinsfield = 1, Brandon = 2, Icklingham = 3, Lankhills = 4, Lechlade = 5, Portway = 6, Queenford = 7.

2.9.3.3 Multidimensional Scaling (MDS)

A dendrogram from a distance matrix of the size generated by this analysis is nearly as incomprehensible as the raw matrix itself. As with the population level statistics, Multidimensional Scaling is used to examine the "hidden structure" of the data (Kruskal and Wish, 1978: 7). While this procedure is available in both SPSS and SYSTAT, these programs allow only 100 cases and are therefore inadequate for this sample. S-Plus is a less user-friendly program, but it does not have restrictions on the number of individuals to be tested. As with the hierarchical cluster analysis, the different methods for deriving the plot were tested against one another. There were no appreciable differences seen among the different graphs using the different MDS distance measures. This helps support the previously mentioned conclusion of Cavalli-Sforza et al. (1994), that distances "calculated by different formulas are always highly correlated" (Cavalli-Sforza et al., 1994: 30; Jorde, 1985: 345). As no real differences were seen among the different graphs, only the graph which employed the Euclidean distance is shown.

3 RESULTS

3.1 POPULATION LEVEL STATISTICS

3.1.1 MMD

The calculations of the MMD, standard deviation and the standardised MMD (MMD_{stan}) were carried out to a precision of 12 decimal places in the program written in dBase. The results presented here use those same numbers, rounded to the nearest three decimal places. As may be expected, there is a certain amount of rounding error and the values shown for the MMD_{stan} may differ from values obtained by dividing the raw MMD scores shown here by their corresponding standard deviation.

The MMD scores are presented in table 5 with the raw MMD score and corresponding standard deviation below the diagonal and the standardised MMD score above the diagonal.

Sites	BER	BRD	IKL	LANK	LBF	PW	QF
BER	—	5.080*	1.596	4.181*	31.243*	3.296*	0.851
BRD	0.083	—	-0.664	4.761*	21.746*	5.093*	3.431*
St Dev	0.016						
IKL	0.062	-0.023	—	1.055	8.451*	1.843	1.422
St Dev	0.039	0.035					
LANK	0.057	0.046	0.034	—	35.609*	5.486*	7.421*
St Dev	0.014	0.009	0.032				
LBF	0.445	0.222	0.277	0.265	—	19.049*	33.097*
St Dev	0.014	0.010	0.033	0.007			
PW	0.072	0.091	0.074	0.083	0.299	—	7.613*
St Dev	0.022	0.018	0.040	0.015	0.016		
QF	0.016	0.052	0.054	0.093	0.434	0.158	—
St Dev	0.019	0.015	0.038	0.012	0.013	0.021	

Table 5. MMD scores for seven sites. Abbreviations for sites are as given in the text. The upper triangle of the matrix shows the standardised MMD scores (MMD/MMD_{stdev}). An asterisk denotes significant difference. The lower half of the matrix gives the raw MMD score and the standard deviations for each comparison.

The only site that is statistically different from all the other sites is Lechlade. The differences for all of the scores are highly significant. The magnitude of difference between Lechlade and another site is between 2.5 and 6.1 times greater than the largest comparison of any other combination of sites. For example, the score for Lechlade and Berinsfield is 31.243 while the next highest score for Berinsfield is with Brandon at 5.080. The difference between these two scores is 26.163. To put it another way, the Berinsfield/Lechlade score is approximately 6.1 times the Berinsfield/Brandon score.

Perhaps the most startling outcome is the comparison between Icklingham (IKL) and Brandon (BRD). A raw score of -0.023 (standardised = -0.664) seems to make no sense. A negative score would seem to suggest that the two populations are more than exactly alike. In real populations this is not possible, yet it happens, thanks to mathematics and is often seen in published reports (e.g., Berry, 1974; Ishida and Dodo, 1993). The mathematical reason for this is that the smaller the n , the larger the denominator in several of the sections of the MMD formula. This results in a larger error term which, when subtracted from the value of $[\theta_{1i}-\theta_{2i}]^2$ in closely related populations yields a negative value. Sjøvold (1973) asserts that this type of result is due to the relationship of the MMD to the chi-squared distribution and that it represents a chi-square value that does not exceed the expectation. Exceeding the expected chi-square is very likely if the hypothesis of equal proportions is true (Sjøvold, 1973: 209). He goes on to state that some have interpreted this paradox as if the score were zero, in other words, that there is no way of distinguishing between the populations (Berry, Evans and Sennitt (1967) cited in Sjøvold, 1973: 209). That is a good heuristic method for interpreting such scores, and much more easily understood by non-statisticians than the explanation given by Sjøvold himself.

The next result of note is that of the three site pairs, Berinsfield (BER) and Queenford (QF) ($MMD_{stan} = 0.851$), Brandon and Icklingham ($MMD_{stan} = -0.664$), and Portway (PW) and Lankhills (LANK) ($MMD_{stan} = 5.486$), only the last differ significantly from one another. One of the possible reasons for this difference is that the geographic distance between these two sites is great enough to provide a slight barrier to interbreeding between the people of Lankhills and the ancestors of the population from Portway was alluded to in the Geo-distance vs. Bio-distance section above, and will be discussed further in the section on the results for that section below.

Icklingham has consistently lower scores than the other sites. These low scores and relatively high standard deviations suggest that the small sample size presents a problem for interpretation. One explanation could be that the people from

Icklingham are consistently more closely related to the people found in the other cemeteries regardless of how the other populations are related to one another. However, the pattern of variation exhibited by Icklingham presents another, more likely explanation. The pattern is consistent with all the other sites in that it is most closely related to its neighbour (Brandon) with an MMD score of -0.664 , and most distantly related to Lechlade (MMD score 8.451). This suggests that, while the absolute values are out of line with the other sites, the Icklingham scores are a reflection of a relationship with each of the other sites that is similar to how the other sites are related. Furthermore, this indicates that if the sample had been larger, the scores would probably have been more like the other sites given the magnitude of the differences.

3.1.1.1 Cluster analysis

As was discussed in section 2.14.1, the judgement of whether the results of hierarchical cluster analysis are stable and show natural groupings of data can be facilitated by examining dendrograms derived from the use of several competing methods. The first, and arguably most simplistic (Baxter, 1994), method examined is 'single linkage'. The resultant dendrogram is shown in figure 19. The second dendrogram (figure 20) shows the results of complete linkage. The third and fourth dendrograms (figures 21 and 22) show the results of average linkage and Ward's Method, respectively. The scale on the left-hand side of each figure gives the height of the point where clusters join and is determined by the algorithm used by S-Plus and does not, therefore, relate directly to the MMD_{stan} score for the sites.

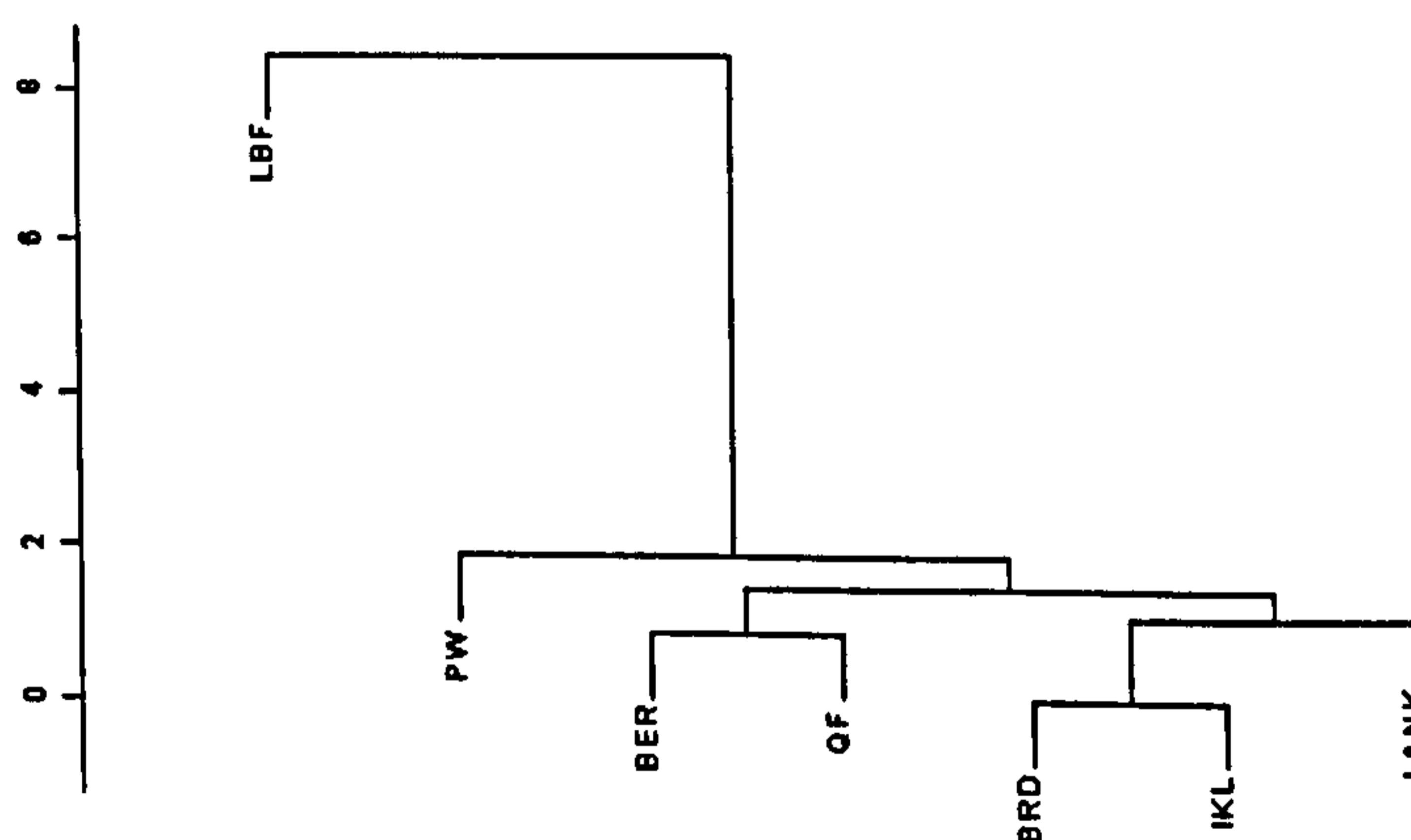


Figure 19 Dendrogram with single linkage

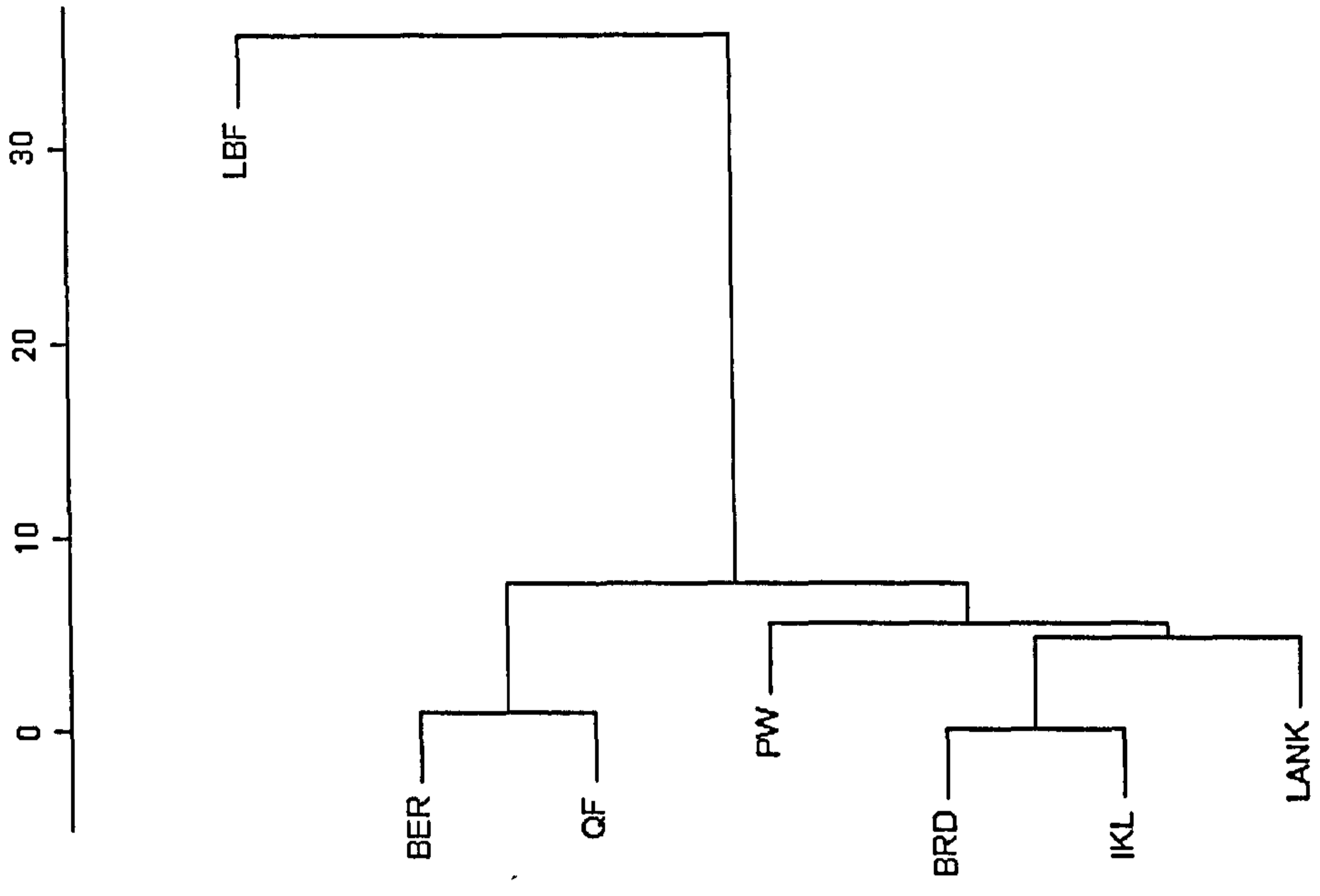


Figure 20. Dendrogram using complete linkage.

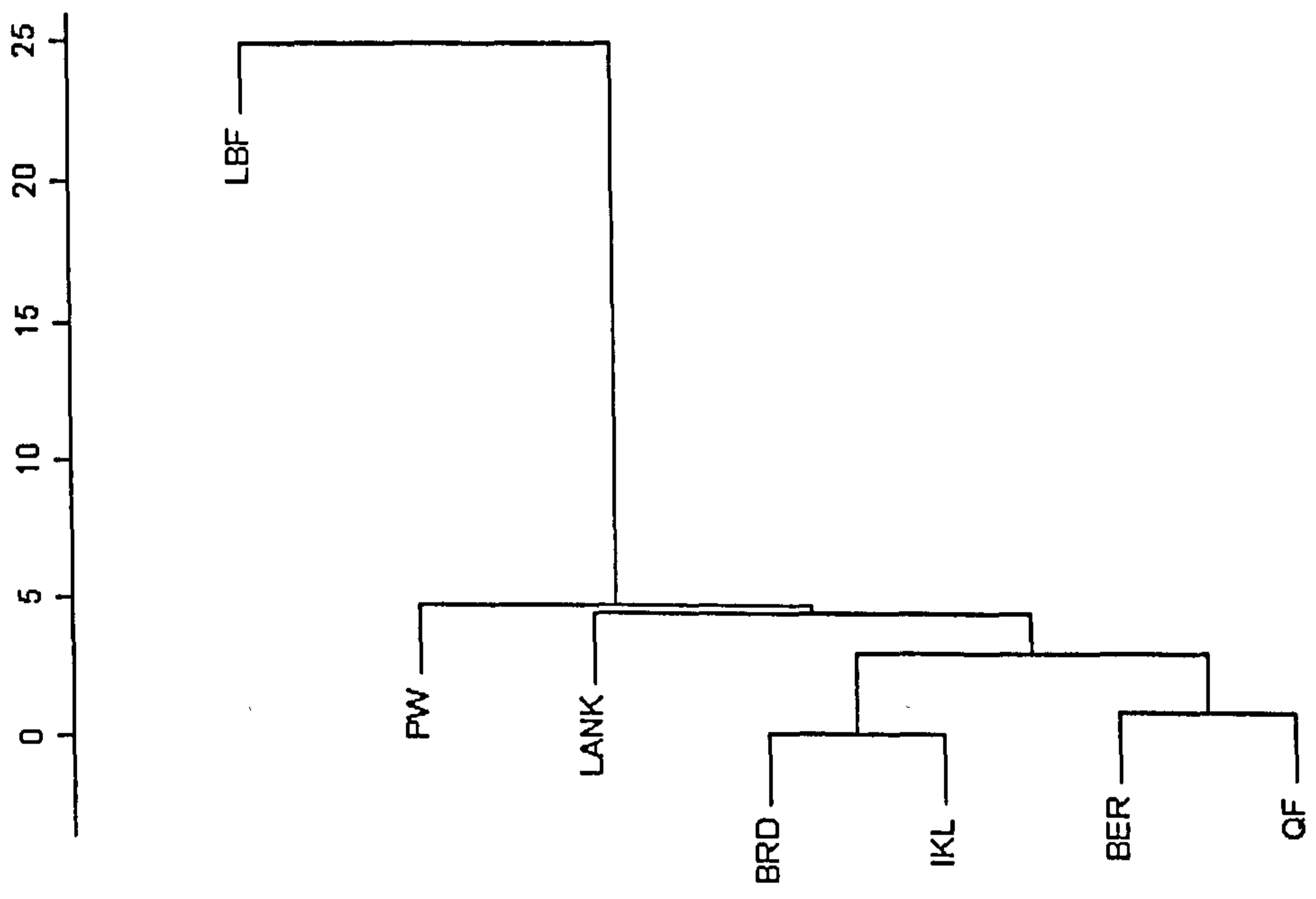


Figure 21 Dendrogram showing average linkage

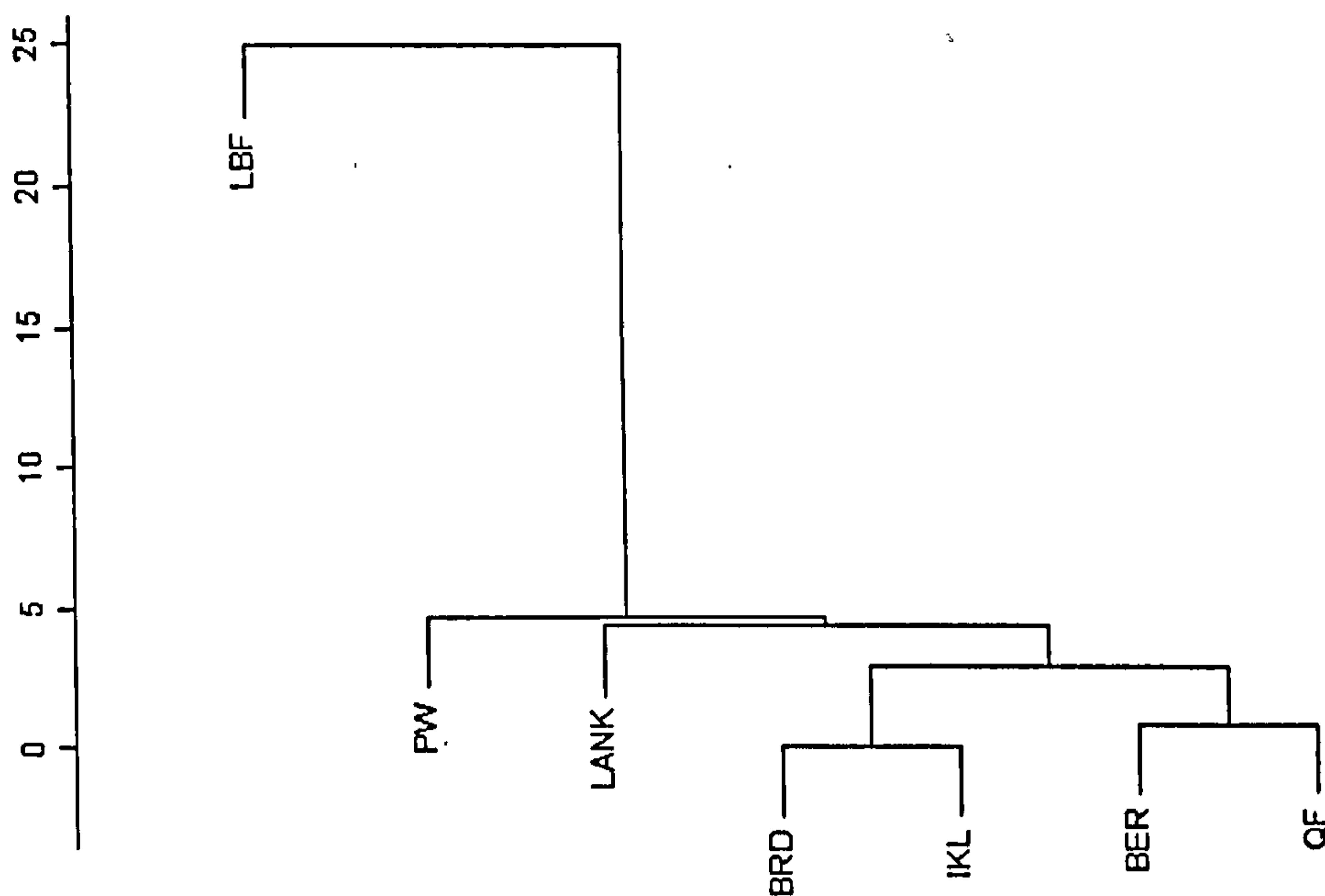


Figure 22 Dendrogram showing Ward's Method

By examining these four dendrograms, one can clearly see the close relationship between Brandon and Icklingham and between Berinsfield and Queenford. The similarities among the general structures of all of the dendrograms also suggest that the groups are real in the sense that they are very similar in all of the dendrograms. The main differences are seen in the heights of the points where the clusters combine.

In the single linkage dendrogram, Lankhills joins with the Brandon/Icklingham cluster. The Berinsfield/Queenford cluster then joins this new cluster followed by Portway Down. In the complete linkage dendrogram, Lankhills again joins with the Brandon/Icklingham cluster but in this case, Portway Down is next to join the clusters followed by the Berinsfield/Queenford cluster. The average linkage and Ward's Method dendrograms are identical to one another. Both show Brandon and Icklingham as the first pair to cluster. The next pair to cluster is that of Berinsfield and Queenford. These two pairs cluster together and are then joined by Lankhills followed by Portway Down and last by Lechlade.

While there are slight differences in the order in which the sites join the clusters the general relationships are not very different from single linkage to complete linkage or then to average linkage and Ward's Method. This general stability suggests that the hierarchical cluster analysis does reveal 'real' groups rather than dividing a normal distribution into arbitrary groups. It is also worth noting that

way that all four dendrograms show the dramatic distance of Lechlade from all of the other sites. They fully illustrate the magnitude of difference between Lechlade and any other site it is compared to as shown by the MMD_{stan} scores.

3.1.1.2 Multidimensional Scaling Results

The map of the MMD results generated by the Multidimensional Scaling procedure (figure 23) shows how the sites relate to one another when a hierarchical structure is not imposed on them by hierarchical cluster analysis. Some of the specific comparisons shown in this map seem to be at odds with the dendrograms presented above in figures 19-22. Brandon and Icklingham group together well, but Berinsfield and Queenford are separated on the Y-axis (Dimension 2) by a wider margin than one would initially expect when considering the original scores and the results of the hierarchical cluster analysis. The positions of Portway and Lankhills seem to better reflect their geographic relationship and the MMD scores when compared to what one would have expected from inspection of the dendrograms. It may not be obvious on first glance that the relationships of these six sites compared to Lechlade are obviously greater than the distances among those six sites. This is because the scales for the two axes reflect the ranges of their respective variables. The X-axis (Dimension 1) ranges from -20 to 30 and the Y-axis (Dimension 2) ranges from -4 to 5. This exaggerates the top-to-bottom differences between sites on the Y-axis compared to the left-to-right differences on the X-axis. If the axes were re-scaled with equivalent scales, the resultant graph would better illustrate the distance of Lechlade from the other sites, but it would be either so short as to be difficult to read or so long that it would stretch off the page. It should also be noted that there is no connection between this map and a geographic map. Even though Lankhills is closest to the bottom of the graph and Portway is slightly above it, as if they were located in the South half of the map, this is an accident of the calculation process and has no real meaning. The sites could be flipped 180 degrees on any axis and the results would have the same meaning.

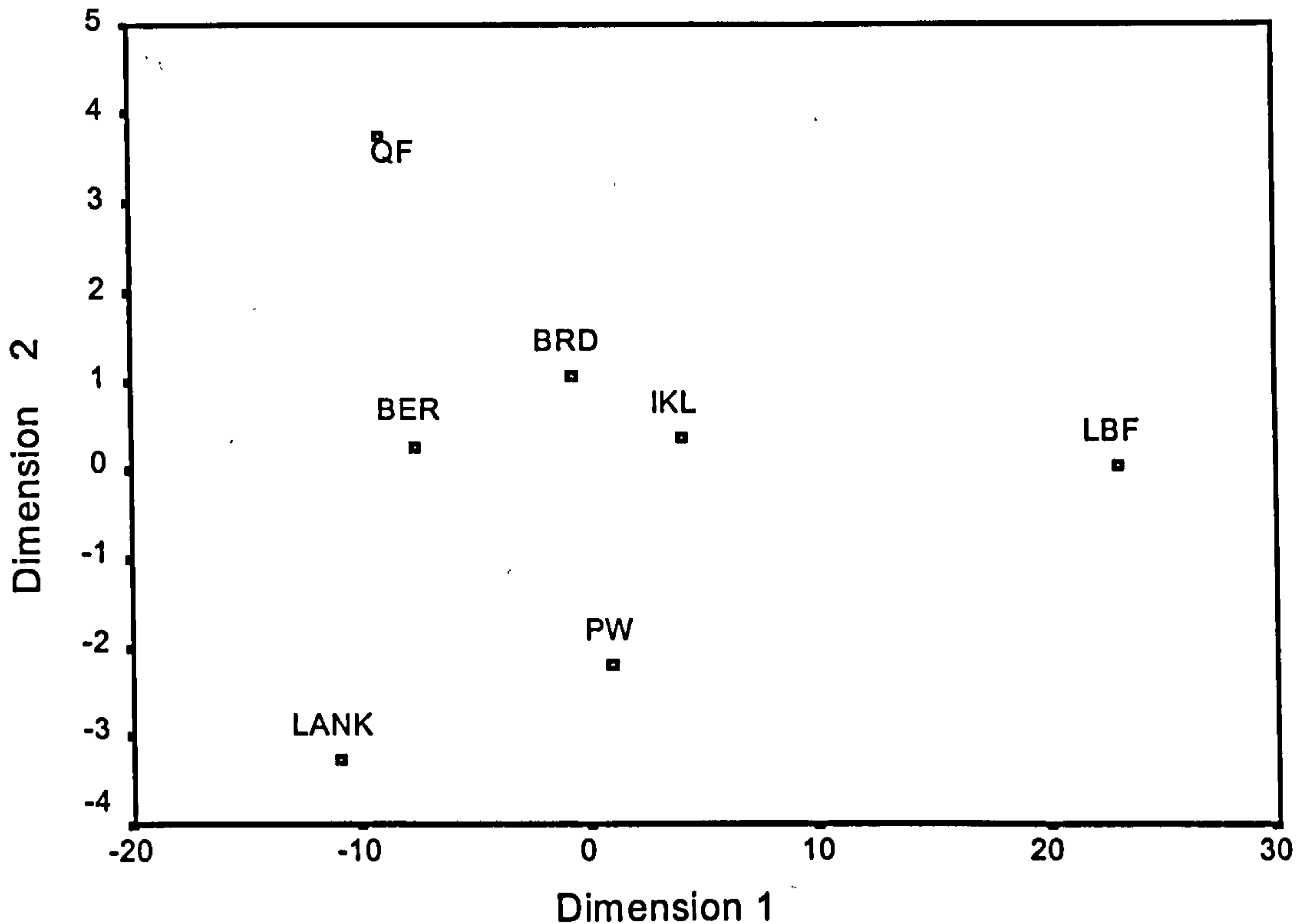


Figure 23. Multidimensional Scaling of Standardised MMD results

3.1.1.3 Biodistance v Geodistance

By plotting the biological distance calculated between two sites, as shown by the MMD scores, against the geographic distance (in kilometres) between those sites results in an XY scatter plot of the 21 comparisons shown in figure 24. As with figure 23, figure 24 uses different axes. The X axis (Geodistance) ranges from 0-300 km while the Y axis (Biodistance) is from -5 to 40 units of the MMD_{stan} distance. These differences in scale make the exaggeration of the top-to-bottom spread compared to the left-to-right spread even greater in figure 24 than it was in figure 23.

Berinsfield is about one kilometre (km) from Queenford. Brandon and Icklingham are separated by about twenty kilometres. Portway and Lankhills are roughly 24 km apart. Lechlade is just under 50 km from Queenford travelling upstream along the Thames. The Suffolk sites (Brandon and Icklingham) are around 180 km from the Oxfordshire sites (Berinsfield and Queenford), 230 km from Lechlade and 240 km from the Hampshire pair (Portway and Lankhills). The Hampshire sites are between 67 and 85 km from the Oxfordshire pair and from 73 to 96 km between the Hampshire sites and Lechlade.

First, this plot shows that, as one would expect in a natural situation, the sites with the smallest MMD scores (most closely related biologically) also tend to be the

sites with the least geographical distance (i.e., the sites in the lower left of the graph have both low MMD scores and are geographically close). As the geographical distance increases there is a slight tendency towards an increase in MMD scores, but that increase is relatively minor. If one were to plot a regression line using all the sites it would show a negative correlation between the two measures. This is due to the extremely high MMD scores for comparisons with Lechlade (especially the BER-LBF, LBF-QF and LANK-LBF scores) and the artificially low MMD scores for comparisons with Icklingham (in particular the BER-IKL, IKL-QF IKL-PW and IKL-LBF scores).

The second and somewhat fortuitous result is that this plot confirms the internal consistency of the MMD statistic. That is to say, the sites group together in predictable patterns. For example, Berinsfield and Queenford are very close to one another both biologically and geographically, and this is reflected by the graph. More importantly, when they are compared to other sites, the point for the comparison of Berinsfield and a third site is near the point for Queenford and that third site (e.g., LBF-QF and Ber-LBF are in the same quadrant of the graph). To put it another way, wherever Queenford goes, Berinsfield is sure to follow.

The Hampshire pair (PW-Lank) has the highest MMD score of the three site-pairs. It is also the pair with the greatest geographic distance (about 24 kilometres apart). Though the geographic distance between Brandon and Icklingham is almost as great as the distance between the two Hampshire sites (about 20 kilometres), the biological distance calculated between those sites does not reflect this. The small sample size of Icklingham is, once again, the probable reason for the MMD score being so low here.

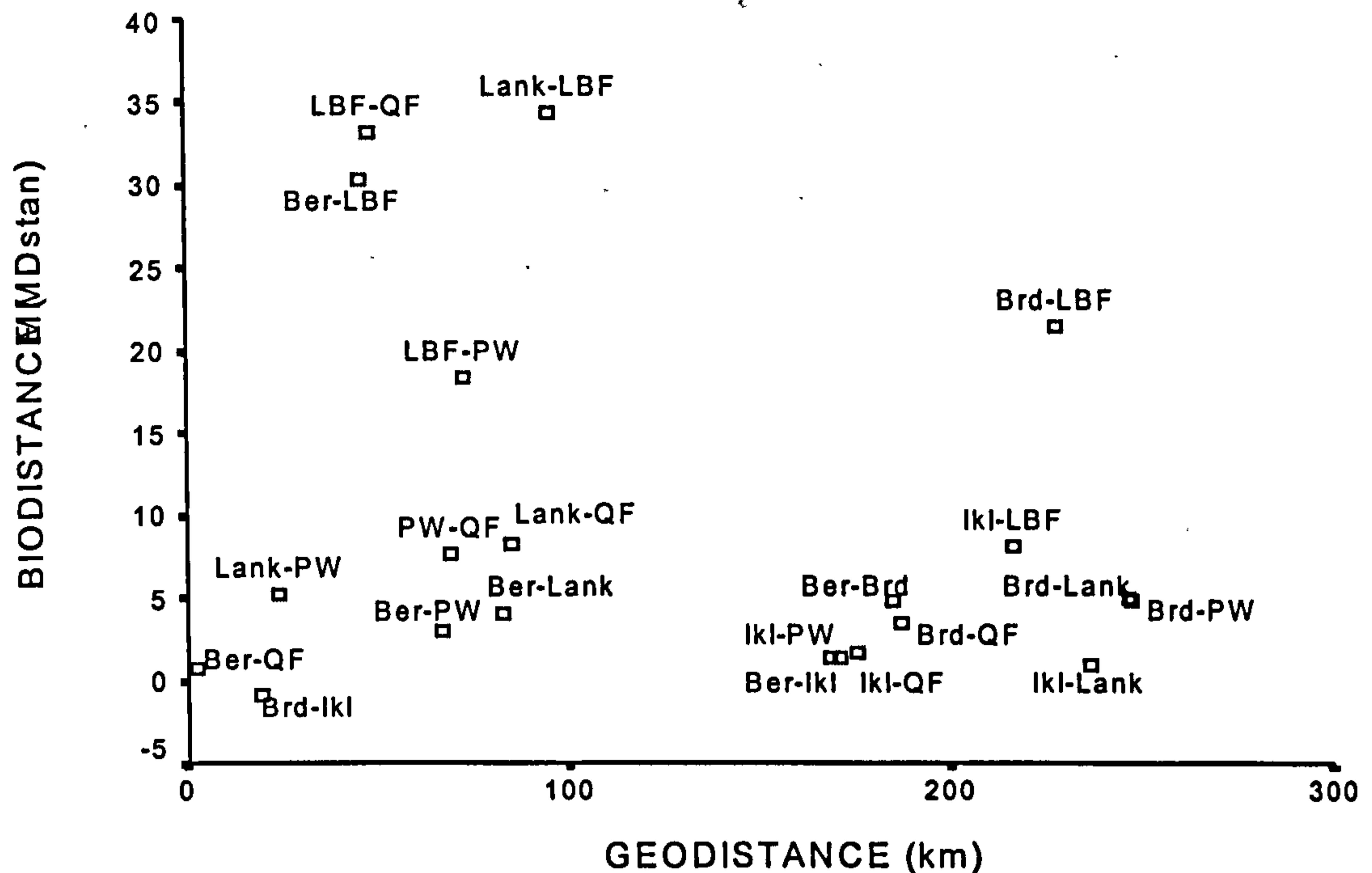


Figure 24. The site pairs plotted by biological distance (MMD_{stan}) against geographical distance (km).

3.1.1.4 Discussion of the Population Level Statistics

The results of the MMD, and the graphical representations of those results, show a very close relationship between Berinsfield and Queenford, both geographically and biologically. The relationship between Brandon and Icklingham is slightly more ambiguous. Theirs is the smallest biological distance of all the sites compared. Icklingham, however, also has the smallest sample size which is the probable reason for the consistently low scores for comparisons between that site and all other sites. Had Icklingham yielded a larger sample, the MMD scores may have been higher when compared to other sites. That conclusion is speculative, however, and is based only on the magnitude of the differences so it cannot be stated categorically on the basis of the available evidence. The biological distance between Lankhills and Portway seems to be a fair reflection of the geographical distance between them.

The most likely explanation for these results is that the population from Berinsfield is directly descended from the population from Queenford. Stated more formally, Berinsfield and Queenford are both derived from the same parent population. The geographic distance between Brandon and Icklingham is greater than the distance between Berinsfield and Queenford, which would suggest that there exists a smaller probability of the inhabitants of Brandon being directly descended from those of Icklingham. It is still highly likely, however, that both populations are

derived from the same parent population because of the very low MMD score. The biological distance between the populations of Lankhills and Portway is statistically significant which indicates a greater degree of biological difference between them. The increased MMD score is consistent with what one would expect to see in a clinal model, i.e., the biological distance increases in proportion to an increase in the geographical distance. In assessing the overall pattern of these six sites, one is left with the impression that the biological differences between regions reflect the geographical distances. It would be easy to speculate that, if one were able to fully correct for the small sample size of Icklingham, the scores for comparisons between these six sites that make up the three site-pairs would show that most of the biological differences were the result of geographic distance.

Lechlade is a 'loner' in more ways than being the only Anglo-Saxon site without a geographically matching Romano-British site. It has statistically different MMD scores from every other site used in this study. The magnitude of the biological differences could lead one to believe that this represents a case of replacement. Another way to interpret such findings would be that Lechlade is a population composed of individuals who have been more completely separated from the other sites used in this study than the other sites have been from one another. While Lechlade includes individuals from areas included in the study, more of them come from outside the study area. It could also be that it represents an older, original population that has some ties to the rest of the sites studied here but has other differences that have built up over time. This idea is similar to the reasons for support of the 'Out of Africa' hypothesis for modern human origins. In that hypothesis, the greater within group variation among African populations shows that they have been in situ longer than other populations and have had more time to accumulate differences in their genetic code (Lewin, 1997; Relethford, 1994; Weiss, 1993). The same line of reasoning is used for the greater variability among native populations in the north-western regions of North America compared to native populations from the rest of the Americas. Greenberg et al (1986) suggest that the populations who crossed the land bridge of the Bering Straits (Beringia) showed greater variability because those who arrived there first were able to build up genetic mutations. Another possible and, to this author, more likely reason for the differences seen between Lechlade and the other sites is that the population of Lechlade includes a significant portion of people who were born in regions of Britain that are not represented, or at least are represented to a much smaller degree, in the other samples. This possibility will be discussed in greater detail below in the Individual Level MDS section, below.

3.2 INDIVIDUAL LEVEL STATISTICS

3.2.1 DISCRIMINANT ANALYSIS

As stated above, the purpose for using Discriminant Analysis in this study is to assess the extent to which dental traits can discriminate members of one population from another. In the first analysis, the test will be to see if individuals can be assigned to the appropriate groups as designated by their cultural affiliation. To do this, we first assign dummy variables of '1' for the Romano-British populations and '2' for the Anglo-Saxon populations.

As there are only two categories, the probability of predicting the correct response would be 50% by chance alone. However, because the groups are of different sizes, the actual probabilities must be calculated from group size. These calculations are one of the options available in SPSS. Examination of table 6 shows that the prior probability of predicting membership in the Romano-British group is about 44%. Prediction of membership in the Anglo-Saxon group is 56%. Discriminant analysis was able to correctly predict that an individual belonged to the Romano-British group 58.6% of the time and to the Anglo-Saxon group 83% of the time. The overall rate of correct predictions of group membership was 72.4%. The classification results for Discriminant Analysis by period is shown in table 6.

	PERIOD	Predicted Group Membership		Prior Probabilities for Groups	Total
		1	2		
Original Count	1	78	55	.438	133
	2	29	142	.563	171
%	1	58.6	41.4		100.0
	2	17.0	83.0		100.0

Table 6. Classification results for Discriminant Analysis by Period. 72.4% of original grouped cases correctly classified.

This implies that the dental traits are slightly better at predicting group membership by time period than is suggested by the prior probabilities. Before deciding that this is proof that the individual relationships are best described by this measure, it is worthwhile to examine the ability to predict membership in a cemetery group.

For the second Discriminant Analysis, the dummy variables are assigned by the cemetery in which the individual was found. In this case, if all samples were of equal size, the chances of correctly predicting group membership should be one in

seven, or roughly 14%. Again, the prior probabilities are calculated by SPSS according to group size. Lankhills (4) and Lechlade (5) have prior probabilities approaching 30%. The probability of correctly guessing the other sites by chance is less than 12% for each of the other five sites, with Icklingham (3) as the least likely at slightly less than 4%. The prior probabilities are shown in table 7.

SITE	PRIOR PROBABILITY
Berinsfield	.089
Brandon	.095
Icklingham	.036
Lankhills	.289
Lechlade	.286
Portway	.092
Queenford	.112

Table 7. Discriminant Analysis, prior probabilities by site.

When the analysis is completed, the results shown in table 8 seem to reveal that the variables do not do a particularly good job of predicting membership in several of the groups. One must keep in mind, however, that the prior probabilities for predicting group membership are also low. The predicted membership for Berinsfield (group 1) is about 26% correct compared to the prior probability of 9%. Correct predictions for Brandon (group 2) are around 34% compared to prior expectations of about 10%. Icklingham (group 3) is 36% correct compared to 4% prior expectation. Lankhills (group 4) is 69% predicted against 29% prior probability. Lechlade (group 5) is 77% correct predictions to 29% prior probability. Portway (group 6) 46% correct compared to 9% prior probability. Queenford (group 7) is 32% correct predictions compared to 11% prior probability. The overall percentage for correct prediction into groups is almost 57% which is much better than the 14% one would have of correctly predicting membership in one of seven groups purely by chance.

		Predicted Group Membership							Total
Original Count	SITE	1	2	3	4	5	6	7	
	1	7	1	1	13	2	2	1	27
	2	1	10	0	13	3	2	0	29
	3	0	1	4	2	3	1	0	11
	4	2	5	2	61	11	4	3	88
	5	0	2	1	14	67	0	3	87
	6	3	1	0	7	3	13	1	28
	7	5	1	0	9	5	3	11	34
Percent of predictions	1	25.9	3.7	3.7	48.1	7.4	7.4	3.7	100.0
	2	3.4	34.5	.0	44.8	10.3	6.9	.0	100.0
	3	.0	9.1	36.4	18.2	27.3	9.1	.0	100.0
	4	2.3	5.7	2.3	69.3	12.5	4.5	3.4	100.0
	5	.0	2.3	1.1	16.1	77.0	.0	3.4	100.0
	6	10.7	3.6	.0	25.0	10.7	46.4	3.6	100.0
	7	14.7	2.9	.0	26.5	14.7	8.8	32.4	100.0

Table 8. Discriminant analysis group membership by site. 56.9% of original grouped cases correctly classified.

One odd result to note is the number of individuals who were predicted to be from Lankhills. Some 48% of the individuals from Berinsfield and 45% of the individuals from Brandon show up in the results as belonging to the Lankhills group, which are greater percentages than those correctly predicted (25.9% for Berinsfield and 34.5% for Brandon). These are the only two cases where Discriminant Analysis predicted membership in one, wrong group more often than in the correct group, although Portway and Queenford also have fairly high percentages of representatives predicted to be in the Lankhills group (25% and 26.5% respectively). As Berinsfield, Brandon and Portway are all Anglo-Saxon sites, and Lankhills is a Romano-British site, the identification of high percentages of individuals from the former three sites with Lankhills suggests that there is considerable biological continuity from the earlier period to the later period. These results also suggest that the ability to predict group membership on the basis of the individual cemetery is much better than predictions made on affiliation with an archaeologically defined time period.

3.2.2 CANONICAL DISCRIMINANT FUNCTIONS

Another way to visualise the results of discriminant analysis is with a scatter plot of the canonical discriminant functions. SPSS gives the option of using several different methods for calculating distances. As with hierarchical cluster analysis, each of the methods were tried and compared. There were no appreciable

differences between the charts so only the chart using the default Mahalanobis' distance of the individual from the group centroid is included in this report. The graph of these results is shown in figure 25.

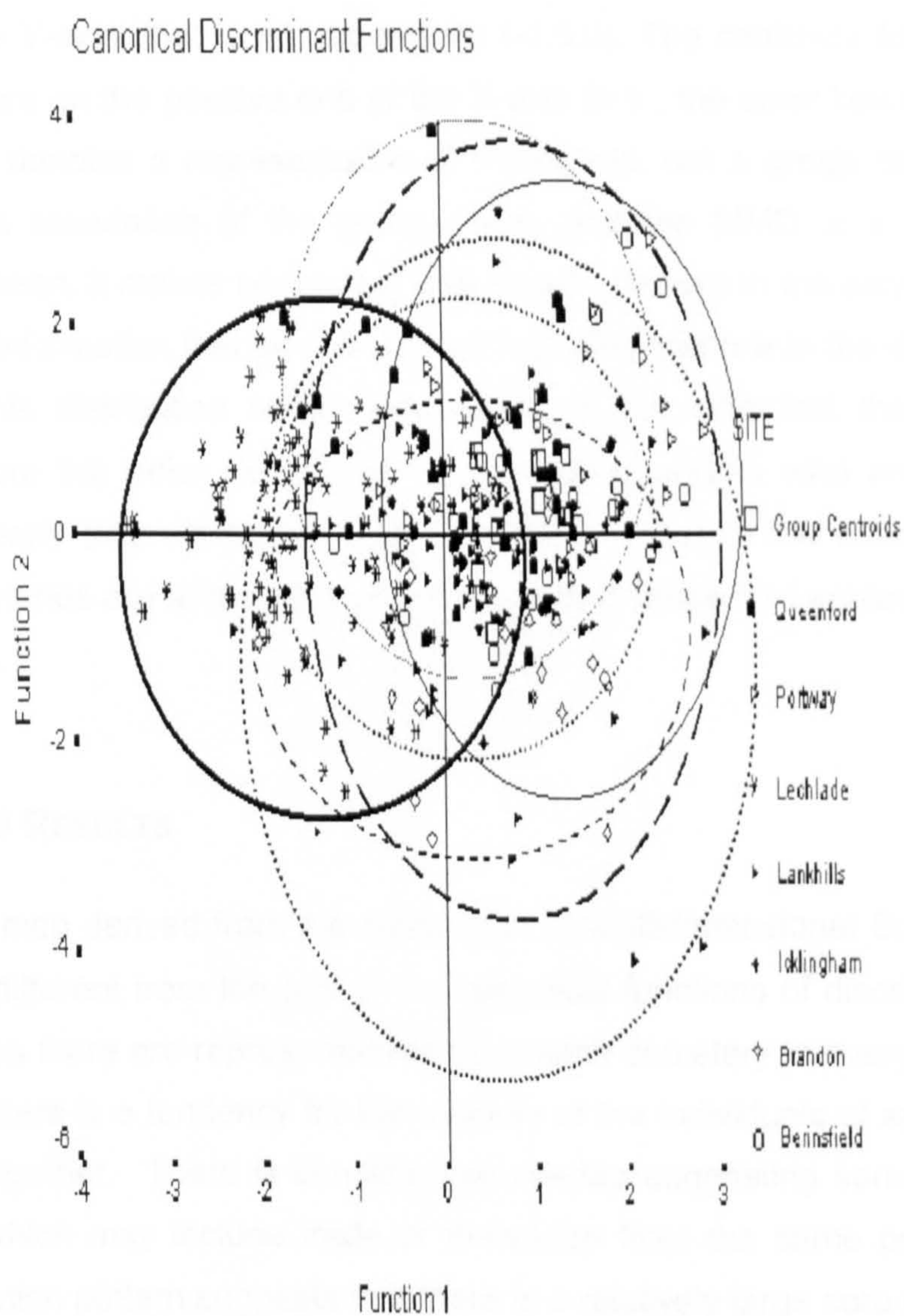


Figure 25. Scatter plot of Canonical Discriminant Functions

It is difficult to interpret this graph because of the number of individuals who are grouped together around the intersection of the axes. This much overlap simply

makes the graph hard to read. The implication, however, is that all of the individuals are fairly closely related, at least in terms of their dental morphology.

Figure 25 shows that the individuals from Lechlade are predominantly clustered on the left side of the graph while the individuals from the other sites tend to lie to the right half of the graph. There is, however, considerable overlap, with individuals from each cemetery in every quadrant of the graph. This graph does help to explain why the MMD results showed such extreme distances for Lechlade. The co-ordinates of the group centroid for Lechlade is between -2 and -1 on the X-axis and 0 on the Y-axis, that is, at about point $(-1.5,0)$. The centroids for the rest of the cemeteries are on the positive end of the X-axis (n.b., the open box symbol at about $(-0.01, -1.2)$ denotes a representative of Berinsfield, not a group centroid). As the centroid is a calculation of the group mean, and the MMD is a measure of the population mean, it makes sense that they should behave in the same manner. The bulk of new information that can be derived from this graph is in the distribution of the outliers. This distribution adds more weight to the idea that the dissimilarity of Lechlade from the other cemeteries is caused by people who are not extremely different, merely different in a different direction. Most of the outliers from the six paired cemeteries are to the right of the graph and those for Lechlade are to the left of the graph.

3.2.3 MDS RESULTS

The map derived from the calculation of Multidimensional Scaling (figure 26) is not very different from the plot of the canonical functions of discriminant analysis. In both cases there are representatives from each cemetery in every quadrant of the graph, but there is a tendency for the majority of the individuals of any one cemetery to cluster together. There is considerable overlap suggesting some sort of contact over time which may include trade or derivation from the same parent population. This distribution pattern suggests that there is a relatively large core population with a common lineage in each cemetery, perhaps as much as three-quarters of the total population, with the remaining one-fourth from other areas.

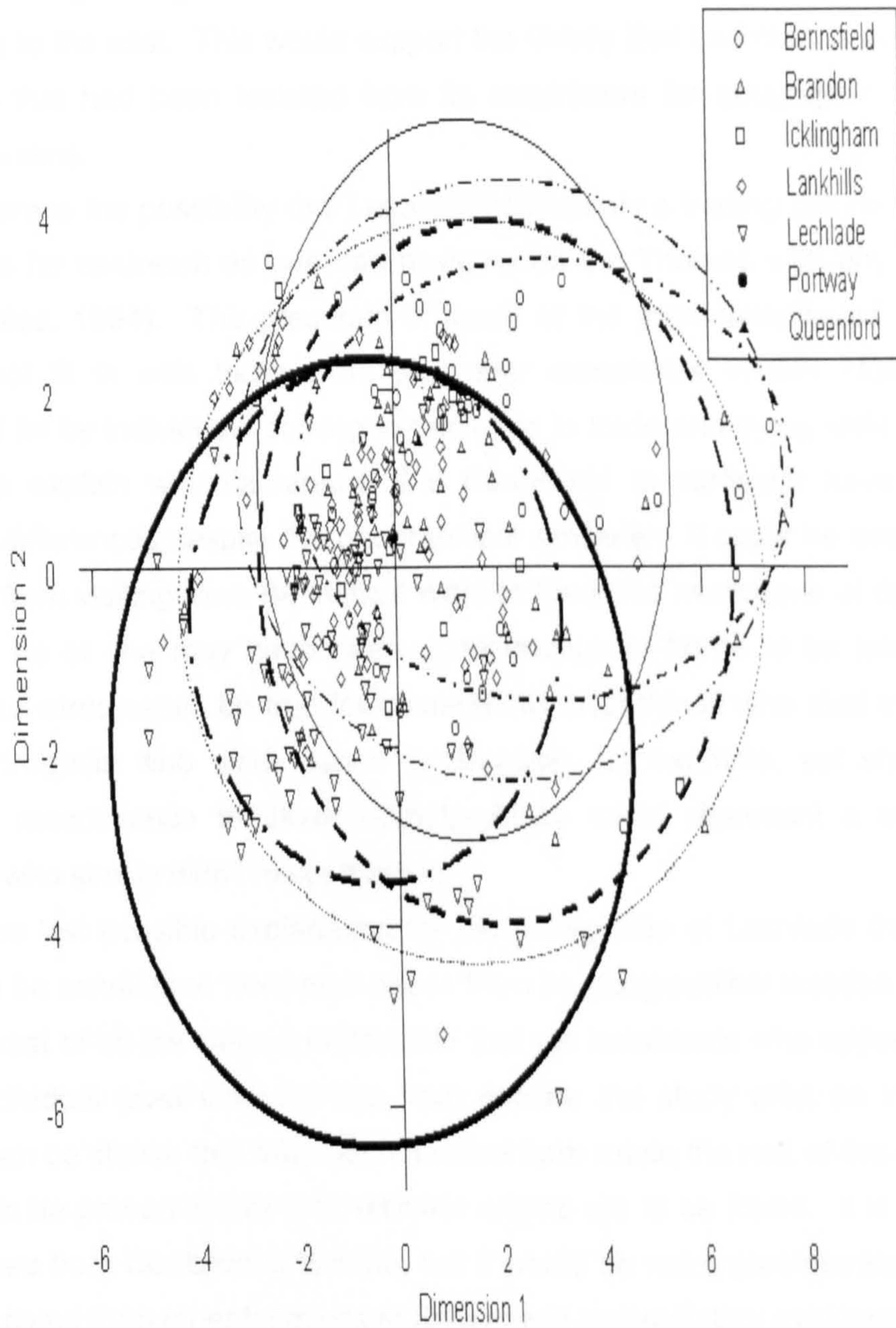


Figure 26. Scatter plot of MDS of individuals

The cluster representing Lechlade is predominantly in the left half of both of these graphs, with much of the cluster intersecting with the other groups. The sprawl of the remainder of this group tends to be away from the rest, which is why the mean

scores represented by the MMD are so divergent from the others. The overlap implies a common ancestry with, or at least some sort of phenotypic resemblance to, 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 geographic or unknown political reasons.

There is the possibility that Lechlade represents a trading centre. Its location is about as far upstream as one can navigate on the Thames with any ease (pers. comm. (Miles, 1994). The presence of many of the individuals found at Lechlade who do not fit in with those from the other cemeteries in this study could be accounted for by individuals coming to Lechlade to trade and dying while there. This could help explain why Queenford and Berinsfield in particular have such large biological differences despite the geographical similarity. It could be assumed that if someone from visiting from Berinsfield were to have the misfortune of dying while in Lechlade, he or she may have been close enough to home to be taken there for burial. The same would be true for someone from Lechlade who died in Berinsfield. Those individuals who were buried in Brandon, for example, yet show a closer biological resemblance to those from Lechlade could represent a traveller from Lechlade who simply didn't make it home.

The last possible explanation for the divergence of Lechlade from the other groups to be considered here also arises from its geographical location. As it is the furthest west of all the sites, it is possible that the individuals who appear as outliers in the individual level statistics are from outside the study area as stated above. While it can be shown that they did not come from within the rest of the study area, it remains to be proven where their ultimate origins are to be found. It is possible that they arrived from Continental Europe, but it would be more parsimonious to assume that they came from other locations in Britain until contradictory evidence is found.

4 CONCLUSIONS

The main purpose of this study was to determine whether the techniques of dental anthropology could be used to provide evidence that would support one or another model of the transition from the Romano-British period to the Anglo-Saxon period. To do this it was first necessary to briefly discuss the background of the debate over whether invasion or biological continuity best describes the reasons for the cultural shift that started in the first half of the fifth century in the area that is now known as England.

Both Anglo-Saxon archaeology and physical anthropology have suffered from the legacy left by early workers in each field. Much of this early work was centred on the construction of typologies. The result of typological systems is that the object being quantified and classified comes to represent another, different concept. In other words, it is reified. At the outset, typological systems may represent a tentative system of classification, but it often becomes a fixed system. To illustrate reification by way of an extremely simplified example, Anglo-Saxon pottery as a class comes to represent 'Anglo-Saxon-ness.' The extent to which a site can be called 'Anglo-Saxon' would then depend on how 'Anglo-Saxon' the pottery is. In the same way, a collection of cranial features, which are to some extent correlated with a geographically defined group, become 'racial' traits. People who exhibit these traits are then said to belong to that race. Once the concept has become reified, it is fixed by its own definition. The process of change that is seen in real populations is conceptually halted and there can be no meaningful deviation from the ideal form of the category. Under such a system the only way for culture to be seen to change is by complete, or at least substantial replacement. If the style of pottery changed from the Romano-British period to the Anglo-Saxon period, the people who lived in the area where the pottery was found must have changed too. This all or nothing way of thinking has slowed the process of developing new models for explaining the process of change. It is probably unfair to suggest that there has ever been a serious study of the Romano-British to Anglo-Saxon transition where these over simplified models of invasion and continuity have been used in their pure forms. Those who do utilise these 'pure forms' usually invoke the pure invasion hypothesis as a short-hand way to explain the transition because it has some minor significance to their own larger field of study.

Race is not a useful concept for this study. All of the groups examined would be considered to be of the same 'major race' as defined by Blumenbach as the origins of the groups would, at some point, be on the European continent. Even if the results of this study showed that invasion was the cause of the Romano-British to Anglo-Saxon transition, the differences may not have been large enough to signify groups that would qualify as 'minor races' under the Blumenbach definition. What is seen here are examples of micro-differentiation which was probably the result of genetic drift. This is appropriate to this research as the ASU system is best applied to cases of genetic drift (Scott and Turner, 1997).

The first step in developing new models is to break away from the reified typological systems that have exemplified previous research. While the terms Romano-British and Anglo-Saxon are used throughout this thesis, it is only as a matter of convenience. These labels were given to the sites by the excavators and reflect the excavators' observations that the site had been in use at a certain time and the cultural items recovered predominantly reflect what is commonly assumed to have been used by the people of that time. Although the terms Romano-British and Anglo-Saxon are used here it should be remembered that the underlying concept is one of dynamic groups.

The abundance of statistical analyses presented should not be taken as an attempt to overwhelm the reader with the weight of numbers. There were, in reality, only three tests presented: 1) reliability of the measuring instrument; 2) population level statistics; and, 3) individual level biological distance measures.

The use of three types of tests for reliability arose because each of the tests makes certain assumptions about the data that may not have been met, or because there are questions about the test itself. For the population level statistics, only one test was used (the Mean Measure of Divergence or MMD), but three different techniques for visualising the data were presented (hierarchical cluster analysis, multidimensional scaling (MDS) and geo-distance v bio-distance plot). Hierarchical cluster analysis is a very commonly used tool, but it has weaknesses such as the imposition of hierarchical structure and one dimensionality. These weaknesses can be avoided by using the mapping technique of MDS. Plotting MMD scores against geographical distance was used as a simple way to visualise the effects of autocorrelation, even though it is not strictly a statistical tool.

The results of the MMD show that the two sites from Suffolk, Brandon and Icklingham, are statistically indistinguishable from one another in biological terms. The Oxfordshire sites, Berinsfield and Queenford Mill, are also biologically

indistinguishable. The pair from Hampshire, Portway and Lankhills, does show a statistically significant difference. It should be noted, however, that these results are only slightly beyond the threshold of statistical significance. One could conclude that the differences between these two sites are due more to geographical distance than to biological distance, as the geo-distance is greater than that of the others. However, comparing the divergence of Lechlade from each of the rest of the sites, and the differences seen between site-pairs from different regions indicate that the ASU system does have the sensitivity to detect even slight differences in the phenotypical profile of groups that would logically be closely related.

Discriminant Analysis, Canonical Discriminant Functions and Multidimensional Scaling of individuals were presented to provide a more in-depth analysis of the relationships among the individuals who contributed to the mean values at the population level. It is not surprising that the population level statistics and the individual level statistics should be confirmatory as the same variables are used in each analysis. What is surprising is the degree to which the similarities could be seen. The discriminant analysis and the individual level MDS show that some 25% of the Lechlade sample overlaps the other sites. This helps support the idea that these groups were dynamic, constantly evolving populations whose membership did not require close kinship with others in the population. The fact that many of those buried at Lechlade have very close relationships to those found at other cemeteries, and indeed, people of other cemeteries closely resemble those buried at Lechlade, also suggests that Lechlade was not as isolated as the population level statistics suggest. Even though these sites can be distinguished from one another, the site that is most biologically dissimilar from the rest (Lechlade) is composed of individuals who are very similar to those found at the other sites.

The methods of visualising the results of the MMD, as well as the MMD scores themselves, show strong support for the hypothesis of biological continuity from the Romano-British period to the Anglo-Saxon period. To support an invasion hypothesis in light of these results, one must make one or more of the following arguments. The first argument is that the cemeteries are not representative of the populations of the time. The problems discussed in the Cemetery Demographics section give several points with which to argue this point. Another argument might be that the ASU system was not sensitive enough or accurate enough to detect a real pattern. It is extremely unlikely, however, that the pattern of biological affinity shown in this study would emerge from examination of a sample of sites selected on the basis of the criteria outlined above and without any attempt to find sites that fit into a

preconceived idea of what should be found if the sites did not reflect at least a sizeable portion of the population.

One of the interesting problems presented by the labelling of sites as Romano-British or Anglo-Saxon by the excavators is seen in the Oxfordshire cemetery pair of Queenford and Berinsfield. If the excavators were correct in assigning the dates of use as late-fourth century to mid-sixth century for Queenford (Chambers, 1987) and mid-fifth to early-seventh century for Berinsfield (Boyle et al., 1995), then these two, apparently culturally distinct cemeteries were in simultaneous use for almost 100 years. As these two cemeteries are separated by less than one mile, it is reasonable to surmise that these are not really two populations, but one population that exhibits a multicultural way of life.

Considering the geographical and chronological similarity of these two cemeteries; it may be advisable to make a slight change to the formal statement of the research design. Rather than the requirement of having two distinct cemeteries in a pair, the statement could be amended to stipulate that there be at least two distinct phases of use in a cemetery as evidenced by a change in cultural treatments of the burials. This change in the formal statement of the design does not, however, change the approach to the basic question at hand, i.e. is a change in cultural identity caused by a change of the biological makeup of the population? Given the results of the dental comparisons made in this study, which show no statistically relevant biological distinctions between the populations of Queenford and Berinsfield, the answer to the question when applied to these two cemeteries is that cultural change took place without biological change. The implications of this result remain the same whether one views the individuals studied as having been members of two distinct cemeteries or as having been in different phases of one cemetery.

When one considers the biological similarities of these two sites and how cultural change would be most likely to happen under the continuity model, it makes sense that there would be a period of overlap between the two sites during which both cultures are represented in the living population. Over time, the original culture would die out as the new culture gradually becomes dominant. A modern example might be in Japan where members of the older generation cling to the older styles of clothing and religion but the younger generations adopt trendy lifestyles that are more similar to European ways. To put it in the terms used by Cavalli-Sforza and Feldman (1981), the amount of vertical transmission of culture in the older population decreased and the vertical and horizontal transmission of culture in the younger population increased.

The biological similarities between Berinsfield and Queenford along with the chronological overlap between the two sites also present difficulties for making the assumptions presented by Härke (1990). The evidence in this study cannot be used to make any assertions about the suggestion that the people who are dissimilar to the bulk of the populations are actually Germanic as no German populations were examined. It is, however, possible to suggest that there were not enough people with dental morphological differences to account for the numbers of people he claimed were of Germanic origin. A simpler explanation of the differences in stature he claimed to have found comes from the tendency of societies to select its largest and/or strongest members to be soldiers.

This type of cultural overlap with biological continuity may even be necessary in some, and possibly a majority of site-pairs where transition from one culture to another is found. If a re-evaluation of Queenford and Berinsfield were to show that these two sites actually were different sections of the same cemetery it could be considered a stroke of luck to have found the transitional form with representatives from both segments of a multicultural society. For these reasons it would be worthwhile to examine all of the material from both of these sites together to examine how they might be related. There is evidence of Romano-British occupation along with the Anglo-Saxon cemetery that was the main focus of the excavations at Berinsfield (Boyle et al., 1995). It may be the case that this Romano-British occupation is also associated with the cemetery at Queenford, but that this relationship was not fully appreciated by the excavators.

A similar re-examination comparing Lankhills and Portway Down may also be of interest. Dates of c. AD 310 to c. 410 were given for the use of Lankhills (Clarke et al., 1979). Cook and Dacre (1985) give late fifth century to about AD 600 for the use of Portway Down. While there is no actual overlap seen in these dates, there may be some cultural similarities that are as yet undetected. The dates for the use of Icklingham, AD 350-420 (West and Plouviez, 1976), and Brandon, AD 600-900 (Carr et al., 1988) suggest that there would be no direct evidence for overlap but a comparison of all the evidence from these sites may show up the lack of transitional forms and, therefore, shed some light on how to more readily detect signs of transition in other site-pairs.

It is difficult, if not impossible to 'prove' a single hypothesis (Madrigal, 1998:2). This is particularly true when studying the movements of ancient populations. Confounding factors such as the types of traits used, verifying the representative nature of the population and the possibility of missing groups that may be

intermediate between the groups actually studied can cast doubts about any findings. The best outcome is to provide evidence in support of one hypothesis over other hypotheses.

Seven sites cannot be said to represent the whole of the transition period. The safest statement that can be made for the results of this study is that in these seven populations, biological continuity from the Romano-British period to the Anglo-Saxon period was the rule. It is highly probable that this situation would be common in much of the rest of Britain, given this pattern of similarities. Studies using more sites from a broader geographical area would help to assess the validity of these results. Obviously these results should not be used in any attempt to explain how the transition from the Romano-British period to the Anglo-Saxon period took place in all areas of Britain. Whether this information will be utilised to discourage the unthinking equation of cultural identity with biological identity remains to be seen.

By reviewing these interpretations of the results of this study, it is the conclusion of this author that the first stated goal of this research has been attained and that dental nonmetric traits are useful tools for exploring the relationships among closely related populations. As discussed in the hypothesis testing section, the fact that sites from different geographical areas were distinguishable, there was no need to go even further afield to find significant differences.

5 FURTHER RESEARCH

Dr. Elizabeth Rega formerly of Sheffield University, now of Claremont College, California, recently received a donation from Professor Barry Brown, recently retired from University College, London (pers. comm. Rega, 1996). The donation consists of all the casts of the teeth of his research subjects which were collected for craniofacial studies. The collection reflects three, and sometimes four generations of families from Ireland. For many individuals there are several casts from different stages of life.

Dr. Rega and this author have already agreed to collaborate on several studies using this collection. One of the first of these studies will be to assess inter-observer concordance and to reassess intra-observer concordance. This will facilitate comparisons between the data collected in this study and any future work by this author to work on other archaeological sites or casts from living populations performed by Dr. Rega. It will also allow even greater expansion of comparability to work carried out by others who may have contact with one of us but not the other.

The logic here being that work carried out separately by researchers A, B, and C may not be comparable if no inter-observer concordance tests are done. The best solution would be for all three researchers to make direct comparisons. If that is not possible, the next best solution is for researchers A and B to test for concordance and for researchers B and C to test for concordance. If the results for A are nearly equal to those for B, and scores for B are nearly equal to those for C, then data collected by A and C should be nearly equal. This is not strictly true, but there is a better chance of it being true than if no tests for concordance were made at all.

Making use of the information provided by the records of the individuals in this sample could also allow for a reassessment of the level of sexual dimorphism. Crown dimensions are known to show low levels of dimorphism for some teeth (Scott and Turner, 1997; Townsend and Brown, 1980; Garn et al., 1967; Lunt, 1969). The reports on morphological traits are contradictory, some report dimorphism (e.g. (Goose and Lee, 1971; Scott et al., 1983) , others do not (e.g. Scott, 1980; Turner, 1969). Using the casts from Professor Brown's collection it will be possible to investigate both metric and nonmetric differences between the sexes. This would tell us how that population compares to some of the other populations that have been studied (e.g. American blacks, New World Indians, Caucasians, Asians, Polynesians and Melanesians (Scott and Turner, 1997: 107).

Another study will involve an assessment of the heritability of the traits used in the ASU system. This is possible due to the nature of the collection. The familial structure will allow for tracking the expression of traits from generation to generation. In some cases, it will be possible to track trait expression from grandparent to grandchild, which, to the best of my knowledge, has never been done before with the ASU system.

There also exists the possibility of developing new classifications for dental traits that are not yet included in the ASU system. Even in the short time since the publication of the ASU system (Turner et al., 1991), the description and reference plaque for another trait has been published (Wu and Turner, 1993). Part of the original vision of how the ASU system would continue to grow in usefulness includes development of new traits (Scott and Turner, 1997; Turner et al., 1991) .

One area neglected by this study is of the demographic nature of the changes found through time and space. One possible study, partly an exercise in data mining, is to examine the extent to which the sex of the individual contributed to the location of burial. For instance, were men more likely to be found at a greater distance from their origins than women, which might indicate that men were more active in trade?

Or were women more likely to be the non-locals which might indicate exogamy to a greater extent than may seem necessary? Another question is what impact age has on location of burial. Are older individuals found at the centre of family groupings (assuming such groupings can be accurately identified), or are they seen as being less important in the general scheme of life and, therefore, buried without much care? Both age and sex were disregarded in this study partly because the nature of teeth and the traits used in the ASU method make it possible to do so. Also, the data in the bone reports were often at odds with this author's own assessments. A careful re-examination of the material may show which set of data is more reliable and could be used for these demographic studies.

Another study that could be carried out using the information from the individual level statistics would involve a search for family groupings within the cemeteries described in the current study. If complete, large-scale maps of the cemeteries and report-number/find-number concordances were available as well as computer software that could identify individuals on the MDS or Canonical Discriminant Function maps, one could, conceivably identify how the bodies in the ground related to the biological distances shown by the dental traits.

Lastly, more sites from more areas and time periods should be studied to fill the gaps left by this research. Would a comparison between a Bronze Age site, for example, show a greater or lesser degree of similarity to a Romano-British site than either would to an Anglo-Saxon site? Would sites in Kent show a greater genetic impact on the part of early Anglo-Saxon immigrants as Historians would argue, or would they fit with the sites in this study to show continuity? Would sites located between the sites used in the current study betray clinal variation in the same way one could interpret the differences between Portway and Lankhills? Sites from more northerly and westerly regions may be helpful in gaining greater understanding of the range of variation across Britain. It would also be interesting to examine sites from a range of continental European countries. This would help in explaining the variation across an even wider area and add to our understanding of micro-evolutionary processes. It would be important to ensure that any further dental morphological studies include inter-observer tests so that observations made by other researchers could be compared to the observations in this study and any future studies by this author.

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6 APPENDICES

6.1 APPENDIX I SCORING SHEETS FOR THE ASU METHOD

The following two pages show the scoring sheet for the Arizona State University Dental Anthropology Scoring Method. Samples of the sheets are included with the casts when purchased from ASU. The examples shown here reflect the slight modifications that have been made by the author. At the bottom of page one there are spaces for the recording of shape, size and number of openings in the incisive fossa. This is a trait that the author began to record early in the data collection phase of this study. The trait is not included in that ASU system. As this trait is still in the developmental phase, the range of variation, classification system, level of genetic influence and liability to environmental change as well as its usefulness in anthropological studies have not yet been determined.

The original sheets were photocopies of a sheet that was created using a typewriter for the text and hand-drawn boxes. Some changes in the layout were made when the sheets were redrawn by Kari A. Lloyd-Jones using Microsoft Excel. Most of the changes involve spacing and placement of the boxes. It is felt by this author that the redrawn sheets are much easier to read and use.

ARIZONA STATE UNIVERSITY

Dental Anthropology Laboratory

Date _____

Facility _____

File Name & No. _____

Age _____ Sex _____

UPPER I1R I1L I2R I2L CR CL P1R P1L P2R P2L M1R M1L M2R M2L M3R M3L
JAW

Status/wear															
Caries															
Winging															Torus: None ___ Tr ___ Med ___ Mark ___
Labial Curve															Abscess _____
Shovel															Perio _____
Double Shovel															Chipping _____
Interrup. Groove															Cult. Treat _____
I & C.t.d.															Other treat _____
C mesial ridge															TMJ damage R _____ L _____
C d.a.r.															Extra teeth _____
P m.&d. Cusps															
Uto-Aztec P															
Metacone															
Hypocone															
Cusp 5															
Carabelli															
Parastyle															
Enamel ext.															
Root number															
Radical no.															
Reg(<7)/reduce															
Odontome															
Cong. Absence															
Hypoplasia age															
Incisive Fossa:	Shape _____		Size _____				Openings _____								

Cran.def. None ___ Occip ___ Lamb ___

Cribr. Orb. 0 ___ 1 ___ 2 ___ 3 ___ 4 ___

Por. Hyp. 0 ___ 1 ___ 2 ___ 3 ___ 4 ___

ARIZONA STATE UNIVERSITY
Dental Anthropology Laboratory

LOWER JAW I1L I1R I2L I2R CL CR P1L P1R P2L P2R M1L M1R M2L M2R M3L M3R

Status/wear																
Caries																
Shovel																
C.d.a.r																
P. ling. Cusps																
Anterior fovia	Torus: None ___ Tr ___ Med ___ Mark ___															
Groove pattern	Rocker: None ___ Near ___ Rocker ___															
M. Cusp no.	Abscess _____															
Def. Wrinkle	Perio _____															
DT crest	Chipping _____															
Protostylid	Cult. Treat _____															
Cusp 5	Other treat _____															
Cusp 6																
Cusp 7																
Tomes root																
Enamel ext.																
Root number																
Radical no.																
Odontome																
Cong. Absence																
Hypoplasia age																
Torsomolar angle																

Color roll frame # _____ B/W roll frame # _____ Subject _____
 # _____ # _____
 New variants:

6.2 APPENDIX II CODE FOR THE DENTAL ANTHROPOLOGY PROGRAM

```
*****
*DENTAL.PRG
*THIS IS THE WORKING NAME FOR THE PROGRAM WHICH CONTROLS THE MENUS AND
*FLOW OF*THE PROGRAM FOR THE DENTAL ANTHROPOLOGY SCORING METHOD
*****
*set environment

CLOSE DATABASES
SET HEADING OFF
set status off
SET SAFETY OFF
SET TALK OFF
SET CONSOLE ON
SET DEVICE TO SCREEN
SET PRINT OFF
SET SCOREBOARD OFF
CLEAR

*define variables

msite=space(25)
mAbbrev=SPACE(5)
MDIR=" "
mdrive=" "
RESTORE FROM LAST && to return to the last site used in the last session

Fname=MDRIVE+ ":"+RTRIM(MDIR)+"\"+RTRIM(mAbbrev)
*@ 23,20 SAY "CURRENT SITE" GET MSITE
uppera=(fname)+"upa"
lowera=(fname)+"loa"
measurea=(fname)+"mea"
upperd=(fname)+"upd"
lowerd=(fname)+"lod"
measured=(fname)+"med"
result=(fname)+"res"
MNSITE=MSITE

*define windows for screen
DEFINE WINDOW Fulscree FROM 1,0 TO 21,79 none
DEFINE WINDOW entry FROM 4,0 TO 21,79
DEFINE WINDOW GETINFO FROM 4,10 TO 18,60 panel COLOR +gr/g, r/w,n/g
DEFINE WINDOW wrong FROM 2,2 TO 17,75 PANEL COLOR R/GR+

*Define the main menu
DEFINE MENU First
DEFINE PAD entry OF First PROMPT "DATA" AT 0,1 MESSAGE "ADD, EDIT ETC."
DEFINE PAD stats OF First PROMPT "STATISTICS" AT 0,15 MESSAGE "START STATISTICS
PROGRAMS"
DEFINE PAD exit OF First PROMPT "EXIT" AT 0,60 MESSAGE "EXIT"
ON PAD entry OF First activate popup addpop
ON PAD stats OF First activate popup statspop
ON PAD exit OF First activate popup outpop

* Define the popup "add"
SET BORDER TO DOUBLE
DEFINE POPUP Addpop FROM 1,1
DEFINE BAR 1 OF Addpop PROMPT "SET UP A NEW SITE" MESSAGE "MAKE ALL THE FILES FOR
A NEW SITE"
DEFINE BAR 2 OF Addpop PROMPT "PERMANENT TEETH" MESSAGE "USE DATA ENTRY FOR
ADULTS"
DEFINE BAR 3 OF Addpop PROMPT "DECIDUOUS TEETH" MESSAGE "USE DATA ENTRY FOR
KIDS"
```

DEFINE BAR 4 OF Addpop PROMPT "VIEW RECORDS" MESSAGE "VIEW RECORDS"
DEFINE BAR 5 OF Addpop PROMPT "DELETE RECORDS" MESSAGE "MARK RECORDS FOR
DELETION, AND DELETE"
DEFINE BAR 6 OF Addpop PROMPT "EDIT RECORDS" MESSAGE "EDIT RECORDS"
DEFINE BAR 7 OF Addpop PROMPT "Change Sites" MESSAGE "CHANGE TO A NEW SITE"

*Define the popup "out"
SET BORDER TO DOUBLE
DEFINE POPUP outpop FROM 1,60
DEFINE BAR 1 OF outpop PROMPT "EXIT TO DBASE" MESSAGE "EXIT TO DOT PROMPT OR
CONTROL CENTER"
DEFINE BAR 2 OF outpop PROMPT "EXIT TO DOS" MESSAGE "EXIT TO DOS"
DEFINE BAR 3 OF outpop PROMPT "CLOSE ALL DATABASES"

*Define the popup "stats"
SET BORDER TO DOUBLE
DEFINE POPUP statspop FROM 1,15
DEFINE BAR 1 OF statspop PROMPT "DO COUNTS"
DEFINE BAR 2 OF statspop PROMPT "DO MMD"
DEFINE BAR 3 OF STATSPOP PROMPT "SHOW RESULTS"

*Define popup "lookpop"
SET BORDER TO DOUBLE
DEFINE POPUP lookpop FROM 3,17
DEFINE BAR 1 OF lookpop PROMPT "UPPER JAW"
DEFINE BAR 2 OF lookpop PROMPT "LOWER JAW"
DEFINE BAR 3 OF lookpop PROMPT "MEASUREMENTS"

ON SELECTION POPUP ADDPOP DO Addproc WITH MSITE
ON SELECTION POPUP STATSPOP DO Statproc
ON SELECTION POPUP OUTPOP DO Outproc
ON SELECTION POPUP LOOKPOP DO Lookproc WITH UPPERA, LOWERA, MEASUREA

@ 24,5 SAY "CURRENT SITE" GET MNSITE
ACTIVATE MENU First
CLOSE ALL
*deactivate window ALL
*RELEASE WINDOWS Fulscree,entry,GETINFO,wrong
RELEASE ALL LIKE m*
RELEASE ALL LIKE n*
RELEASE POPUPS
RELEASE MENUS
RETURN

6.3 APPENDIX III CODE FOR PROCEDURES ADDPROC AND MAKEFILE

```
*****
*ADDPROC
*Program for the data entry/ housekeeping menu
*****
PARAMETER MNSITE

DO CASE

    CASE BAR()=1
        @ 24,5 SAY "CURRENT SITE" GET MNSITE picture "!!!!!!!!!!!!!!!!!!!!!!!!!!!!"
        DO MAKEFILE WITH MDIR,MDRIVE,MABBREV,MSITE,FNAME

    CASE BAR()= 2
        @ 24,5 SAY "CURRENT SITE" GET MNSITE
        ACTIVATE WINDOW FULSCREEN
        DO ADULPROC WITH FNAME, MNSITE,uppera,lowera,measurea &&THE
DATA ENTRY PROGRAM FOR ADULT DENTITION
        DEACTIVATE WINDOW FULSCREEN

    CASE BAR()=3
        @ 24,5 SAY "CURRENT SITE" GET MNSITE
        ACTIVATE WINDOW FULSCREEN
        DO KIDSPROC WITH FNAME,mNsite,upperd,lowerd,measured && THE
ENTRY PROGRAM FOR DECIDIOUS TEETH
        DEACTIVATE WINDOW FULSCREEN

    CASE BAR ()=4
        @ 24,5 SAY "CURRENT SITE" GET MNSITE
        ACTIVATE POPUP LOOKPOP

    CASE BAR ()=5
        @ 24,5 SAY "CURRENT SITE" GET MNSITE
        ACTIVATE WINDOW Fulscreeen
        DO OUST with uppera, lowera,measurea
        DEACTIVATE WINDOW Fulscreeen

    CASE BAR ()= 6
        @ 24,5 SAY "CURRENT SITE" GET MNSITE
        ACTIVATE WINDOW FULSCREEN
        DO EDITPROC
        DEACTIVATE WINDOW FULSCREEN

    CASE BAR()= 7
        @ 24,5 SAY "CURRENT SITE" GET MNSITE
        ACTIVATE WINDOW FULSCREEN
        DO changem
        DEACTIVATE WINDOW FULSCREEN
    OTHERWISE
        ? BAR()
        WAIT

ENDCASE
RETURN

PROCEDURE MAKEFILE
```



```

PARAMETERS MSITE, MABBREV, MDIR, MDRIVE, FNAME
*****
*MAKEFILE.PRG
*Creates a set of empty datafiles for the site passed in "name".
*The sites file is currently open and positioned at this site's data.
*****
*****
*This program uses 7 files. They all start with the word "MASTER" plus a suffix
* which relates the the structure of the relevant database. For example, the
* dbf file for the upperjaw of adults is called "**UPA.dbf" where the global
* refers to the abbreviation given by the user.
*****

```

```
close databases
```

```

CLEAR SCREEN
SET TALK OFF
msite=space(25)
mAbbrev=SPACE(5)
MDIR=" "
mdrive=" "
Activate window getinfo
@ 2,2 SAY "Site Name: " GET msite PICTURE "!!!!!!!!!!!!!!!!!!!!!!!!!!!!";
MESSAGE "The unique name by which this site is known"
@ 4,2 SAY "Abbreviation: " GET mAbbrev PICTURE "!!!!!";
MESSAGE "A unique 5 letter abbreviation to identify the files for the site"
@ 6,2 SAY "Drive: " GET mdrive PICTURE "!";
MESSAGE "The letter of the drive on which these files will be stored"
@ 8,2 SAY "Directory: " GET mdir PICTURE "!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!";
MESSAGE "The name of the directory for these files"
read
DEACTIVATE WINDOW GETINFO
Fname= "\"+RTRIM(MDIR)+"\"+RTRIM(mAbbrev) &&Get the site details
USE SITES
SET ORDER TO TAG SITE
SEEK TRIM(MSITE)

```

```

IF .NOT. FOUND()
DO MAKEPROC
ELSE

```

```

    ACTIVATE WINDOW wrong
    @ 6,8 SAY "Sorry, "+ TRIM(MSITE)+" already exists in the database."
    @ 8,20 say " Try another name,"
    WAIT
    CLOSE DATABASES
    DEACTIVATE WINDOW wrong, GETINFO

```

```
ENDIF
```

```
PROCEDURE MAKEPROC
```

```

USE MASTERUP
CREATE (FNAME)+"UPA" FROM MASTERUP
USE MASTERLO
CREATE (FNAME)+"LOA" FROM MASTERLO
USE MASTERMA
CREATE (FNAME)+"MEA" FROM MASTERMA
USE MASTERUD
CREATE (FNAME)+"UPD" FROM MASTERUD
USE MASTERLD

```

```
CREATE (FNAME)+"LOD" FROM MASTERLD
USE MASTERMD
CREATE (FNAME)+"MED" FROM MASTERMD
use mastres
create (fname)+"RES" from mastres
deactivate window getinfo
USE SITES
APPEND BLANK
REPLACE SITE WITH m->MSITE ,ABBREV WITH m->mabbrev,DRIVE WITH m->mDRIVE,
DIRECT WITH m->MDIR
SET DEFAULT TO &MDRIVE
SET PATH TO &MDIR
Close databases
DELETE FILE LAST.MEM
SAVE TO LAST
@ 23,33
*@ 23,33 GET MSITE
return
```

6.4 APPENDIX IV CODE FOR DATA ENTRY

```
*****
*-Procedure for data entry for permanent teeth
*PROCEDURE ADULPROC
*****
PARAMETER FNAME, MSITE, UPPERA, LOWERA, MEASUREA
CLOSE DATABASES
CLEAR
SET TALK OFF

SELECT 1
use &uppera
set order to tag filename
SELECT 2
use &lowera
SELECT 3
USE &MEASUREA
DO WHILE .T.
    mfile= SPACE(10)
    SELECT 1
    @ 0,20 SAY "THE DENTAL ANTHROPOLOGY SCORE SHEET"
    @ 2,30 SAY "FILE NAME" GET mfile PICTURE "!!!!!!!";
    VALID (.NOT. SEEK(mfile)).AND.(.NOT.LEN(TRIM(mfile))<1) ERROR "THAT ONE
HAS ALREADY BEEN DONE"
    READ
    ACTIVATE WINDOW entry
    APPEND BLANK
    SET FORMAT TO UPPER.FMT
    REPLACE Filename WITH mfile
    READ
    SET FORMAT TO
    SELECT 2
    SET FORMAT TO LOWER.FMT
    APPEND BLANK
    REPLACE Filename WITH mfile
    READ
    SET FORMAT TO
    SELECT 3
    SET FORMAT TO MEASURME.FMT
    APPEND BLANK
    REPLACE Filename WITH mfile
    READ
    SET FORMAT TO
    mget= ''
    @ 15,15 SAY "ENTER MORE RECORDS NOW? (Y/N)";
    GET mget picture "I" VALID (mget)$'YN'ERROR "YES OR NO";
    DEFAULT "N"
    READ
        IF UPPER(mget) <> 'Y'
            EXIT
        ENDIF
    ENDDO
DEACTIVATE WINDOW entry
CLOSE DATABASES
CLOSE FORMAT
CLEAR
* PROCEDURE FOR ENTERING RECORDS ABOUT DECIDIOUS TEETH
PROCEDURE KIDSPROC
```

```

PARAMETER FNAME,msite, UPPERD, LOWERD, MEASURED
CLOSE DATABASES
CLEAR
SET TALK OFF
SELECT 1
use &upperd
set order to tag filename
SELECT 2
use &lowerd
SELECT 3
USE &measured
DO WHILE .T.
    mfile= SPACE(10)
    SELECT 1
    @ 0,20 SAY "THE DENTAL ANTHROPOLOGY SCORE SHEET"
    @ 2,30 SAY "FILE NAME" GET mfile PICTURE "!!!!!!!";
    VALID (.NOT. SEEK(mfile)).AND.(.NOT.LEN(TRIM(mfile))<1) ERROR "THAT ONE
HAS ALREADY BEEN DONE"
    READ
    ACTIVATE WINDOW entry
    APPEND BLANK
    SET FORMAT TO UPPERDEC.FMT
    REPLACE Filename WITH mfile
    READ
    SET FORMAT TO
    SELECT 2
    SET FORMAT TO LOWERDEC.FMT
    APPEND BLANK
    REPLACE Filename WITH mfile
    READ
    SET FORMAT TO
    SELECT 3
    SET FORMAT TO MEASRDEC.FMT
    APPEND BLANK
    REPLACE Filename WITH mfile
    READ
    SET FORMAT TO
    mget= ''
    @ 15,15 SAY "ENTER MORE RECORDS NOW? (Y/N)";
    GET mget picture "I" VALID (mget)$'YN'ERROR "YES OR NO";
    DEFAULT "N"
    READ
        IF UPPER(mget) <> 'Y'
            EXIT
        ENDIF
    ENDDO
DEACTIVATE WINDOW entry
RELEASE ALL
CLOSE DATABASES
CLOSE FORMAT
CLEAR

```

6.5 APPENDIX V FORMAT CODE FOR UPPER JAW DATA ENTRY

```
*-- Name.....: UPPER.FMT
*-- Date.....: 10-22-91
*-- Version....: dBASE IV, Format 1.1
*-- Notes.....: Format files use "" as delimiters!
```

```
*-- Format file initialization code -----
```

```
*-- Some of these PRIVATE variables are created based on CodeGen and may not
*-- be used by your particular .fmt file
```

```
PRIVATE lc_talk, lc_cursor, lc_display, lc_status, lc_carry, lc_proc,;
      ln_typeahd, gc_cut
```

```
IF SET("TALK") = "ON"
```

```
  SET TALK OFF
```

```
  lc_talk = "ON"
```

```
ELSE
```

```
  lc_talk = "OFF"
```

```
ENDIF
```

```
lc_cursor = SET("CURSOR")
```

```
SET CURSOR ON
```

```
lc_status = SET("STATUS")
```

```
*-- SET STATUS was ON when you went into the Forms Designer.
```

```
IF lc_status = "OFF"
```

```
  SET STATUS ON
```

```
ENDIF
```

```
*-- Window for memo field Sexcrit.
```

```
DEFINE WINDOW wndow1 FROM 1,14 TO 20,65
```

```
*-- Window for memo field Agecrit.
```

```
DEFINE WINDOW wndow2 FROM 1,14 TO 20,65
```

```
*-- Window for memo field Burialtype.
```

```
DEFINE WINDOW wndow3 FROM 1,14 TO 20,65
```

```
*-- Window for memo field Chipping.
```

```
DEFINE WINDOW wndow4 FROM 1,14 TO 20,65
```

```
*-- Window for memo field Upabcess.
```

```
DEFINE WINDOW wndow5 FROM 1,14 TO 20,65
```

```
*-- Window for memo field Extrateeth.
```

```
DEFINE WINDOW wndow6 FROM 1,14 TO 20,65
```

```
*-- Window for memo field Perio.
```

```
DEFINE WINDOW wndow7 FROM 1,14 TO 20,65
```

```
*-- Window for memo field Culttreat.
```

```
DEFINE WINDOW wndow8 FROM 1,14 TO 20,65
```

```
*-- Window for memo field Comments.
```

```
DEFINE WINDOW wndow9 FROM 1,14 TO 20,65
```

```
*-- Window for memo field Newvariant.
```

```
DEFINE WINDOW wndow10 FROM 1,14 TO 20,65
```

```
*-- Window for memo field Othertreat.
```

```
DEFINE WINDOW wndow11 FROM 1,14 TO 20,65
```

```
*-- Window for memo field Lowabcess.
```

```
DEFINE WINDOW wndow12 FROM 1,14 TO 20,65
```

```
*-- Window for memo field Lowperio.
```

```
DEFINE WINDOW wndow13 FROM 1,14 TO 20,65
```

*-- Window for memo field Film.
DEFINE WINDOW wndow14 FROM 1,14 TO 20,65

*-- @ SAY GETS Processing. -----
on escape return to master
*-- Format Page: 1
@ 1,25 TO 3,46
@ 2,26 SAY "DATE SCORED"
@ 2,38 GET Date
@ 4,5 TO 6,19
@ 4,34 TO 6,70
@ 5,6 SAY "SEX " GET Sex PICT "@M ?,M,F"
@ 5,35 SAY "CRITERIA FOR DETERMINING SEX "
@ 5,66 GET Sexcrit WINDOW wndow1
@ 7,5 TO 9,22
@ 7,34 TO 9,70
@ 8,6 SAY "AGE"
@ 8,18 GET Age PICTURE "XXXX"
@ 8,35 SAY "CRITERIA FOR DETERMINING AGE"
@ 8,66 GET Agecrit WINDOW wndow2
@ 10,5 TO 12,28
@ 10,53 TO 12,70
@ 11,6 SAY "PERIOD"
@ 11,18 GET Period PICTURE "XXXXXXXXXX"
@ 11,54 SAY "BURIALTYPE"
@ 11,66 GET Burialtype WINDOW wndow3
READ

*-- Format Page: 2

@ 1,25 SAY "*****UPPER JAW*****"
@ 3,3 SAY "UPPER TORUS "
@ 3,16 GET Uppertorus PICTURE "@M =,NONE,TR,MOD,MARK";
ERROR "IS IT NONE, TRACE, MEDIUM OR MARKED?"
@ 3,26 SAY "CHIPPING"
@ 3,39 GET Chipping WINDOW wndow4
@ 3,49 SAY "ABCESSING ON UPPER JAW"
@ 3,73 GET Upabcess WINDOW wndow5
@ 5,3 SAY "CRIBRA ORB."
@ 5,16 GET Cribraorb PICTURE "XXXX"
@ 5,26 SAY "EXTRATEETH"
@ 5,39 GET Extrateeth WINDOW wndow6
@ 5,49 SAY "PERIODONTAL DISEASE"
@ 5,73 GET Perio WINDOW wndow7
@ 7,3 SAY "PORHYP"
@ 7,16 GET Porhyp PICTURE "XXXX"
@ 7,26 SAY "CRANIAL DEF."
@ 7,39 GET Crandef PICTURE "XXXX"
@ 7,49 SAY "CULTURAL TREATMENTS"
@ 7,73 GET Culttreat WINDOW wndow8
@ 9,3 SAY "COMMENTS"
@ 9,16 GET Comments WINDOW wndow9
@ 9,26 SAY "NEW VARIANTS"
@ 9,39 GET Newvariant WINDOW wndow10
@ 9,49 SAY "OTHER TREATMENTS "
@ 9,69 GET Othertreat WINDOW wndow11
READ

*-- Format Page: 3

@ 1,2 TO 7,77
 @ 1,28 SAY "STAUS AND WEAR"
 @ 2,7 SAY "I1R"
 @ 2,14 SAY "I1L"
 @ 2,21 SAY "I2R"
 @ 2,28 SAY "I2L"
 @ 2,35 SAY "CR"
 @ 2,42 SAY "CL"
 @ 2,49 SAY "P1R"
 @ 2,56 SAY "P1L"
 @ 2,63 SAY "P2R"
 @ 2,70 SAY "P2L"
 @ 3,7 GET Ui1rsw PICTURE "!!!!";
 VALID (TRIM (Ui1rsw) \$ " =APICU0-1-2-3-4") DEFAULT "="
 @ 3,14 GET Ui1lsw PICTURE "!!!!";
 VALID (TRIM (Ui1lsw) \$ " =APICU0-1-2-3-4") DEFAULT "="
 @ 3,21 GET Ui2rsw PICTURE "!!!!";
 VALID (TRIM (Ui2rsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 3,28 GET Ui2lsw PICTURE "!!!!";
 VALID (TRIM (Ui2lsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 3,35 GET Ucrsw PICTURE "!!!!";
 VALID (TRIM (Ucrsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 3,42 GET Uclsw PICTURE "!!!!";
 VALID (TRIM (Uclsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 3,49 GET Up1rsw PICTURE "!!!!";
 VALID (TRIM (Up1rsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 3,56 GET Up1lsw PICTURE "!!!!";
 VALID (TRIM (Up1lsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 3,63 GET Up2rsw PICTURE "!!!!";
 VALID (TRIM (Up2rsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 3,70 GET Up2lsw PICTURE "!!!!";
 VALID (TRIM (Up2lsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 5,19 SAY "M1R"
 @ 5,26 SAY "M1L"
 @ 5,33 SAY "M2R"
 @ 5,40 SAY "M2L"
 @ 5,47 SAY "M3R"
 @ 5,54 SAY "M3L"
 @ 6,19 GET Um1rsw PICTURE "!!!!";
 VALID (TRIM (Um1rsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 6,26 GET Um1lsw PICTURE "!!!!";
 VALID (TRIM (Um1lsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 6,33 GET Um2rsw PICTURE "!!!!";
 VALID (TRIM (Um2rsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 6,40 GET Um2lsw PICTURE "!!!!";
 VALID (TRIM (Um2lsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 6,47 GET Um3rsw PICTURE "!!!!";
 VALID (TRIM (Um3rsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 6,54 GET Um3lsw PICTURE "!!!!";
 VALID (TRIM (Um3lsw) \$ " =APICU0-1-2-3-4")DEFAULT "="
 @ 8,2 TO 14,77
 @ 8,33 SAY "CARIES"
 @ 9,7 SAY "I1R"
 @ 9,14 SAY "I1L"
 @ 9,21 SAY "I2R"
 @ 9,28 SAY "I2L"
 @ 9,35 SAY "CR"
 @ 9,42 SAY "CL"
 @ 9,49 SAY "P1R"

@ 9,56 SAY "P1L"
 @ 9,63 SAY "P2R"
 @ 9,70 SAY "P2L"
 @ 10,7 GET Ui1rcav PICTURE "!!!!"
 @ 10,14 GET Ui1lcav PICTURE "!!!!"
 @ 10,21 GET Ui2rcav PICTURE "!!!!"
 @ 10,28 GET Ui2lcav PICTURE "!!!!"
 @ 10,35 GET Ucrav PICTURE "!!!!"
 @ 10,42 GET Uclcav PICTURE "!!!!"
 @ 10,49 GET Up1rcav PICTURE "!!!!"
 @ 10,56 GET Up1lcav PICTURE "!!!!"
 @ 10,63 GET Up2rcav PICTURE "!!!!"
 @ 10,70 GET Up2lcav PICTURE "!!!!"
 @ 12,19 SAY "M1R"
 @ 12,26 SAY "M1L"
 @ 12,33 SAY "M2R"
 @ 12,40 SAY "M2L"
 @ 12,47 SAY "M3R"
 @ 12,54 SAY "M3L"
 @ 13,19 GET Um1rcav PICTURE "!!!!"
 @ 13,26 GET Um1lcav PICTURE "!!!!"
 @ 13,33 GET Um2rcav PICTURE "!!!!"
 @ 13,40 GET Um2lcav PICTURE "!!!!"
 @ 13,47 GET Um3rcav PICTURE "!!!!"
 @ 13,54 GET Um3lcav PICTURE "!!!!"
 READ

*-- Format Page: 4

@ 1,19 SAY "I1R"
 @ 1,25 SAY "I1L"
 @ 1,31 SAY "I2R"
 @ 1,37 SAY "I2L"
 @ 1,43 SAY "CR"
 @ 1,49 SAY "CL"
 @ 1,55 SAY "P1R"
 @ 1,61 SAY "P1L"
 @ 1,67 SAY "P2R"
 @ 1,73 SAY "P2L"
 @ 2,2 SAY "_____ "

@ 3,2 SAY "WINGING"
 @ 3,20 GET Ui1rwing PICTURE "X" VALID (Ui1rwing) \$ "=1234 "
 @ 3,26 GET Ui1lwing PICTURE "X" VALID (Ui1lwing) \$ "=1234 "
 @ 4,2 SAY "_____ "

@ 5,2 SAY "LABIAL CURVE"
 @ 5,20 GET Ui1rlabcur PICTURE "X" VALID (Ui1rlabcur) \$ "=01234 "
 @ 5,26 GET Ui1llabcur PICTURE "X" VALID (Ui1llabcur) \$ "=01234 "
 @ 6,2 SAY "_____ "

@ 7,2 SAY "SHOVELING"
 @ 7,20 GET Ui1rshovel PICTURE "X" VALID (Ui1rshovel) \$ "=0123456 "
 @ 7,26 GET Ui1lshovel PICTURE "X" VALID (Ui1lshovel) \$ "=0123456 "
 @ 7,32 GET Ui2rshovel PICTURE "X" VALID (Ui2rshovel) \$ "=01234567 "
 @ 7,38 GET Ui2lshovel PICTURE "X" VALID (Ui2lshovel) \$ "=01234567 "
 @ 7,44 GET Ucrshovel PICTURE "X" VALID (Ucrshovel) \$ "=0123456 "
 @ 7,50 GET Uclshovel PICTURE "X" VALID (Uclshovel) \$ "=0123456 "
 @ 8,2 SAY "_____ "

@ 9,2 SAY "DOUBLE SHOVELING" _____ "

@ 9,20 GET Ui1rdshove PICTURE "X" VALID (Ui1rdshove) \$"=012345 "
@ 9,26 GET Ui1ldshove PICTURE "X" VALID (Ui1ldshove) \$"=012345 "
@ 9,32 GET Ui2rdshove PICTURE "X" VALID (Ui2rdshove) \$"=012345 "
@ 9,38 GET Ui2ldshove PICTURE "X" VALID (Ui2ldshove) \$"=012345 "
@ 9,44 GET Ucrdshove PICTURE "X" VALID (Ucrdshove) \$"=012345 "
@ 9,50 GET Uclldshove PICTURE "X" VALID (Uclldshove) \$"=012345 "
@ 9,56 GET Up1rdshove PICTURE "X" VALID (Up1rdshove) \$"=012345 "
@ 9,62 GET Up1ldshove PICTURE "X" VALID (Up1ldshove) \$"=012345 "
@ 10,2 SAY "_____"

@ 11,2 SAY "INT. GROOVE"
@ 11,19 GET Ui1rintgro PICTURE "!!!" VALID (TRIM (Ui1rintgro)\$"=0MDMED ")
@ 11,25 GET Ui1lintgro PICTURE "!!!" VALID (TRIM (Ui1lintgro)\$"=0MDMED ")
@ 11,31 GET Ui2rintgro PICTURE "!!!" VALID (TRIM (Ui2rintgro)\$"=0MDMED ")
@ 11,37 GET Ui2lintgro PICTURE "!!!" VALID (TRIM (Ui2lintgro)\$"=0MDMED ")
@ 12,2 SAY "_____"

@ 13,2 SAY "T.DENT."
@ 13,20 GET Ui1rtdent PICTURE "X" VALID (Ui1rtdent)\$"=0123456 "
@ 13,26 GET Ui1ltdent PICTURE "X" VALID (Ui1ltdent)\$"=0123456 "
@ 13,32 GET Ui2rtdent PICTURE "X" VALID (Ui2rtdent)\$"=0123456 "
@ 13,38 GET Ui2ltdent PICTURE "X" VALID (Ui2ltdent)\$"=0123456 "
@ 13,44 GET Ucrtdent PICTURE "X" VALID (Ucrtdent)\$"=0123456 "
@ 13,50 GET Ucltdent PICTURE "X" VALID (Ucltdent)\$"=0123456 "
@ 14,2 SAY "_____"

READ

*- Format Page: 5

@ 1,2 SAY "_____"

@ 1,19 SAY "I1R"
@ 1,25 SAY "I1L"
@ 1,31 SAY "I2R"
@ 1,37 SAY "I2L"
@ 1,43 SAY "CR"
@ 1,49 SAY "CL"
@ 1,55 SAY "P1R"
@ 1,61 SAY "P1L"
@ 1,67 SAY "P2R"
@ 1,73 SAY "P2L"
@ 2,2 SAY "CANINE MESIAL RIDGE"
@ 2,44 GET Ucrmesridg PICTURE "X" VALID (Ucrmesridg) \$"=0123 "
@ 2,50 GET Uclmesridg PICTURE "X" VALID (Uclmesridg) \$"=0123 "
@ 3,2 SAY "_____"

@ 4,2 SAY "CANINE D.A.R."
@ 4,44 GET Ucrdar PICTURE "X" VALID (Ucrdar) \$ "012345=" "
@ 4,50 GET Ucldar PICTURE "X" VALID (Ucldar) \$ "012345=" "
@ 5,2 SAY "_____"

@ 6,2 SAY "PREMOLAR CUSPS"
@ 6,56 GET Up1rcusps PICTURE "X" VALID (Up1rcusps) \$ "01=" "
@ 6,62 GET Up1lcsusps PICTURE "X" VALID (Up1lcsusps) \$ "01=" "
@ 6,68 GET Up2rcusps PICTURE "X" VALID (Up2rcusps) \$ "01=" "
@ 6,74 GET Up2lcsusps PICTURE "X" VALID (Up2lcsusps) \$ "01=" "
@ 7,2 SAY "_____"

@ 8,2 SAY "UTO-AZTECAN PREMOLAR"
@ 8,56 GET UP1rutoazt PICTURE "X" VALID (UP1rutoazt) \$ "01=" "
@ 8,62 GET UP1lutoazt PICTURE "X" VALID (UP1lutoazt) \$ "01=" "

@ 9,2 SAY "

@ 10,2 TO 14,77
@ 10,31 SAY "ENAMAL EXTENSION"
@ 11,6 SAY "P1R"
@ 11,13 SAY "P1L"
@ 11,20 SAY "P2R"
@ 11,27 SAY "P2L"
@ 11,34 SAY "M1R"
@ 11,41 SAY "M1L"
@ 11,48 SAY "M2R"
@ 11,55 SAY "M2L"
@ 11,62 SAY "M3R"
@ 11,69 SAY "M3L"
@ 12,6 GET Up1renamx PICTURE "X" VALID (TRIM (Up1renamx) \$ "0123= ")
@ 12,13 GET Up1lenamx PICTURE "X" VALID (TRIM (Up1lenamx) \$ "0123= ")
@ 12,20 GET Up2renamx PICTURE "X" VALID (TRIM (Up2renamx) \$ "0123= ")
@ 12,27 GET Up2lenamx PICTURE "X" VALID (TRIM (Up2lenamx) \$ "0123= ")
@ 12,34 GET Um1renamx PICTURE "X" VALID (TRIM (Um1renamx) \$ "0123= ")
@ 12,41 GET Um1lenamx PICTURE "X" VALID (TRIM (Um1lenamx) \$ "0123= ")
@ 12,48 GET Um2renamx PICTURE "X" VALID (TRIM (Um2renamx) \$ "0123= ")
@ 12,55 GET Um2lenamx PICTURE "X" VALID (TRIM (Um2lenamx) \$ "0123= ")
@ 12,62 GET Um3renamx PICTURE "X" VALID (TRIM (Um3renamx) \$ "0123= ")
@ 12,69 GET Um3lenamx PICTURE "X" VALID (TRIM (Um3lenamx) \$ "0123= ")
READ

*- Format Page: 6

@ 1,2 TO 7,77
@ 1,33 SAY "ROOT NUMBER"
@ 2,7 SAY "I1R"
@ 2,14 SAY "I1L"
@ 2,21 SAY "I2R"
@ 2,28 SAY "I2L"
@ 2,35 SAY "CR"
@ 2,42 SAY "CL"
@ 2,49 SAY "P1R"
@ 2,56 SAY "P1L"
@ 2,63 SAY "P2R"
@ 2,70 SAY "P2L"
@ 3,8 GET Ui1rootno PICTURE "X" VALID (Ui1rootno) \$ "=123 "
@ 3,15 GET Ui1lrootno PICTURE "X" VALID (Ui1lrootno) \$ "=123 "
@ 3,22 GET Ui2rootno PICTURE "X" VALID (Ui2rootno) \$ "=123 "
@ 3,29 GET Ui2lrootno PICTURE "X" VALID (Ui2lrootno) \$ "=123 "
@ 3,36 GET Ucrrootno PICTURE "X" VALID (Ucrrootno) \$ "=123 "
@ 3,43 GET Uclrootno PICTURE "X" VALID (Uclrootno) \$ "=123 "
@ 3,50 GET Up1rootno PICTURE "X" VALID (Up1rootno) \$ "=123 "
@ 3,57 GET Up1lrootno PICTURE "X" VALID (Up1lrootno) \$ "=123 "
@ 3,64 GET Up2rootno PICTURE "X" VALID (Up2rootno) \$ "=123 "
@ 3,71 GET Up2lrootno PICTURE "X" VALID (Up2lrootno) \$ "=123 "
@ 5,19 SAY "M1R"
@ 5,26 SAY "M1L"
@ 5,33 SAY "M2R"
@ 5,40 SAY "M2L"
@ 5,47 SAY "M3R"
@ 5,54 SAY "M3L"
@ 6,20 GET Um1rootno PICTURE "X" VALID (Um1rootno) \$ "=1234 "
@ 6,27 GET Um1lrootno PICTURE "X" VALID (Um1lrootno) \$ "=1234 "
@ 6,34 GET Um2rootno PICTURE "X" VALID (Um2rootno) \$ "=1234 "
@ 6,41 GET Um2lrootno PICTURE "X" VALID (Um2lrootno) \$ "=1234 "
@ 6,48 GET Um3rootno PICTURE "X" VALID (Um3rootno) \$ "=1234 "
@ 6,55 GET Um3lrootno PICTURE "X" VALID (Um3lrootno) \$ "=1234 "

@ 8,2 TO 14,77
 @ 8,32 SAY "RADICAL NUMBER"
 @ 9,7 SAY "I1R"
 @ 9,14 SAY "I1L"
 @ 9,21 SAY "I2R"
 @ 9,28 SAY "I2L"
 @ 9,35 SAY "CR"
 @ 9,42 SAY "CL"
 @ 9,49 SAY "P1R"
 @ 9,56 SAY "P1L"
 @ 9,63 SAY "P2R"
 @ 9,70 SAY "P2L"
 @ 10,8 GET Ui1rradno PICTURE "X"
 @ 10,15 GET Ui1lradno PICTURE "X"
 @ 10,22 GET Ui2rradno PICTURE "X"
 @ 10,29 GET Ui2lradno PICTURE "X"
 @ 10,36 GET Ucrradno PICTURE "X"
 @ 10,43 GET Uclradno PICTURE "X"
 @ 10,50 GET Up1rradno PICTURE "X"
 @ 10,57 GET Up1lradno PICTURE "X"
 @ 10,64 GET Up2rradno PICTURE "X"
 @ 10,71 GET Up2lradno PICTURE "X"
 @ 12,19 SAY "M1R"
 @ 12,26 SAY "M1L"
 @ 12,33 SAY "M2R"
 @ 12,40 SAY "M2L"
 @ 12,47 SAY "M3R"
 @ 12,54 SAY "M3L"
 @ 13,20 GET Um1rradno PICTURE "X"
 @ 13,27 GET Um1lradno PICTURE "X"
 @ 13,34 GET Um2rradno PICTURE "X"
 @ 13,41 GET Um2lradno PICTURE "X"
 @ 13,48 GET Um3rradno PICTURE "X"
 @ 13,55 GET Um3lradno PICTURE "X"
 READ

*-- Format Page: 7

@ 1,32 SAY "M1R"
 @ 1,40 SAY "M1L"
 @ 1,48 SAY "M2R"
 @ 1,56 SAY "M2L"
 @ 1,64 SAY "M3R"
 @ 1,72 SAY "M3L"
 @ 2,2 SAY "_____
 @ 3,2 SAY "METACONE"
 @ 3,33 GET Um1rmetaco PICTURE "X" VALID (Um1rmetaco) \$ "=012345 "
 @ 3,41 GET Um1lmetaco PICTURE "X" VALID (Um1lmetaco) \$ "=012345 "
 @ 3,49 GET Um2rmetaco PICTURE "X" VALID (Um2rmetaco) \$ "=012345 "
 @ 3,57 GET Um2lmetaco PICTURE "X" VALID (Um2lmetaco) \$ "=012345 "
 @ 3,65 GET Um3rmetaco PICTURE "X" VALID (Um3rmetaco) \$ "=012345 "
 @ 3,73 GET Um3lmetaco PICTURE "X" VALID (Um3lmetaco) \$ "=012345 "
 @ 4,2 SAY "_____
 @ 5,2 SAY "HYPOCONE"
 @ 5,33 GET Um1rhypoco PICTURE "X" VALID (Um1rhypoco) \$ "=012345 "
 @ 5,41 GET Um1lhypoco PICTURE "X" VALID (Um1lhypoco) \$ "=012345 "
 @ 5,49 GET Um2rhypoco PICTURE "X" VALID (Um2rhypoco) \$ "=012345 "
 @ 5,57 GET Um2lhypoco PICTURE "X" VALID (Um2lhypoco) \$ "=012345 "
 @ 5,65 GET Um3rhypoco PICTURE "X" VALID (Um3rhypoco) \$ "=012345 "
 @ 5,73 GET Um3lhypoco PICTURE "X" VALID (Um3lhypoco) \$ "=012345 "
 @ 6,2 SAY "_____"

@ 7,2 SAY "CUSP 5"
 @ 7,33 GET Um1rcusp5 PICTURE "X" VALID (Um1rcusp5) \$ "=012345 "
 @ 7,41 GET Um1lcusp5 PICTURE "X" VALID (Um1lcusp5) \$ "=012345 "
 @ 7,49 GET Um2rcusp5 PICTURE "X" VALID (Um2rcusp5) \$ "=012345 "
 @ 7,57 GET Um2lcusp5 PICTURE "X" VALID (Um2lcusp5) \$ "=012345 "
 @ 7,65 GET Um3rcusp5 PICTURE "X" VALID (Um3rcusp5) \$ "=012345 "
 @ 7,73 GET Um3lcusp5 PICTURE "X" VALID (Um3lcusp5) \$ "=012345 "
 @ 8,2 SAY "_____
 @ 9,2 SAY "CARABELLI'S CUSP"
 @ 9,33 GET Um1rcarabl PICTURE "X" VALID (Um1rcarabl) \$ "=01234567 "
 @ 9,41 GET Um1lcarabl PICTURE "X" VALID (Um1lcarabl) \$ "=01234567 "
 @ 9,49 GET Um2rcarabl PICTURE "X" VALID (Um2rcarabl) \$ "=01234567 "
 @ 9,57 GET Um2lcarabl PICTURE "X" VALID (Um2lcarabl) \$ "=01234567 "
 @ 9,65 GET Um3rcarabl PICTURE "X" VALID (Um3rcarabl) \$ "=01234567 "
 @ 9,73 GET Um3lcarabl PICTURE "X" VALID (Um3lcarabl) \$ "=01234567 "
 @ 10,2 SAY "_____
 @ 11,2 SAY "PARASTYLE"
 @ 11,33 GET Um1rparast PICTURE "X" VALID (Um1rparast) \$ "=0123456 "
 @ 11,41 GET Um1lparast PICTURE "X" VALID (Um1lparast) \$ "=0123456 "
 @ 11,49 GET Um2rparast PICTURE "X" VALID (Um2rparast) \$ "=0123456 "
 @ 11,57 GET Um2lparast PICTURE "X" VALID (Um2lparast) \$ "=0123456 "
 @ 11,65 GET Um3rparast PICTURE "X" VALID (Um3rparast) \$ "=0123456 "
 @ 11,73 GET Um3lparast PICTURE "X" VALID (Um3lparast) \$ "=0123456 "
 @ 12,2 SAY "_____
 @ 13,2 SAY "PREMOLAR"
 @ 13,18 SAY "P1R"
 @ 13,26 SAY "P1L"
 @ 13,34 SAY "P2R"
 @ 13,42 SAY "P2L"
 @ 14,2 SAY "ODONTOMES"
 @ 14,19 GET Up1rodonto PICTURE "X" VALID (Up1rodonto) \$ "=01 "
 @ 14,27 GET Up1lodonto PICTURE "X" VALID (Up1lodonto) \$ "=01 "
 @ 14,35 GET Up2rodonto PICTURE "X" VALID (Up2rodonto) \$ "=01 "
 @ 14,43 GET Up2lodonto PICTURE "X" VALID (Up2lodonto) \$ "=01 "
 @ 15,2 SAY "

SAY

READ

*-- Format Page: 8
 @ 1,2 SAY "CONGENITAL ABSENCE"
 @ 1,22 SAY "I2R"
 @ 1,28 SAY "I2L"
 @ 1,35 SAY "P2R"
 @ 1,42 SAY "P2L"
 @ 1,49 SAY "M3R"
 @ 1,56 SAY "M3L"
 @ 2,23 GET Ui2rcongab PICTURE "X" VALID (Ui2rcongab) \$ "01= "
 @ 2,29 GET Ui2lcongab PICTURE "X" VALID (Ui2lcongab) \$ "01= "
 @ 2,36 GET Up2rcongab PICTURE "X" VALID (Up2rcongab) \$ "01= "
 @ 2,43 GET Up2lcongab PICTURE "X" VALID (Up2lcongab) \$ "01= "
 @ 2,50 GET Um3rcongab PICTURE "X" VALID (Um3rcongab) \$ "01= "
 @ 2,57 GET Um3lcongab PICTURE "X" VALID (Um3lcongab) \$ "01= "
 @ 3,2 SAY "_____
 @ 4,2 SAY "PEG/ REDUCED"
 @ 4,22 SAY "I2R"
 @ 4,28 SAY "I2L"
 @ 4,34 SAY "M3R"
 @ 4,40 SAY "M3L"
 @ 5,23 GET Ui2rpeg PICTURE "X" VALID (Ui2rpeg) \$ "=012 "
 @ 5,29 GET Ui2lpeg PICTURE "X" VALID (Ui2lpeg) \$ "=012 "

```

@ 5,35 GET Um3rreduce PICTURE "X" VALID (Um3rreduce) $ "=012 "
@ 5,41 GET Um3lreduce PICTURE "X" VALID (Um3lreduce) $ "=012 "
@ 6,2 SAY "-----"
@ 7,2 TO 13,77
@ 7,27 SAY "HYPOPLASIA"
@ 8,6 SAY "I1R"
@ 8,13 SAY "I1L"
@ 8,20 SAY "I2R"
@ 8,27 SAY "I2L"
@ 8,34 SAY "CR"
@ 8,41 SAY "CL"
@ 8,48 SAY "P1R"
@ 8,55 SAY "P1L"
@ 8,62 SAY "P2R"
@ 8,69 SAY "P2L"
@ 9,7 GET Ui1rhypopl PICTURE "X"
@ 9,14 GET Ui1lhypopl PICTURE "X"
@ 9,21 GET Ui2rhypopl PICTURE "X"
@ 9,28 GET Ui2lhypopl PICTURE "X"
@ 9,35 GET Ucrhypopl PICTURE "X"
@ 9,42 GET Uclhypopl PICTURE "X"
@ 9,49 GET Up1rhypopl PICTURE "X"
@ 9,56 GET Up1lhypopl PICTURE "X"
@ 9,63 GET Up2rhypopl PICTURE "X"
@ 9,70 GET Up2lhypopl PICTURE "X"
@ 11,20 SAY "M1R"
@ 11,27 SAY "M1L"
@ 11,34 SAY "M2R"
@ 11,41 SAY "M2L"
@ 11,48 SAY "M3R"
@ 11,55 SAY "M3L"
@ 12,21 GET Um1rhypopl PICTURE "X"
@ 12,28 GET Um1lhypopl PICTURE "X"
@ 12,35 GET Um2rhypopl PICTURE "X"
@ 12,42 GET Um2lhypopl PICTURE "X"
@ 12,49 GET Um3rhypopl PICTURE "X"
@ 12,56 GET Um3lhypopl PICTURE "X"
READ
*-- Format file exit code -----
*-- SET STATUS was ON when you went into the Forms Designer.
IF lc_status = "OFF" && Entered form with status off
  SET STATUS OFF && Turn STATUS "OFF" on the way out
ENDIF
SET CURSOR &lc_cursor.
SET TALK &lc_talk.
RELEASE
window1,window2,window3,window4,window5,window6,window7,window8,;
window9,window10,window11,window12,window13,window14
RELEASE lc_talk,lc_fields,lc_status
*-- EOP: LOWER.FMT

```

WINDOWS

6.6 APPENDIX VI FORMAT CODE FOR LOWER JAW DATA ENTRY

```
*****
*-- Name.....: LOWER.FMT
*-- Date.....: 10-22-91
*-- Version....: dBASE IV, Format 1.1
*-- Notes.....: Format files use "" as delimiters!
*****

*-- Format file initialization code -----

*-- Some of these PRIVATE variables are created based on CodeGen and may not
*-- be used by your particular .fmt file
PRIVATE lc_talk, lc_cursor, lc_display, lc_status, lc_carry, lc_proc,;
      ln_typeahd, gc_cut

IF SET("TALK") = "ON"
  SET TALK OFF
  lc_talk = "ON"
ELSE
  lc_talk = "OFF"
ENDIF
lc_cursor = SET("CURSOR")
SET CURSOR ON

lc_status = SET("STATUS")
*-- SET STATUS was ON when you went into the Forms Designer.
IF lc_status = "OFF"
  SET STATUS ON
ENDIF
*-- Window for memo field Lowabcess.
DEFINE WINDOW wndow1 FROM 1,14 TO 20,65
*-- Window for memo field Lowperio.
DEFINE WINDOW wndow2 FROM 1,14 TO 20,65
*-- Window for memo field Film.
DEFINE WINDOW wndow3 FROM 1,14 TO 20,65

*-- @ SAY GETS Processing. -----

*-- Format Page: 1
@ 0,25 SAY "*****LOWER JAW*****"
@ 2,4 SAY "LOWER TORUS"
@ 2,17 GET Lowtorus PICT "@M =,NONE, TR, MED, MARK"
@ 2,27 SAY "ROCKER JAW"
@ 2,39 GET Rocker PICTURE "@M =,NONE, NEAR, ROCK"
@ 2,49 SAY "ABCESSING LOWER JAW  "
@ 2,72 GET Lowabcess WINDOW wndow1
@ 4,11 SAY "LOWSHOVEL"
@ 4,23 GET Lowshovel PICTURE "X"
@ 4,47 SAY "PERIODONTAL DISEASE  "
@ 4,70 GET Lowperio WINDOW wndow2
@ 6,26 SAY "PHOTOS"
@ 6,38 GET Film WINDOW wndow3
@ 9,2 TO 15,77
@ 9,27 SAY "STATUS AND WEAR"
@ 10,6 SAY "I1L"
@ 10,13 SAY "I1R"
@ 10,20 SAY "I2L"
@ 10,27 SAY "I2R"
```

@ 10,34 SAY "CL"
 @ 10,41 SAY "CR"
 @ 10,48 SAY "P1L"
 @ 10,55 SAY "P1R"
 @ 10,62 SAY "P2L"
 @ 10,69 SAY "P2R"
 @ 11,6 GET Li1lsw PICTURE "!!!!" VALID (TRIM (Li1lsw) \$ " ACPIU0-1-2-3-4")
 @ 11,13 GET Li1rsw PICTURE "!!!!" VALID (TRIM (Li1rsw) \$ " ACPIU0-1-2-3-4")
 @ 11,20 GET Li2lsw PICTURE "!!!!" VALID (TRIM (Li2lsw) \$ " ACPIU0-1-2-3-4")
 @ 11,27 GET Li2rsw PICTURE "!!!!" VALID (TRIM (Li2rsw) \$ " ACPIU0-1-2-3-4")
 @ 11,34 GET Lclsw PICTURE "!!!!" VALID (TRIM (Lclsw) \$ " ACPIU0-1-2-3-4")
 @ 11,41 GET Lcrsw PICTURE "!!!!" VALID (TRIM (Lcrsw) \$ " ACPIU0-1-2-3-4")
 @ 11,48 GET Lp1lsw PICTURE "!!!!" VALID (TRIM (Lp1lsw) \$ " ACPIU0-1-2-3-4")
 @ 11,55 GET Lp1rsw PICTURE "!!!!" VALID (TRIM (Lp1rsw) \$ " ACPIU0-1-2-3-4")
 @ 11,62 GET Lp2lsw PICTURE "!!!!" VALID (TRIM (Lp2lsw) \$ " ACPIU0-1-2-3-4")
 @ 11,69 GET Lp2rsw PICTURE "!!!!" VALID (TRIM (Lp2rsw) \$ " ACPIU0-1-2-3-4")
 @ 13,19 SAY "M1L"
 @ 13,26 SAY "M1R"
 @ 13,33 SAY "M2L"
 @ 13,40 SAY "M2R"
 @ 13,47 SAY "M3L"
 @ 13,54 SAY "M3R"
 @ 14,19 GET Lm1lsw PICTURE "!!!!" VALID (TRIM (Lm1lsw) \$ " ACPIU0-1-2-3-4")
 @ 14,26 GET Lm1rsw PICTURE "!!!!" VALID (TRIM (Lm1rsw) \$ " ACPIU0-1-2-3-4")
 @ 14,33 GET Lm2lsw PICTURE "!!!!" VALID (TRIM (Lm2lsw) \$ " ACPIU0-1-2-3-4")
 @ 14,40 GET Lm2rsw PICTURE "!!!!" VALID (TRIM (Lm2rsw) \$ " ACPIU0-1-2-3-4")
 @ 14,47 GET Lm3lsw PICTURE "!!!!" VALID (TRIM (Lm3lsw) \$ " ACPIU0-1-2-3-4")
 @ 14,54 GET Lm3rsw PICTURE "!!!!" VALID (TRIM (Lm3rsw) \$ " ACPIU0-1-2-3-4")
 READ

*-- Format Page: 2

@ 1,2 TO 7,77
 @ 1,30 SAY "CARRIES"
 @ 2,6 SAY "I1L"
 @ 2,13 SAY "I1R"
 @ 2,20 SAY "I2L"
 @ 2,27 SAY "I2R"
 @ 2,34 SAY "CL"
 @ 2,41 SAY "CR"
 @ 2,48 SAY "P1L"
 @ 2,55 SAY "P1R"
 @ 2,62 SAY "P2L"
 @ 2,69 SAY "P2R"
 @ 3,6 GET Li1lcav PICTURE "!!!!"
 @ 3,13 GET Li1rcav PICTURE "!!!!"
 @ 3,20 GET Li2lcav PICTURE "!!!!"
 @ 3,27 GET Li2rcav PICTURE "!!!!"
 @ 3,34 GET Lclcav PICTURE "!!!!"
 @ 3,41 GET Lcrcav PICTURE "!!!!"
 @ 3,48 GET Lp1lcav PICTURE "!!!!"
 @ 3,55 GET Lp1rcav PICTURE "!!!!"
 @ 3,62 GET Lp2lcav PICTURE "!!!!"
 @ 3,69 GET Lp2rcav PICTURE "!!!!"
 @ 5,19 SAY "M1L"
 @ 5,26 SAY "M1R"
 @ 5,33 SAY "M2L"
 @ 5,40 SAY "M2R"
 @ 5,47 SAY "M3L"
 @ 5,54 SAY "M3R"

@ 6,19 GET Lm1lcav PICTURE "!!!!"
 @ 6,26 GET Lm1rcav PICTURE "!!!!"
 @ 6,33 GET Lm2lcav PICTURE "!!!!"
 @ 6,40 GET Lm2rcav PICTURE "!!!!"
 @ 6,47 GET Lm3lcav PICTURE "!!!!"
 @ 6,54 GET Lm3rcav PICTURE "!!!!"
 @ 9,2 TO 12,15
 @ 9,3 SAY "CANINE D.A.R"
 @ 9,16 TO 12,40
 @ 9,17 SAY "PREMOLAR LINGUAL CUSPS"
 @ 9,41 TO 12,53
 @ 9,42 SAY "TOME'S ROOT"
 @ 9,54 TO 12,77
 @ 9,61 SAY "ODONTOMES"
 @ 10,6 SAY "CL"
 @ 10,10 SAY "CR"
 @ 10,18 SAY "P1L"
 @ 10,25 SAY "P1R"
 @ 10,30 SAY "P2L"
 @ 10,36 SAY "P2R"
 @ 10,43 SAY "P1L"
 @ 10,49 SAY "P1R"
 @ 10,57 SAY "P1L"
 @ 10,62 SAY "P1R"
 @ 10,67 SAY "P2L"
 @ 10,72 SAY "P2R"
 @ 11,7 GET Lcldar PICTURE "X" VALID (Lcldar) \$ "012345 "
 @ 11,11 GET Lcrdar PICTURE "X" VALID (Lcrdar) \$ "012345 "
 @ 11,19 GET Lp1llcusps PICTURE "I" VALID (Lp1llcusps) \$ "A0123456789 "
 @ 11,25 GET Lp1rlcusps PICTURE "I" VALID (Lp1rlcusps) \$ "A0123456789 "
 @ 11,31 GET Lp2llcusps PICTURE "I" VALID (Lp2llcusps) \$ "A0123456789 "
 @ 11,37 GET Lp2rlcusps PICTURE "I" VALID (Lp2rlcusps) \$ "A0123456789 "
 @ 11,44 GET Lp1ltomesr PICTURE "X" VALID (Lp1ltomesro) \$ "012345 "
 @ 11,50 GET Lp1rtomesr PICTURE "X" VALID (Lp1rtomesro) \$ "012345 "
 @ 11,58 GET Lp1lodonto PICTURE "X" VALID (Lp1lodonto) \$ "01 "
 @ 11,63 GET Lp1rodonto PICTURE "X" VALID (Lp1rodonto) \$ "01 "
 @ 11,68 GET Lp2lodonto PICTURE "X" VALID (Lp2lodonto) \$ "01 "
 @ 11,73 GET Lp2rodonto PICTURE "X" VALID (Lp2rodonto) \$ "01 "

READ

*-- Format Page: 3

@ 1,32 SAY "M1L"
 @ 1,39 SAY "M1R"
 @ 1,46 SAY "M2L"
 @ 1,53 SAY "M2R"
 @ 1,60 SAY "M3L"
 @ 1,67 SAY "M3R"
 @ 2,2 SAY "_____
 @ 3,2 SAY "ANTERIOR FOVIA"
 @ 3,33 GET Lm1lantfov PICTURE "X" VALID (Lm1lantfov) \$ "01234 "
 @ 3,40 GET Lm1rantfov PICTURE "X" VALID (Lm1rantfov) \$ "01234 "
 @ 4,2 SAY "_____
 @ 5,2 SAY "GROOVE PATTERN"
 @ 5,33 GET Lm1lgroove PICTURE "I" VALID (Lm1lgroove) \$ "XY+ "
 @ 5,40 GET Lm1rgroove PICTURE "I" VALID (Lm1rgroove) \$ "XY+ "
 @ 5,47 GET Lm2lgroove PICTURE "I" VALID (Lm2lgroove) \$ "XY+ "
 @ 5,54 GET Lm2rgroove PICTURE "I" VALID (Lm2rgroove) \$ "XY+ "
 @ 5,61 GET Lm3lgroove PICTURE "I" VALID (Lm3lgroove) \$ "XY+ "

@ 5,68 GET Lm3rgroove PICTURE "I" VALID (Lm3rgroove) \$ "XY+ "
 @ 6,2 SAY "_____
 @ 7,2 SAY "CUSP NUMBER"
 @ 7,33 GET Lm1lucuspno PICTURE "X" VALID (Lm1lucuspno) \$ "3456 "
 @ 7,40 GET Lm1rcuspno PICTURE "X" VALID (Lm1rcuspno) \$ "3456 "
 @ 7,47 GET Lm2lucuspno PICTURE "X" VALID (Lm2lucuspno) \$ "3456 "
 @ 7,54 GET Lm2rcuspno PICTURE "X" VALID (Lm2rcuspno) \$ "3456 "
 @ 7,61 GET Lm3lucuspno PICTURE "X" VALID (Lm3lucuspno) \$ "3456 "
 @ 7,68 GET Lm3rcuspno PICTURE "X" VALID (Lm3rcuspno) \$ "3456 "
 @ 8,2 SAY "_____
 @ 9,2 SAY "DEFLECTING WRINKLE"
 @ 9,33 GET Lm1ldefwri PICTURE "X" VALID (Lm1ldefwri) \$ "0123 "
 @ 9,40 GET Lm1rdefwri PICTURE "X" VALID (Lm1rdefwri) \$ "0123 "
 @ 9,47 GET Lm2ldefwri PICTURE "X" VALID (Lm2ldefwri) \$ "0123 "
 @ 9,54 GET Lm2rdefwri PICTURE "X" VALID (Lm2rdefwri) \$ "0123 "
 @ 9,61 GET Lm3ldefwri PICTURE "X" VALID (Lm3ldefwri) \$ "0123 "
 @ 9,68 GET Lm3rdefwri PICTURE "X" VALID (Lm3rdefwri) \$ "0123 "
 @ 10,2 SAY "_____
 @ 11,2 SAY "DISTAL TRIGONID CREST"
 @ 11,33 GET Lm1ldtcre PICTURE "X" VALID (Lm1ldtcre) \$ "01 "
 @ 11,40 GET Lm1rdtcre PICTURE "X" VALID (Lm1rdtcre) \$ "01 "
 @ 11,47 GET Lm2ldtcre PICTURE "X" VALID (Lm2ldtcre) \$ "01 "
 @ 11,54 GET Lm2rdtcre PICTURE "X" VALID (Lm2rdtcre) \$ "01 "
 @ 11,61 GET Lm3ldtcre PICTURE "X" VALID (Lm3ldtcre) \$ "01 "
 @ 11,68 GET Lm3rdtcre PICTURE "X" VALID (Lm3rdtcre) \$ "01 "
 @ 12,2 SAY "_____
 _____"

@ 13,2 SAY "PROTOSTYLID"
 @ 13,33 GET Lm1lpstyld PICTURE "X" VALID (Lm1lpstyld) \$ "01234567 "
 @ 13,40 GET Lm1rpstyld PICTURE "X" VALID (Lm1rpstyld) \$ "01234567 "
 @ 13,47 GET Lm2lpstyld PICTURE "X" VALID (Lm2lpstyld) \$ "01234567 "
 @ 13,54 GET Lm2rpstyld PICTURE "X" VALID (Lm2rpstyld) \$ "01234567 "
 @ 13,61 GET Lm3lpstyld PICTURE "X" VALID (Lm3lpstyld) \$ "01234567 "
 @ 13,68 GET Lm3rpstyld PICTURE "X" VALID (Lm3rpstyld) \$ "01234567 "
 @ 14,2 SAY "_____
 READ

*-- Format Page: 4

@ 1,32 SAY "M1L"
 @ 1,39 SAY "M1R"
 @ 1,46 SAY "M2L"
 @ 1,53 SAY "M2R"
 @ 1,60 SAY "M3L"
 @ 1,67 SAY "M3R"
 @ 2,2 SAY "_____
 @ 3,2 SAY "CUSP 5"
 @ 3,33 GET Lm1lucusp5 PICTURE "X" VALID (Lm1lucusp5) \$ "012345 "
 @ 3,40 GET Lm1rcusp5 PICTURE "X" VALID (Lm1rcusp5) \$ "012345 "
 @ 3,47 GET Lm2lucusp5 PICTURE "X" VALID (Lm2lucusp5) \$ "012345 "
 @ 3,54 GET Lm2rcusp5 PICTURE "X" VALID (Lm2rcusp5) \$ "012345 "
 @ 3,61 GET Lm3lucusp5 PICTURE "X" VALID (Lm3lucusp5) \$ "012345 "
 @ 3,68 GET Lm3rcusp5 PICTURE "X" VALID (Lm3rcusp5) \$ "012345 "
 @ 4,2 SAY "_____
 @ 5,2 SAY "CUSP 6"
 @ 5,33 GET Lm1lucusp6 PICTURE "X" VALID (Lm1lucusp6) \$ "012345 "
 @ 5,40 GET Lm1rcusp6 PICTURE "X" VALID (Lm1rcusp6) \$ "012345 "
 @ 5,47 GET Lm2lucusp6 PICTURE "X" VALID (Lm2lucusp6) \$ "012345 "
 @ 5,54 GET Lm2rcusp6 PICTURE "X" VALID (Lm2rcusp6) \$ "012345 "

@ 5,61 GET Lm3lculp6 PICTURE "X" VALID (Lm3lculp6) \$ "012345 "
@ 5,68 GET Lm3rcusp6 PICTURE "X" VALID (Lm3rcusp6) \$ "012345 "
@ 6,2 SAY "_____"

@ 7,2 SAY "CUSP 7"
@ 7,33 GET Lm1lculp7 PICTURE "X" VALID (Lm1lculp7) \$ "0123456 "
@ 7,40 GET Lm1rcusp7 PICTURE "X" VALID (Lm1rcusp7) \$ "0123456 "
@ 7,47 GET Lm2lculp7 PICTURE "X" VALID (Lm2lculp7) \$ "0123456 "
@ 7,54 GET Lm2rcusp7 PICTURE "X" VALID (Lm2rcusp7) \$ "0123456 "
@ 7,61 GET Lm3lculp7 PICTURE "X" VALID (Lm3lculp7) \$ "0123456 "
@ 7,68 GET Lm3rcusp7 PICTURE "X" VALID (Lm3rcusp7) \$ "0123456 "
@ 8,2 SAY "_____"
@ 10,2 TO 13,77
@ 10,31 SAY "ENAMAL EXTENSION"
@ 11,7 SAY "P1L"
@ 11,14 SAY "P1R"
@ 11,20 SAY "P2L"
@ 11,27 SAY "P2R"
@ 11,34 SAY "M1L"
@ 11,41 SAY "M1R"
@ 11,48 SAY "M2L"
@ 11,54 SAY "M2R"
@ 11,61 SAY "M3L"
@ 11,68 SAY "M3R"
@ 12,8 GET Lp1lenamx PICTURE "X"
@ 12,15 GET Lp1renamx PICTURE "X"
@ 12,21 GET Lp2lenamx PICTURE "X"
@ 12,28 GET Lp2renamx PICTURE "X"
@ 12,35 GET Lm1lenamx PICTURE "X"
@ 12,42 GET Lm1renamx PICTURE "X"
@ 12,49 GET Lm2lenamx PICTURE "X"
@ 12,55 GET Lm2renamx PICTURE "X"
@ 12,62 GET Lm3lenamx PICTURE "X"
@ 12,69 GET Lm3renamx PICTURE "X"
READ

*-- Format Page: 5

@ 1,2 TO 7,77
@ 1,28 SAY "ROOT NUMBER"
@ 2,7 SAY "I1L"
@ 2,14 SAY "I1R"
@ 2,21 SAY "I2L"
@ 2,28 SAY "I2R"
@ 2,35 SAY "CL"
@ 2,42 SAY "CR"
@ 2,49 SAY "P1L"
@ 2,56 SAY "P1R"
@ 2,63 SAY "P2L"
@ 2,70 SAY "P2R"
@ 3,8 GET Li1rootno PICTURE "X" VALID (Li1rootno) \$ "12 "
@ 3,15 GET Li1rootno PICTURE "X" VALID (Li1rootno) \$ "12 "
@ 3,22 GET Li2rootno PICTURE "X" VALID (Li2rootno) \$ "12 "
@ 3,29 GET Li2rootno PICTURE "X" VALID (Li2rootno) \$ "12 "
@ 3,36 GET Lclrootno PICTURE "X" VALID (Lclrootno) \$ "12 "
@ 3,43 GET Lcrrootno PICTURE "X" VALID (Lcrrootno) \$ "12 "
@ 3,50 GET Lp1rootno PICTURE "X" VALID (Lp1rootno) \$ "123 "
@ 3,57 GET Lp1rootno PICTURE "X" VALID (Lp1rootno) \$ "123 "
@ 3,64 GET Lp2rootno PICTURE "X" VALID (Lp2rootno) \$ "123 "
@ 3,71 GET Lp2rootno PICTURE "X" VALID (Lp2rootno) \$ "123 "

@ 5,17 SAY "M1L"
 @ 5,24 SAY "M1R"
 @ 5,31 SAY "M2L"
 @ 5,38 SAY "M2R"
 @ 5,45 SAY "M3L"
 @ 5,52 SAY "M3R"
 @ 6,18 GET Lm1lrootno PICTURE "X" VALID (Lm1lrootno) \$ "1234 "
 @ 6,25 GET Lm1rrootno PICTURE "X" VALID (Lm1rrootno) \$ "1234 "
 @ 6,32 GET Lm2lrootno PICTURE "X" VALID (Lm2lrootno) \$ "1234 "
 @ 6,39 GET Lm2rrootno PICTURE "X" VALID (Lm2rrootno) \$ "1234 "
 @ 6,46 GET Lm3lrootno PICTURE "X" VALID (Lm3lrootno) \$ "1234 "
 @ 6,53 GET Lm3rrootno PICTURE "X" VALID (Lm3rrootno) \$ "1234 "
 @ 8,2 TO 14,77
 @ 8,27 SAY "RADICAL NUMBER"
 @ 9,7 SAY "I1L"
 @ 9,14 SAY "I1R"
 @ 9,21 SAY "I2L"
 @ 9,28 SAY "I2R"
 @ 9,35 SAY "CL"
 @ 9,42 SAY "CR"
 @ 9,49 SAY "P1L"
 @ 9,56 SAY "P1R"
 @ 9,63 SAY "P2L"
 @ 9,70 SAY "P2R"
 @ 10,8 GET Li1lradno PICTURE "X" VALID (Li1lradno) \$ "12345678 "
 @ 10,15 GET Li1rradno PICTURE "X" VALID (Li1rradno) \$ "12345678 "
 @ 10,22 GET Li2lradno PICTURE "X" VALID (Li2lradno) \$ "12345678 "
 @ 10,29 GET Li2rradno PICTURE "X" VALID (Li2rradno) \$ "12345678 "
 @ 10,36 GET Lclradno PICTURE "X" VALID (Lclradno) \$ "12345678 "
 @ 10,43 GET Lcrradno PICTURE "X" VALID (Lcrradno) \$ "12345678 "
 @ 10,50 GET Lp1lradno PICTURE "X" VALID (Lp1lradno) \$ "12345678 "
 @ 10,57 GET Lp1rradno PICTURE "X" VALID (Lp1rradno) \$ "12345678 "
 @ 10,64 GET Lp2lradno PICTURE "X" VALID (Lp2lradno) \$ "12345678 "
 @ 10,71 GET Lp2rradno PICTURE "X" VALID (Lp2rradno) \$ "12345678 "
 @ 12,17 SAY "M1L"
 @ 12,24 SAY "M1R"
 @ 12,31 SAY "M2L"
 @ 12,38 SAY "M2R"
 @ 12,45 SAY "M3L"
 @ 12,52 SAY "M3R"
 @ 13,18 GET Lm1lradno PICTURE "X" VALID (Lm1lradno) \$ "12345678 "
 @ 13,25 GET Lm1rradno PICTURE "X" VALID (Lm1rradno) \$ "12345678 "
 @ 13,32 GET Lm2lradno PICTURE "X" VALID (Lm2lradno) \$ "12345678 "
 @ 13,39 GET Lm2rradno PICTURE "X" VALID (Lm2rradno) \$ "12345678 "
 @ 13,46 GET Lm3lradno PICTURE "X" VALID (Lm3lradno) \$ "12345678 "
 @ 13,53 GET Lm3rradno PICTURE "X" VALID (Lm3rradno) \$ "12345678 "

READ

*-- Format Page: 6

@ 1,2 TO 4,44
 @ 1,14 SAY "CONGENITAL ABSENCE"
 @ 1,46 TO 4,68
 @ 1,49 SAY "TORSO-MOLAR ANGLE"
 @ 2,4 SAY "I1L"
 @ 2,11 SAY "I1R"
 @ 2,18 SAY "P2L"
 @ 2,25 SAY "P2R"
 @ 2,32 SAY "M3L"

```

@ 2,39 SAY "M3R"
@ 2,52 SAY "M3L"
@ 2,60 SAY "M3R"
@ 3,5 GET Li1lcongab PICTURE "X" VALID (Li1lcongab) $ "01 "
@ 3,12 GET Li1rcongab PICTURE "X" VALID (Li1rcongab) $ "01 "
@ 3,19 GET Lp2lcongab PICTURE "X" VALID (Lp2lcongab) $ "01 "
@ 3,26 GET Lp2rcongab PICTURE "X" VALID (Lp2rcongab) $ "01 "
@ 3,33 GET Lm3lcongab PICTURE "X" VALID (Lm3lcongab) $ "01 "
@ 3,40 GET Lm3rcongab PICTURE "X" VALID (Lm3rcongab) $ "01 "
@ 3,53 GET Lm3lt_mang PICTURE "X"
@ 3,61 GET Lm3rt_mang PICTURE "X"
@ 6,2 TO 12,77
@ 6,29 SAY "HYPOPLASIA"
@ 7,7 SAY "I1L"
@ 7,14 SAY "I1R"
@ 7,21 SAY "I2L"
@ 7,28 SAY "I2R"
@ 7,35 SAY "CL"
@ 7,42 SAY "CR"
@ 7,49 SAY "P1L"
@ 7,56 SAY "P1R"
@ 7,63 SAY "P2L"
@ 7,70 SAY "P2R"
@ 8,7 GET Li1lhypopl PICTURE "XXX"
@ 8,14 GET Li1rhypopl PICTURE "XXX"
@ 8,21 GET Li2lhypopl PICTURE "XXX"
@ 8,28 GET Li2rhypopl PICTURE "XXX"
@ 8,35 GET Lclhypopl PICTURE "XXX"
@ 8,42 GET Lcrhypopl PICTURE "XXX"
@ 8,49 GET Lp1lhypopl PICTURE "XXX"
@ 8,56 GET Lp1rhypopl PICTURE "XXX"
@ 8,63 GET Lp2lhypopl PICTURE "XXX"
@ 8,70 GET Lp2rhypopl PICTURE "XXX"
@ 10,18 SAY "M1L"
@ 10,25 SAY "M1R"
@ 10,32 SAY "M2L"
@ 10,39 SAY "M2R"
@ 10,46 SAY "M3L"
@ 10,53 SAY "M3R"
@ 11,18 GET Lm1lhypopl PICTURE "XXX"
@ 11,25 GET Lm1rhypopl PICTURE "XXX"
@ 11,32 GET Lm2lhypopl PICTURE "XXX"
@ 11,39 GET Lm2rhypopl PICTURE "XXX"
@ 11,46 GET Lm3lhypopl PICTURE "XXX"
@ 11,53 GET Lm3rhypopl PICTURE "XXX"
READ

```

*-- Format file exit code -----

```

*-- SET STATUS was ON when you went into the Forms Designer.
IF lc_status = "OFF" && Entered form with status off
  SET STATUS OFF && Turn STATUS "OFF" on the way out
ENDIF
SET CURSOR &lc_cursor.
SET TALK &lc_talk.

```

RELEASE WINDOWS wndow1,wndow2,wndow3

RELEASE lc_talk,lc_fields,lc_status

*--

EOP:

LOWER.FMT

6.7 APPENDIX VII PROCEDURE FOR INDIVIDUAL COUNT

```
*PROCEDURE INDVCOUN
PARAMETERS FNAME,UPPERA,LOWERA
result=fname+"res"
close all
use &UPPERA in 1
use &LOWERA in 2
use &RESULT in 3
use tothabb in 4
use nameabbr in 5
clear
*set dele on
*sele 1
*delete for recno(>)>70
*sele 2
*delete for recno(>)>70
mstring= " "
sele 5
go top
sele 4
go top
mfield=5
mtooth=1
muplow=1
mside=1
mfieldname=" "
mcounter=1
mloop=1
mzippo=1
*in_d=fcreate("DATA.DAT","rw")
*****poss fields=37*****

do while muplow<=2

    if muplow=1 && Select the upper or lower jaw files
        mupdo="U"
    else
        mupdo="L"
    endif

    do while mtooth<=8 && Select the tooth to be scanned
        if mside=1 && Get the right or left tooth scores
            moside="R"
            MOPSIDE="L"
        else
            moside="L"
            MOPSIDE="R"
        endif

        do case
        case mtooth=1
            mid="I1"
        case mtooth =2
            mid="I2"
        case mtooth=3
            mid="C"
        case mtooth=4
            mid="P1"
        case mtooth=5
            mid="P2"
        case mtooth=6
            mid="M1"
```

```

        case mtooth=7
            mid="M2"
        case mtooth=8
            mid="M3"
        endcase

    sele 4
        mget=mupdo+mid
        locate for abbreviati=mget
        mfieldname=field(mfield)

    MTIT=MUPDO+MID+TRIM(MFIELDNAME)
    MORIGST=mupdo+mid+moside+trim(mfieldname)
    MOPPSTR=MUPDO+MID+MOPSIDE+TRIM(MFIELDNAME)
    store &mfieldname to mtrue
        if mtrue=.T. .AND. TRIM(MFIELDNAME)<>"INTGRO" .AND.
    TRIM(MFIELDNAME)<>"GROOVE"

    sele 5
        locate for abbrev="&mfieldname" && Find out if the trait matches the tooth
        if .not. found()
            @ 10,2 say mfieldname
            @ 11,2 say mstring
            wait
            endif
        store poss_score to Sscore
        MSCORE=VAL(SSCORE)+1
        MSCORE=STR(MSCORE)

        if muplow=1 .AND. TRIM(MFIELDNAME)<>"INTGRO" && Choose the right
    database for upper or lower jaw
            sele 1
        else
            muplow=2
            sele 2
        endif
        do countem with MTIT,MOPPSTR,MORIGST, mscore && The sub-routine for doing
    the actual count

            if mcounter=2
                sele 4
                if mloop>16
                    go top
                    mtooth=1
                else
                    skip
                endif
            endif
        else
            if mloop=>16
                mtooth=1
                go top
            else
                @ 20,5 say "NOT FOUND"
            endif
        endif
    endif

    *mside=2
    mcounter=mcounter+1
    mloop=mloop+2
        if mloop>16
            mtooth=0
            mloop=1
            mfield=mfield+1
        endif
            if mcounter>1

```

```

        mtooth=mtooth+1
        mside=1
        mcounter=1
        endif
        sele 3
        mfinal=0
        store recno() to mfinal
        if mfinal=68 .and. mzippo=1
            muplow=muplow+1
            mupdo="L"
            mfield=5
            mzippo=mzippo+1
        endif
        if mfinal=133
            mloop=18
            mtooth=15
        endif
    CLEAR
    enddo
    muplow=3
enddo
close all
release all
procedure countem
parameter MTIT,MOPPSTR,MORIGST, mscore
matooth=" "

```

set talk off

MSPACE=" "

STORE 0 TO MSPACE,M0,M1,M2,M3,M4,M5,M6,M7,M8,M9

SET EXACT ON

*calc min((&MORIGST)) for (&MORIGST)=>0 to Mmin

*calc max((&MORIGST)) to MMAX

*calc std((&MORIGST)) to mstd

go top

DO WHILE .NOT. EOF()

IF (&MORIGST)=>0 .OR.(&MOPPSTR)=>0

DO CASE

CASE (&MORIGST)> (&MOPPSTR)

MSTRING=(&MORIGST)

CASE (&MOPPSTR)>(&MORIGST)

MSTRING=(&MOPPSTR)

CASE (&MOPPSTR)=(&MORIGST)

IF (&MORIGST)>0

MSTRING=(&MORIGST)

ELSE

MSTRING=(&MOPPSTR)

ENDIF

ENDCASE

DO CASE

CASE mstring=0.01

M0=M0+1

CASE MSTRING=1

M1=M1+1

CASE MSTRING=2

M2=M2+1

CASE MSTRING=3

M3=M3+1

CASE MSTRING= 4

M4=M4+1

CASE MSTRING=5

M5=M5+1

CASE MSTRING=6

M6=M6+1

```

CASE MSTRING= 7
    M7=M7+1
CASE MSTRING= 8
    M8=M8+1
CASE MSTRING=9
    M9=M9+1
otherwise
    MSPACE=MSPACE+1
ENDCASE
ENDIF
fn=filename
    **ln_c=fwrite(ln_d, fn+" "+ mstring+", "+CHR(10)+chr(13))
SKIP
@ 3,1 SAY mTIT
@ 4,1 SAY "MISSING " + STR(MSPACE)
@ 5,1 SAY "0 " + str(M0)
@ 6,1 SAY "1 " + str(M1)
if val(mscore)=>4
@ 7,1 SAY "2 " + str(M2)
else
m2=0
endif
if val(mscore)=>5
@ 8,1 SAY "3 " + str(M3)
else
m3=0
endif
if val(mscore)=>6
@ 9,1 SAY "4 " + str(M4)
else
m4=0
endif
if val(mscore)=>7
@ 10,1 SAY "5 " + str(m5)
else
m5=0
endif
if val(mscore)=>8
@ 11,1 SAY "6 " + str(m6)
else
m6=0
endif
if val(mscore)=>9
@ 12,1 SAY "7 " + str(m7)
else
m7=0
endif
if val(mscore)=>10
@ 13,1 SAY "8 " + str(m8)
else
m8=0
endif
if val(mscore)=>11
@ 14,1 SAY "9 " + str(m9)
else
m9=0
endif
MTOT=MSPACE+M0+M1+M2+M3+M4+M5+M6+M7+M8+M9
@ 15,1 SAY "TOTAL" +STR(MTOT)
ENDDO
MVALID=M0+M1+m2+m3+M4+m5+m6+m7+m8+m9
VALPC=(MVALID/MTOT)*100
    two=m2*2
    three=m3*3
    four=m4*4
    five=m5*5
    six=m6*6

```



```
seven=m7*7
eight=m8*8
nine=m9*9
mmean=(m0+m1+two+three+four+five+six+seven+eight+nine)/mvalid
set status on
sele 3
```

```
APPEND BLANK
replace string with MTIT
REPLACE TOTAL WITH MVALID
REPLACE VALID_PC WITH VALPC
REPLACE MISSING WITH MSPACE
REPLACE d0 WITH M0
REPLACE d1 WITH m1
if val(mscore)=>4
REPLACE d2 WITH m2
endif
if val(mscore)=>5
REPLACE d3 WITH m3
endif
if val(mscore)=>6
REPLACE d4 WITH m4
endif
if val(mscore)=>7
REPLACE d5 WITH m5
endif
if val(mScore)=>8
REPLACE d6 WITH m6
endif
if val(mscore)=>9
REPLACE d7 WITH m7
endif
if val(mscore)=>10
REPLACE d8 WITH m8
endif
if val(mscore)=>11
REPLACE d9 WITH m9
ENDIF
replace poss_score with val(mscore)
*replace min with mmin
*replace max with mmax
*replace mean with mmean
*replace stddev with mstd
return
```

6.8 APPENDIX VIII CODE FOR MMD PROGRAM

```
*****
* PROGRAM: MMD.PRG
* This program asks the user several questions about which sites and traits
* are to be used for calculating MMDs and then does the MMD calculations
*****

DEFINE WINDOW GETINFO FROM 4,10 TO 18,60 panel COLOR +gr/g, r/w,n/g
close all
clear
set talk off
*set dbtrap off
store 0 to sites,traits,number,recnum
store " " to reply, MSITe, MDIR, MABBREV, MDRIVE, combscore1, combscore2, mtot2
YUP="Y"
siteno=1
mtooth=Space(20)
matooth=" "
mtrait=space(30)
matrait=" "
mside=" "
mscore=" "
traitloop=3
BP=0
outname=" "
seleloop=1
seletrait=1
s=4
define popup toothpop from 8,5 prompt field tooth_type
define popup traitpop from 8,45 prompt field trait
define popup sitepop from 5,5 prompt field site

@ 10,10 say "How many sites would you like?" get sites picture "99"
@ 12,10 say "How many traits would you like to do?" get traits picture "99"
@ 15,10 say "What name would you like to give to the output file?" get outname picture "!!!!!!!"
read
DATNAME=LTRIM(rtrim(OUTNAME))+".DAT"
totsites=sites+2
tottrait=(traits+1)*2
public array namer [totsites,tottrait]
store sites to namer [1,1]
store traits to namer [1,2]
clear
do while yup="Y"

use tothabb in 1
use nameabbr in 2
use sites in 3
    do while seleloop<=sites
        on selection popup sitepop do getsites with reply,number,recnum
            sele 3
            set order to tag site
            activate popup sitepop
            seleloop=seleloop+1
        enddo

        s=s+1
        malias=str(s)
        sele &malias
        use list &&the dbase file to keep track of traits
        sele list
        zap
        s=s+1
        malias=str(s)
        sele &malias
        use mmd && the file the holds the mmd calculations
```

```
enddo
do seletrait
```

```
*****
```

```
procedure seletrait
```

```
*****
```

```
    on selection popup toothpop do tonameproc with mtooth, matooth
do while seletrait<=traits
    sele 1
    activate popup toothpop
    do scan
enddo
do mmdcalc
return
```

```
*****
```

```
procedure getsites && for identifying and storing the site name
```

```
*****
```

```
parameter reply,number,recnum
```

```
    store prompt() to reply
    store bar() to number
    store recno() to recnum
```

```
    SEEK reply
    if found()
    STORE site TO msite
    STORE abbrev TO MABBREV
    STORE drive TO MDRIVE
    STORE Direct TO MDIR
```

```
    ACTIVATE WINDOW GETINFO
```

```
    @ 0,5 SAY "Current Site"
    @ 2,2 SAY "Site Name: " GET msite &&PICTURE "!!!!!!!!!!!!!!!!!!!!!!!!!!!!";
    MESSAGE "The unique name by which this site is known"
    @ 4,2 SAY "Abbreviation: " GET mAbbrev &&PICTURE "!!!!!!";
    Message "A unique 5 letter abbreviation to identify the files for the site"
    @ 6,2 SAY "Drive: " GET mdrive && PICTURE "!" ;
    MESSAGE "The letter of the drive on which these files will be stored"
    @ 8,2 SAY "Directory: " GET mdir && PICTURE "!!!!!!!!";
    MESSAGE "The name of the directory for these files"
    CLEAR GETS
    yup="Y"
    @ 10,2 SAY "Is This the Site you want to use?" GET YUP PICT "@M Y,N"
    READ
```

```
        if YUP="Y"
            mresfile=rtrim(mabbrev)+"res"
            res=MDRIVE+ ":\"+RTRIM(MDIR)+"\"+RTRIM(mresfile)
            DEACTIVATE WINDOW GETINFO
            siteno=siteno+1
```

```
        if yup="Y"
            malias=str(s)    && variable for the work areas
            sele &malias    && sets the work area to next in line
            use &res && opens the most recently requested
                *&& site in the new work area
            s=s+1
            sele 3
        else
            return
        endif
```

```
    @ 18,10 say "ADD ANOTHER SITE?"
```

```
    @ 19,12 get yup picture "!"
```

```
    read
```

```
        DEACTIVATE WINDOW OKAY
```

```
deactivate popup
ENDIF
ENDIF
```

```
*****
PROCEDURE SCAN && to get the right traits and the right teeth
*****

clear
*do while seletrait<=traits
@ 2,5 say "Which tooth?"
select 1
@ 2,19 SAY MTOOTH

@ 4,5 say "Which trait?"
select 2
SET ORDER TO TAG TRAIT
on selection popup traitpop do tnameproc WITH MTRAIT,MATRAIT,mscore
activate popup traitpop
@ 4,19 SAY MTRAIT
mstring=trim(matooth)+trim(matrait)
select 1
set filter to tooth_type=mtooth
if &matrait=.t.
set filter to
@ 20,10 SAY "What breakpoint would you like to use for this triat?" get bp picture "9"

read

sele list
append blank
replace site_trait with mstring
replace breakpoint with bp
store mstring to namer[1,traitloop]
store bp to namer[totsites,traitloop]
traitloop=traitloop+2
bp=0
else
@ 7,7 say "That trait is not found on that Tooth"
wait
endif
@ 7,7 clear to 7,76
@ 7,7 say "Would you like to add another Trait?"
@ 8,10 get yup picture "I"
read
seletrait=seletrait+1
*enddo
return
*****

procedure tnameproc && for identifying and storing the tooth name
*****

parameter mtooth,matooth,MTRAIT, MATRAIT, mscore
GO TOP
store prompt() to mtooth
locate for tooth_type="&mtooth"
store abbreviati to matooth
DEACTIVATE POPUP

*****

procedure tnameproc && for identifying and storing the trait name
*****

parameter MTRAIT, MATRAIT, mscore
store prompt() to mtrait
locate for trait="&mtrait"
store abbrev to matrait
```

```
store poss_score to mscore
deactivate popup
deactivate popup
```

```
*****
```

```
procedure mmdcalc
```

```
*****
```

```
sele list
go top
s=s+1
t=s
smmd=s+1
Inc=fcreate("MMDS.DAT", "RW")
DECLARE THETAS[sites,traits]
DECLARE NS[sites,traits]
*SITE=""
S=1
R=traits
DO WHILE S<=sites
malias=str(s+3)
*s=s+1
sele &malias
msitenm=dbf()
sele sites
go top
lsite="D:"+trim(abbrev)+"RES.DBF"
do while msitenm<>lsite
*locate for lsite=msitenm
skip
lsite="D:"+trim(abbrev)+"RES.DBF"
enddo
store abbrev to msite

SELE mmd
APPEND BLANK
REPLACE SITE_TRAIT WITH mSITE
LNH=FWRITE(LNC,mSITE+" ")
SELE list
GO TOP
R1=1
DO WHILE .NOT.EOF()
STORE SITE_TRAIT TO FI
STORE BREAKPOINT TO BP
*SI=STR(S)
*SELE &SI
sele &malias
LOCATE FOR TRIM(STRING) = TRIM(FI)
DO CASE
CASE BP=0
DK=D1+D2+D3+D4+D5+D6+D7+D8+D9
CASE BP=1
DK=D2+D3+D4+D5+D6+D7+D8+D9
CASE BP=2
DK=D3+D4+D5+D6+D7+D8+D9
CASE BP=3
DK=D4+D5+D6+D7+D8+D9
CASE BP=4
DK=D5+D6+D7+D8+D9
CASE BP=5
DK=D6+D7+D8+D9
CASE BP=6
DK=D7+D8+D9
CASE BP=7
DK=D8+D9
ENDCASE
STORE TOTAL TO DN
```

```

THE=.5*(ASIN(1-((2*DK)/(DN+1))))+.5*(ASIN(1-(2*(DK+1))/(DN+1)))
THETAS[S,R1]=THE
NS[S,R1]=DN
SELE mmd
APPEND BLANK
REPLACE SITE_TRAIT WITH FI
REPLACE N WITH DN
REPLACE K WITH DK
REPLACE THETA WITH THE
REPLACE BREAKPOINT WITH BP
SELE list
R1=R1+1
SKIP
ENDDO
S=S+1
ENDDO
LNH=FWRITE(LNC, CHR(10)+CHR(13))
DECLARE MMDS[sites,sites]
declare sigs[sites,sites]
declare stdmmd[sites,sites]
R1=1
DO WHILE R1<sites
R2=R1+1
    DO WHILE R2<=sites
        C=1
        MD=0
        vr=0
        DO WHILE C<=r
            M1=THETAS[R1,C]-THETAS[R2,C]
            M1=M1**2
            *LNH=FWRITE(LNC,STR(m1,18,16)+chr(10)+chr(13))
            M2=1/(NS[R1,C]+.5)
            M3=1/(NS[R2,C]+.5)
            M4=M2+M3
            MM=M1-M4
            MD=MD+MM
            vr=vr+((M2+M3)**2)

            store 0 to m1,m2,m3,m4,mm

            C=C+1
        ENDDO
        MF=MD/R
        var=(2/(R)**2)*vr
        sig=(sqrt(var))
        IF 2*SIG<(MF)
            STAR=""
        ELSE
            STAR=""
        ENDIF
        MMDS[R1,R2]=MF
        MMDS[R2,R1]=MF
        MMDS[R1,R1]=0
        sigs[R1,R2]=sig
        sigs[R2,R1]=sig
        sigs[R1,R1]=0
        stdmmd[r1,r2]=mf/sig
        stdmmd[r2,r1]=mf/sig
        stdmmd[r1,r1]=0
        R2=R2+1
    ENDDO
    LNHF=FWRITE(LNC,"RAW: "+STR(MF,10,6)+star+" SD: "+STR(SIG,10,6)+CHR(10)+CHR(13))
    ENDDO
    R1=R1+1
    MMDS[sites,sites]=0
    stdmmd[sites,sites]=0
    ENDDO
A=1

```

```
DO WHILE A<=sites
B=1
DO WHILE B<=sites
LNH=FWRITE(LNC,STR(stdmmd[A,B],10,6)+" ")
B=B+1
ENDDO
LNH=FWRITE(LNC,CHR(10)+CHR(13))
A=A+1
ENDDO
LNH=FCLOSE(LNC)
```

6.9 APPENDIX IX DATA FROM THE SEVEN SITES

6.9.1 THE DATA FOR WALLY CORNER, BERINSFIELD, OXFORDSHIRE

FILENAME	UI2	UP1	UC	UC	UM2	UM2	UM2	UM2	UM2	UM1	LP2	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TIDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR			
BERWC61	1.00	2.00	4.00	4.00	4.00	2.00	1.00	3.00	9.00	0.01	0.01	0.01	4.00		
BERWC77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	1.00			
BERWC26	0.00	2.00	0.00	4.00	4.00	0.00	0.00	0.00	6.00	0.00	0.01	2.00			
BERWC128	2.00	0.01	3.00	0.00	5.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00			
BERWC149	0.00	1.00	0.00	0.00	0.00	0.00	1.00	1.00	0.00	0.01	2.00	0.00			
BERWC86	0.00	1.00	0.00	0.00	3.00	0.01	1.00	0.01	0.00	0.00	0.00	0.00			
BERWC125	0.01	2.00	4.00	3.00	5.00	2.00	0.01	0.01	3.00	1.00	0.01	0.01			
BERWC5	3.00	2.00	3.00	4.00	4.00	2.00	0.00	0.01	2.00	0.01	2.00	1.00			
BERWC10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	1.00	0.01	0.00			
BERWC14	2.00	0.00	0.00	0.01	4.00	1.00	2.00	0.01	0.00	0.01	0.01	0.00			
BERWC32	0.00	0.00	4.00	5.00	0.00	0.00	0.00	0.00	6.00	0.00	0.00	0.00			
BERWC92	0.00	2.00	0.00	4.00	4.00	0.01	2.00	0.01	0.00	0.00	0.00	0.00			
BERWC91	4.00	2.00	4.00	0.00	4.00	2.00	4.00	0.01	3.00	0.01	3.00	0.01			
BERWC81	0.00	0.00	0.00	5.00	4.00	0.01	2.00	0.01	0.00	0.00	0.00	0.00			
BERWC20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00			
BERWC150/1	2.00	1.00	3.00	4.00	4.00	0.01	3.00	1.00	0.01	0.01	3.00	1.00			
BERWC56-B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	1.00	0.01	0.00			
BERWC56	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	6.00	3.00	0.01	1.00			
BERWC4	1.00	1.00	1.00	5.00	4.00	0.01	1.00	0.01	3.00	0.01	0.01	0.00			
BERWC133	0.00	0.01	0.00	5.00	4.00	0.00	0.00	1.00	6.00	0.00	0.00	1.00			
BERWC135	2.00	0.00	0.01	0.00	4.00	0.01	3.00	3.00	0.00	3.00	3.00	0.00			
BERWC147	7.00	1.00	4.00	5.00	4.00	0.01	3.00	0.01	0.00	0.01	5.00	0.00			
BERWC126	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	0.00	0.00	0.00	0.00			
BERWC82	3.00	0.01	4.00	4.00	5.00	0.01	0.00	0.00	3.00	4.00	0.01	3.00			
BERWC107-2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8.00	1.00	0.01	0.00			
BERWC107-1	1.00	2.00	2.00	4.00	4.00	2.00	2.00	0.01	3.00	0.01	0.01	1.00			

FILENAME	UI2	SHOVEL	UP1	UC	UC	MESRIDG	UC	UC	UM2	UM2	CUSP5	CARABL	UM1	LP2	LCUSPS	PSTYLD	LM2	CUSP5	LM2	LP1	TOMESR
BERWC37-1	2.00		1.00	4.00	5.00		4.00	4.00	0.01	3.00	3.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BERWC8	3.00		2.00	4.00	5.00		5.00	5.00	0.01	0.00	0.00	1.00	3.00	3.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00
BERWC127	4.00		1.00	4.00	5.00		4.00	4.00	0.01	7.00	0.01	0.01	8.00	8.00	0.00	0.01	3.00	3.00	0.00	1.00	0.00
BERWC103	1.00		0.00	2.00	4.00		0.00	0.00	0.00	0.00	3.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BERWC104	0.00		1.00	0.00	4.00		0.00	0.00	0.00	0.00	1.00	1.00	3.00	3.00	0.00	0.01	5.00	0.00	1.00	0.01	0.00
BERWC108	2.00		1.00	4.00	4.00		4.00	4.00	1.00	0.00	0.01	0.01	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.01	0.00
BERWC122	0.01		0.01	0.00	0.00		0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BERWC18	0.00		2.00	0.00	0.00		0.00	5.00	4.00	5.00	3.00	3.00	6.00	6.00	2.00	2.00	3.00	3.00	0.01	0.00	0.00
BERWC101	0.00		1.00	4.00	4.00		4.00	5.00	0.01	0.00	0.00	0.00	8.00	8.00	1.00	1.00	0.01	0.00	0.00	0.00	0.00
BERWC6	0.00		0.00	0.00	4.00		4.00	5.00	0.01	0.00	1.00	1.00	3.00	3.00	3.00	3.00	0.01	0.00	0.00	0.00	0.00
BERWC48	2.00		1.00	4.00	0.01		0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BERWC47	0.00		0.00	0.00	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BERWC130	0.00		2.00	0.00	4.00		0.00	0.00	0.00	0.00	0.00	0.00	9.00	9.00	0.00	0.00	0.01	0.00	3.00	0.00	0.00
BERWC129	0.01		0.00	4.00	0.00		0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BERWC49	0.00		1.00	0.00	0.00		0.00	0.00	0.00	0.00	0.00	0.00	4.00	4.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00
BERWC73	5.00		0.01	0.01	4.00		4.00	4.00	0.01	0.01	1.00	1.00	2.00	2.00	1.00	1.00	0.01	0.00	0.01	0.01	0.00
BERWC73-B	0.01		2.00	1.00	4.00		4.00	4.00	0.01	5.00	0.01	0.01	0.01	0.01	0.01	1.00	0.01	0.00	0.00	0.00	0.00
BERWC68	0.00		0.00	0.00	0.00		0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BERWC72	3.00		2.00	4.00	5.00		3.00	3.00	0.01	1.00	0.01	0.01	0.01	0.01	1.00	1.00	0.01	0.00	0.00	1.00	0.00
BERWC29	4.00		3.00	0.01	5.00		5.00	5.00	0.01	4.00	0.01	0.01	0.00	0.00	6.00	6.00	0.01	0.00	0.00	0.00	0.00
CB2	0.00		0.00	0.00	0.00		0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	4.00	4.00	0.01	0.00	0.00	0.00	0.00
BERWC5F152	4.00		0.00	4.00	4.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BERWC5EEND	0.00		0.00	0.00	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BERWC5UNSTR	0.00		0.00	0.00	0.00		0.00	4.00	0.01	0.00	0.00	0.00	3.00	3.00	1.00	1.00	0.01	0.00	0.00	0.00	0.00
BERWC141-1	3.00		0.00	4.00	5.00		5.00	5.00	0.01	0.00	0.00	0.00	4.00	4.00	0.01	0.01	0.01	0.00	0.00	1.00	0.00
BERWC110	0.00		0.00	0.00	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BERWC102	1.00		2.00	4.00	4.00		4.00	5.00	0.01	0.01	0.01	0.01	3.00	3.00	1.00	1.00	0.01	0.00	0.01	0.01	0.00
BERWC42	3.00		2.00	4.00	0.00		0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00
BERWC34	1.00		2.00	4.00	4.00		4.00	4.00	0.01	3.00	0.00	0.00	5.00	5.00	1.00	1.00	3.00	3.00	0.00	3.00	0.00
BERWC58	0.00		2.00	0.00	0.00		0.00	4.00	1.00	3.00	0.01	0.01	2.00	2.00	1.00	1.00	0.01	0.00	0.00	1.00	0.00
BERWC53	0.00		0.00	0.00	0.00		0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	0.00	0.00	0.01	0.00	0.00	1.00	0.00
BERWC106	0.00		0.00	0.00	0.00		4.00	4.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

FILENAME	UI2	UP1	UC	UC	UM2	UM2	UM2	UM2	UM2	UM2	UM1	LP2	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR				
BERWC35	1.00	2.00	1.00	3.00	5.00	1.00	0.01	0.01	3.00	1.00	0.01	3.00	0.01	1.00	0.01	1.00
BERWC9	0.00	0.00	0.00	0.00	5.00	3.00	0.01	0.00	2.00	1.00	0.00	2.00	3.00	3.00	3.00	3.00
BERWC152	2.00	1.00	5.00	5.00	4.00	0.01	2.00	0.01	2.00	1.00	0.01	2.00	2.00	2.00	0.00	0.00
BERWC2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BERWC1	3.00	2.00	5.00	4.00	0.00	0.00	0.00	1.00	0.00	0.00	1.00	0.00	0.00	0.00	0.01	0.01
BERWC3	0.00	2.00	0.00	4.00	5.00	0.01	0.01	1.00	6.00	0.01	1.00	6.00	0.01	0.01	3.00	3.00
BERWC28	0.00	0.00	0.00	0.00	5.00	0.01	0.00	1.00	4.00	0.00	1.00	4.00	0.00	0.00	0.01	0.01
BERWC15	2.00	2.00	5.00	5.00	3.00	0.01	0.01	0.01	0.00	2.00	0.01	0.00	0.01	0.01	0.00	0.00
BERWC57	0.01	1.00	5.00	3.00	4.00	3.00	0.01	0.01	0.00	0.00	0.01	0.00	0.01	0.01	0.00	0.00
BERWC59	3.00	0.00	5.00	5.00	0.00	0.00	0.00	0.01	2.00	1.00	0.01	2.00	0.01	0.01	0.00	0.00
BERWC55	0.00	0.00	0.00	1.00	4.00	0.01	0.01	0.01	0.00	0.01	0.01	0.00	0.01	0.01	0.00	0.00
BERWC74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
BERWC22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	0.00	3.00	0.01	0.01	0.01	0.01
BERWC67	4.00	1.00	4.00	5.00	5.00	0.01	0.00	1.00	2.00	1.00	1.00	2.00	0.01	1.00	1.00	1.00
BERWC30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	3.00	0.01	0.01	0.01	0.01

6.9.2 THE DATA FOR BRANDON, STAUNCH MEADOW, SUFFOLK

FILENAME	UI2 SHOVEL	UP1 DSHOVE	UC TDENT	UC MESRIDG	UM2 METACO	UM2 CUSP5	UM2 CARABL	UM1 PARAST	LP2 LCUSPS	LM2 PSTYLD	LM2 CUSP5	LP1 TOMESR
BRD3122	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	1.00	0.01	1.00
BRD3128A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3128B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
BRD4010	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.01	0.00
BRD4011A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD4011B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD4011C	0.00	1.00	0.00	0.00	4.00	0.01	3.00	1.00	0.00	0.00	0.00	0.00
BRD4011D	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	4.00	0.00
BRD4011E	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.01	0.00
BRD3065	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00
BRD3111	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.00	0.00	0.00	2.00
BRD3127A	1.00	1.00	3.00	4.00	0.00	0.00	0.00	0.00	0.00	1.00	4.00	0.01
BRD3127B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	0.00	0.00	3.00
BRD3127C	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
BRD3123A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.01	4.00
BRD3123B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3124	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD4005A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	0.01
BRD4005B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00
BRD4005C	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD4015	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD4028B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD4028A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00
BRD3095	1.00	2.00	5.00	0.00	3.00	0.01	0.00	0.00	0.00	1.00	0.01	0.01
BRD3060	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00
BRD3070	0.00	0.00	0.00	0.00	5.00	0.01	0.00	0.00	0.01	0.00	0.00	0.01
BRD3074	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00
BRD4003	0.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3091	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

FILENAME	U2 SHOVEL	UP1 DSHOVE	UC TDENT	UC MESRIDG	UM2 METACO	UM2 CUSP5	UM2 CARABL	UM1 PARAST	LP2 LCUSPS	LM2 PSTYLD	LM2 CUSP5	LP1 TOMESR
BRD3104	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
BRD3079	0.00	2.00	0.00	5.00	4.00	0.01	0.00	1.00	0.00	0.00	0.00	0.00
BRD3084	0.00	3.00	0.00	4.00	4.00	0.01	6.00	0.01	0.00	0.01	0.01	0.00
BRD3098	0.00	1.00	4.00	4.00	4.00	0.01	0.00	1.00	6.00	0.01	0.01	0.01
BRD3096	0.01	1.00	0.01	4.00	3.00	4.00	5.00	0.01	0.00	0.00	0.00	0.00
BRD3096-B	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3086	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	0.01	0.01	0.00
BRD3073	1.00	2.00	4.00	4.00	4.00	0.01	0.00	0.01	4.00	1.00	3.00	0.01
BRD3073-B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3083	1.00	1.00	1.00	5.00	4.00	0.01	0.01	0.01	3.00	0.01	0.01	1.00
BRD3093	1.00	0.01	4.00	5.00	4.00	0.01	0.01	2.00	0.01	1.00	0.01	0.01
BRD3081	0.00	0.00	4.00	0.01	3.00	0.01	0.00	0.00	4.00	0.00	0.00	1.00
BRD3072	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.01	0.01
BRD3062	0.00	3.00	0.00	0.00	4.00	0.01	0.00	0.00	0.00	5.00	4.00	0.00
BRD4050	0.00	0.00	0.00	0.00	4.00	0.01	3.00	0.00	0.00	0.00	0.00	0.00
BRD4558	0.01	1.00	0.01	0.00	3.00	4.00	3.00	0.00	3.00	0.01	0.01	3.00
BRD4038	0.00	0.00	0.00	4.00	4.00	0.01	0.00	0.00	4.00	1.00	0.01	0.01
BRD4054	0.00	0.00	4.00	0.00	4.00	0.01	0.00	0.00	2.00	0.01	0.01	1.00
BRD4048	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7.00	0.00	0.00	0.01
BRD4057	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	4.00	0.00	0.00	0.00
BRD4042	2.00	0.00	5.00	4.00	0.00	0.00	0.00	1.00	5.00	1.00	4.00	2.00
BRD4557	0.01	0.00	2.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
BRD4580	1.00	0.01	3.00	0.00	4.00	0.01	0.01	0.01	2.00	3.00	0.01	0.00
BRD3068	0.00	0.00	0.00	0.00	4.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00
BRD4009	0.00	0.00	0.00	0.00	3.00	0.01	6.00	0.00	5.00	3.00	0.01	1.00
BRD4020	0.00	3.00	0.00	3.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00
BRD3142	0.00	1.00	0.00	5.00	4.00	0.01	0.00	1.00	0.00	0.00	0.00	0.00
BRD3109	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3133	0.00	0.01	0.00	0.00	4.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00
BRD3108	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3075	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
BRD3076	0.00	0.01	0.00	0.00	4.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00

FILENAME	UI2 SHOVEL	UP1 DSHOVE	UC TDENT	UC MESRIDG	UM2 METACO	UM2 CUSP5	UM2 CARABL	UM1 PARAST	LP2 LCUSPS	LM2 PSTYLD	LM2 CUSP5	LP1 TOMESR
BRD4587	0.01	1.00	4.00	4.00	3.00	0.01	0.00	0.00	2.00	0.01	0.01	2.00
BRD4584	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
BRD4563	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00
BRD4602	0.00	0.00	4.00	3.00	0.00	0.00	0.00	0.00	5.00	0.00	0.00	0.01
BRD1555	1.00	3.00	5.00	5.00	4.00	0.01	0.01	1.00	3.00	0.01	0.01	0.00
BRD1554	0.00	2.00	0.00	0.00	4.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00
BRD1861	0.00	0.01	0.00	0.00	3.00	0.01	0.00	1.00	0.00	0.00	0.00	0.00
BRD1496	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	1.00	0.01	0.00
BRD1854	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7.00	1.00	1.00	0.00
BRD1498	0.00	0.00	0.00	0.00	4.00	0.01	0.00	1.00	2.00	5.00	0.01	1.00
BRD0187	0.01	0.00	1.00	4.00	5.00	1.00	4.00	0.01	2.00	0.01	0.01	1.00
BRD1500	0.00	0.00	0.00	2.00	4.00	0.01	3.00	0.01	0.01	0.00	0.00	0.00
BRD1839	0.00	0.00	0.00	0.00	4.00	3.00	0.01	1.00	0.00	0.00	0.00	0.00
BRD1859	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	5.00	0.00	0.01	0.00
BRD1859-A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00
BRD1556	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
BRD1862	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD1831	0.00	3.00	0.00	3.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
BRD1837	0.00	3.00	0.00	4.00	4.00	0.01	4.00	0.00	0.00	0.00	0.00	0.00
BRD1779-B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD1779	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	0.01	1.00
BRD1727	0.00	0.00	0.00	0.00	4.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
BRD1774	0.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD1838	0.00	1.00	0.00	5.00	4.00	0.01	0.00	0.00	2.00	1.00	0.01	1.00
BRD1849	1.00	1.00	4.00	4.00	4.00	0.01	0.00	0.00	0.00	1.00	1.00	0.01
BRD1900	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
BRD1919	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
BRD8009	1.00	1.00	3.00	4.00	4.00	0.01	0.00	2.00	2.00	0.00	0.00	0.00
BRD8055	2.00	0.01	4.00	0.00	4.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
BRD8018	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8.00	0.00	0.00	0.01
BRD8004	1.00	0.00	3.00	0.00	4.00	2.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD1893	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

FILENAME	UI2 SHOVEL	UP1 DSHOVE	UC TDENT	UC MESRIDG	UM2 METACO	UM2 CUSP5	UM2 CARABL	UM1 PARAST	LP2 LCUSPS	LM2 PSTYLD	LM2 CUSP5	LP1 TOMESR
BRD1917	2.00	3.00	5.00	0.00	5.00	0.01	0.00	0.00	0.00	0.00	0.00	1.00
BRD1929	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD1927	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
BRD1926	0.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	9.00	0.00	0.00	1.00
BRD1887	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
BRD1911	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	0.00	0.01	3.00
BRD1656	2.00	0.00	0.01	5.00	2.00	0.01	1.00	0.00	8.00	1.00	4.00	0.01
BRD1709	0.00	0.01	0.00	0.00	4.00	0.01	0.00	0.00	0.00	0.01	0.01	3.00
BRD1708	2.00	3.00	4.00	5.00	4.00	3.00	0.01	2.00	7.00	0.01	0.01	3.00
BRD1804	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	0.00	0.00	1.00
BRD1772	1.00	3.00	5.00	2.00	3.00	0.01	0.00	0.01	3.00	0.00	0.00	0.00
BRD1778	4.00	1.00	5.00	5.00	4.00	0.01	1.00	3.00	0.00	1.00	0.01	0.00
BRD1780	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.00
BRD1807	1.00	0.00	5.00	0.00	0.00	0.00	0.00	0.00	2.00	4.00	0.01	0.00
BRD1816	1.00	3.00	5.00	4.00	4.00	0.01	0.00	3.00	3.00	1.00	0.01	0.01
BRD1830	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00
BRD1840	0.01	4.00	4.00	4.00	4.00	2.00	1.00	1.00	2.00	2.00	2.00	0.01
BRD1844	4.00	0.00	5.00	0.00	4.00	1.00	0.01	0.01	0.00	1.00	2.00	0.00
BRD1850	1.00	2.00	4.00	4.00	4.00	0.00	0.00	0.01	4.00	0.01	0.01	3.00
BRD1845	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.01	0.00
BRD1857	0.00	2.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	1.00	2.00	0.00
BRD1882-B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.00	0.00	0.01	3.00
BRD1882-A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	0.00	0.00	0.00
BRD1897	0.01	1.00	4.00	4.00	3.00	0.01	0.00	3.00	4.00	3.00	4.00	2.00
BRD4068-A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	0.01	2.00	0.00
BRD4068-B	0.00	0.00	0.00	0.00	4.00	1.00	6.00	0.01	4.00	0.00	0.00	0.00
BRD4046	1.00	1.00	4.00	5.00	4.00	0.01	0.01	0.01	0.00	0.00	0.00	0.00
BRD4019	0.00	0.00	0.00	0.00	4.00	0.00	0.00	0.00	5.00	0.00	0.01	1.00
BRD4022	0.00	2.00	0.00	4.00	4.00	0.01	0.01	1.00	3.00	0.01	0.01	3.00
BRD4021	0.00	3.00	0.00	4.00	3.00	0.01	2.00	1.00	4.00	1.00	0.01	1.00
BRD4018	0.00	3.00	0.00	0.00	3.00	0.01	0.00	1.00	0.00	2.00	0.01	0.01
BRD4027	0.00	0.00	0.00	0.00	4.00	0.01	0.00	0.00	4.00	0.00	0.01	3.00

FILENAME	UI2 SHOVEL	UP1 DSHOVE	UC TDENT	UC MESRIDG	UM2 METACO	UM2 CUSP5	UM2 CARABL	UM1 PARAST	LP2 LCUSPS	LM2 PSTYLD	LM2 CUSP5	LP1 TOMESR
BRD4016	0.00	0.00	0.00	5.00	4.00	0.01	0.00	0.00	0.00	0.00	0.01	2.00
BRD4017	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
BRD1406	3.00	1.00	5.00	0.00	4.00	0.01	0.00	3.00	4.00	1.00	0.01	0.01
BRD1385	0.00	0.00	0.00	0.00	4.00	3.00	1.00	0.00	3.00	4.00	3.00	0.00
BRD4077	5.00	0.00	5.00	5.00	0.00	0.00	0.00	0.00	0.00	3.00	0.01	0.00
BRD4065	0.00	0.00	0.00	0.00	4.00	3.00	3.00	3.00	5.00	5.00	0.01	2.00
BRD4090	0.00	3.00	0.00	0.00	4.00	0.01	0.00	0.00	4.00	0.00	0.01	0.00
BRD4085	4.00	3.00	3.00	4.00	4.00	0.01	0.01	0.01	0.00	0.00	0.00	0.00
BRD4082	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	3.00	3.00	0.01
BRD4056	0.00	0.00	0.00	4.00	4.00	0.01	0.00	2.00	0.00	0.00	0.00	0.00
BRD4053-B	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
BRD4053-A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7.00	1.00	0.01	1.00
BRD4059	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
BRD1497	2.00	3.00	5.00	3.00	4.00	0.01	0.00	1.00	2.00	3.00	0.01	1.00
BRD1499	0.00	0.00	0.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD1527	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
BRD1440	0.00	0.00	0.00	0.00	4.00	0.01	0.00	0.00	3.00	0.00	0.01	0.01
BRD1541	3.00	0.01	5.00	5.00	3.00	0.01	5.00	3.00	8.00	1.00	5.00	3.00
BRD1553	0.00	1.00	0.00	5.00	4.00	2.00	7.00	3.00	6.00	4.00	3.00	3.00
BRD1588	0.00	1.00	0.00	4.00	4.00	0.01	1.00	0.00	0.00	0.01	0.01	0.00
BRD1587	0.00	1.00	0.00	3.00	4.00	3.00	0.00	0.00	0.00	3.00	3.00	0.01
BRD1594	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	4.00	0.01
BRD4946	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
BRD4807	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00
BRD4818	0.01	0.00	0.00	3.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
BRD4727	0.01	0.00	0.00	5.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00
BRD4817	1.00	0.00	0.00	4.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
BRD4821	1.00	0.01	4.00	0.01	3.00	1.00	0.01	0.01	0.00	0.00	0.00	0.00
BRD4853	2.00	1.00	4.00	4.00	3.00	0.01	4.00	0.01	2.00	3.00	0.01	0.01
BRD1879	2.00	1.00	4.00	5.00	4.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
BRD1874	2.00	0.01	5.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD1863-A	0.00	0.00	0.00	0.00	4.00	0.01	0.00	0.00	0.00	0.01	2.00	0.00

FILENAME	UI2	SHOVEL	UP1	UC	UC	MESRIDG	UM2	METACO	UM2	CUSP5	UM2	CARABL	PARAST	UM1	LCUSPS	LP2	PSTYLD	LM2	CUSP5	LM2	TOMESR	LP1	
BRD1863-C	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD1863-D	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00
BRD1883	2.00	2.00	3.00	4.00	4.00	5.00	5.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3114	0.00	0.01	0.00	0.00	0.00	4.00	0.00	0.01	0.01	0.00	0.00	0.00	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3134	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3094	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3137	0.00	0.00	0.00	5.00	5.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3110	0.00	0.00	0.00	5.00	5.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	2.00	1.00	0.01	0.01	0.01	1.00	1.00	1.00
BRD3135	3.00	0.01	4.00	4.00	4.00	4.00	4.00	4.00	0.01	1.00	1.00	0.01	1.00	1.00	0.00	0.00	1.00	0.01	0.01	0.01	0.01	3.00	3.00
BRD3136	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	0.00	2.00	2.00	2.00	0.00	0.00	0.00
BRD4001	2.00	0.01	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	4.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01
BRD3116	0.00	0.01	0.00	0.00	0.00	4.00	4.00	4.00	2.00	1.00	1.00	2.00	1.00	1.00	2.00	2.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01
BRD4835	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.00	0.00	0.00
BRD4822	0.00	1.00	3.00	4.00	4.00	4.00	4.00	4.00	0.01	0.01	0.01	0.00	0.00	0.00	3.00	3.00	2.00	0.01	0.01	0.01	0.00	0.00	0.00
BRD4665	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00	2.00	2.00	1.00	0.01	0.01	0.01	0.00	0.00	0.00
BRD4738	0.00	1.00	4.00	0.00	0.00	4.00	4.00	4.00	0.00	0.00	0.00	7.00	0.00	0.00	3.00	3.00	1.00	0.01	0.01	0.01	3.00	3.00	3.00
BRD4675	2.00	1.00	5.00	4.00	4.00	4.00	4.00	4.00	0.01	0.01	0.01	0.01	0.01	1.00	6.00	6.00	0.01	0.01	3.00	0.01	0.01	0.01	0.01
BRD4004	0.00	2.00	0.00	0.00	0.00	3.00	3.00	3.00	0.01	0.01	0.01	0.01	2.00	2.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD3145	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.00	6.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01
BRD3144	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00	2.00	2.00	1.00	0.01	0.01	0.01	0.01	0.01	0.01
BRD3113	0.01	1.00	4.00	4.00	4.00	3.00	3.00	3.00	0.01	0.01	0.01	0.01	1.00	1.00	2.00	2.00	1.00	3.00	3.00	3.00	2.00	2.00	2.00
BRD4002	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	3.00
BRD3141	0.00	0.00	0.00	0.00	0.00	4.00	4.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00	1.00
BRD3100	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	3.00	0.01	0.01	0.01	2.00	2.00	2.00
BRD8001	1.00	1.00	4.00	2.00	2.00	4.00	4.00	4.00	0.01	0.01	0.01	0.01	3.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD4045	2.00	1.00	5.00	0.00	0.00	4.00	4.00	4.00	0.01	0.01	0.01	0.00	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD4035-B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.00	5.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01
BRD4035-A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD4035-C	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD4044	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	1.00	3.00	3.00	3.00	0.01	0.01	0.01
BRD4037	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	2.00	0.01	0.01	0.01	0.01	1.00	1.00	1.00
BRD4034	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	0.00	0.00	3.00	3.00	0.01	0.01	0.01

FILENAME	UI2	SHOVEL	UP1	UC	UC	MESRIDG	UM2	METACO	UM2	CUSP5	UM2	CARABL	UM1	PARAST	LCUSPS	LP2	PSTYLD	LM2	CUSP5	LM2	TOMESR
BRD4034-B	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	2.00	5.00	0.01	0.01	0.01	0.01
BRD4034-A	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD4041	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BRD4842	0.00		1.00	0.00	4.00	4.00	4.00	4.00	0.01	0.01	0.00	0.00	0.00	6.00	6.00	1.00	1.00	0.01	0.01	0.01	0.01

6.9.3 THE DATA FOR ICKLINGHAM, SUFFOLK

FILENAME	UI2	SHOVEL	UP1	UC	UC	MESRIDG	UC	UM2	METACO	UM2	CUSP5	CARABL	UM2	PARAST	LCUSPS	PSTYLD	LM2	CUSP5	LM2	LP1	
		DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR									
IKLA47#22	3.00	2.00	0.00	0.00	4.00	0.01	0.00	1.00	0.01	0.01	0.01	0.01	1.00	0.01	0.01	1.00	0.01	0.01	0.01	0.01	0.01
IKLA80#36	0.00	0.01	0.00	0.00	4.00	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.01	0.01	0.00	0.01	0.01	0.01	0.00	0.00
IKLA146#3	0.00	0.00	0.00	0.00	4.00	0.01	0.00	0.01	0.01	0.00	0.00	0.00	0.01	0.01	6.00	1.00	2.00	0.01	0.01	0.01	0.01
IKLA48#16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.00	0.01	0.01	0.01	0.01	3.00	0.00
IKLA12#6	0.00	0.00	0.00	0.00	0.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7.00	0.01	2.00	0.01	0.01	0.00	0.00
IKLA6#2	0.00	1.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01	0.00	0.00	0.00	1.00	0.01	3.00	0.01	0.01	0.01	0.01	0.00	0.00
IKLA42#25	4.00	0.01	0.01	0.00	3.00	0.01	0.00	0.00	0.01	0.00	0.00	0.00	1.00	0.01	3.00	1.00	0.01	0.01	0.01	0.00	0.00
IKLA117#38	0.00	4.00	4.00	5.00	4.00	4.00	0.01	1.00	4.00	0.01	0.00	0.00	1.00	0.01	6.00	1.00	0.01	0.01	0.01	1.00	0.00
IKLA104#27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.01	0.01	0.01	0.01	5.00	0.00
IKLA13#7	3.00	3.00	4.00	5.00	4.00	3.00	0.00	0.01	4.00	3.00	0.00	0.00	0.01	0.01	3.00	0.00	0.01	0.01	0.01	0.01	0.01
IKLA97#1	1.00	1.00	4.00	4.00	4.00	2.00	4.00	4.00	4.00	2.00	4.00	4.00	3.00	3.00	3.00	0.00	0.00	0.00	0.00	0.01	0.01
IKLA141#8	1.00	3.00	4.00	4.00	4.00	2.00	4.00	4.00	4.00	2.00	4.00	4.00	0.00	0.00	3.00	2.00	0.01	0.01	0.01	0.00	0.00
IKLA3WH24	0.01	3.00	0.00	4.00	4.00	0.00	4.00	0.01	4.00	0.00	0.01	0.01	0.01	0.01	2.00	0.01	3.00	0.01	0.01	0.00	0.00
IKLA75#33	0.01	0.01	4.00	4.00	4.00	3.00	4.00	0.01	4.00	3.00	0.01	0.01	0.01	0.01	3.00	4.00	0.01	0.01	0.01	2.00	0.00
IKLA100#47	4.00	3.00	4.00	4.00	4.00	0.01	4.00	0.00	4.00	0.01	0.00	0.00	0.00	0.00	8.00	0.00	0.01	0.01	0.01	0.00	0.00
IKLA11#5	3.00	0.01	4.00	0.00	3.00	2.00	0.01	2.00	3.00	2.00	0.01	0.01	2.00	0.01	5.00	0.01	0.01	0.01	0.01	0.00	0.00
IKL74#12	0.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01
IKLA79#35	4.00	2.00	5.00	4.00	4.00	0.01	4.00	0.01	4.00	0.01	0.00	0.00	0.01	0.01	3.00	1.00	0.00	0.00	0.01	0.01	0.01
IKL0630672	2.00	2.00	2.00	4.00	4.00	0.01	4.00	0.01	4.00	0.01	0.00	0.00	0.00	0.00	2.00	0.01	0.01	0.01	0.00	0.00	0.00
IKLA90#45	0.00	2.00	0.00	4.00	3.00	1.00	4.00	4.00	3.00	1.00	4.00	4.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
IKL0630618	4.00	2.00	3.00	0.01	4.00	3.00	4.00	3.00	4.00	3.00	3.00	3.00	1.00	1.00	8.00	7.00	3.00	3.00	0.01	0.01	0.01
IKL033UNMA	1.00	1.00	4.00	4.00	0.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
IKLA43#23	0.00	0.01	0.00	4.00	0.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00
IKLA91#46	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
IKLA10#4	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
IKL0630546	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.01	0.01	0.01	0.01	0.01

6.9.4 THE DATA FOR LANKHILLS SCHOOL, WINCHESTER, HAMPSHIRE

FILENAME	UI2 SHOVEL	UP1 DSHOVE	UC TDENT	UC MESRIDG	UM2 METACO	UM2 CUSP5	UM2 CARABL	UM1 PARAST	LP2 LCUSPS	LM2 PSTYLD	LM2 CUSP5	LP1 TOMESR
1971293	1.00	1.00	2.00	2.00	4.00	0.01	0.01	0.01	0.00	0.00	0.00	0.00
1971293-A	1.00	0.01	3.00	3.00	5.00	0.01	0.01	0.01	3.00	0.01	2.00	0.01
1970179	1.00	1.00	1.00	0.00	4.00	0.01	1.00	0.01	0.00	0.01	0.01	0.01
1970181	1.00	0.01	1.00	2.00	3.00	0.01	0.00	1.00	3.00	1.00	0.01	3.00
1971212	2.00	1.00	0.01	4.00	4.00	0.01	0.01	1.00	0.00	1.00	0.01	0.01
1970232	0.00	0.01	0.00	4.00	5.00	0.01	3.00	0.00	3.00	0.01	0.01	0.01
1971349	1.00	0.01	4.00	1.00	4.00	0.01	0.00	4.00	0.01	0.00	0.01	0.01
1970186	2.00	2.00	4.00	3.00	4.00	0.01	0.00	0.01	0.00	0.00	4.00	0.00
1970243	4.00	2.00	4.00	4.00	4.00	0.01	4.00	1.00	3.00	1.00	0.01	0.01
1972362	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	0.01	0.00	1.00
1971330	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	2.00
1971217	4.00	0.01	4.00	5.00	3.00	0.01	0.01	0.00	4.00	0.00	0.00	0.00
1970228	2.00	3.00	2.00	3.00	3.00	0.01	1.00	2.00	0.00	0.01	4.00	0.00
1971332	1.00	1.00	4.00	4.00	4.00	0.01	0.01	0.01	5.00	1.00	0.01	3.00
1971299	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.01	0.00
1969138	0.00	0.01	0.00	0.00	5.00	0.01	4.00	0.01	0.00	0.00	0.00	0.00
1972352	2.00	0.01	4.00	0.00	4.00	0.01	0.01	0.00	3.00	0.01	0.01	2.00
1972336	5.00	0.01	5.00	4.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.01
1972220	0.00	2.00	4.00	4.00	3.00	0.01	0.00	0.00	3.00	3.00	2.00	0.01
1972358	0.00	3.00	3.00	5.00	4.00	0.01	0.00	0.01	3.00	0.01	0.01	3.00
1971315	0.00	0.01	4.00	4.00	4.00	4.00	2.00	0.00	2.00	3.00	3.00	0.01
1971231	0.00	1.00	1.00	3.00	0.00	0.00	0.00	1.00	0.00	0.00	0.01	0.01
1971203	0.01	1.00	1.00	4.00	5.00	0.01	0.01	0.01	3.00	1.00	2.00	0.01
1970222	2.00	2.00	0.00	3.00	4.00	0.01	0.01	0.00	0.01	1.00	0.01	0.01
1970226	2.00	0.00	3.00	4.00	4.00	0.01	0.01	0.00	3.00	0.01	0.01	0.01
1970893	0.01	1.00	2.00	3.00	4.00	0.01	2.00	0.01	3.00	0.01	0.01	2.00
1971211	0.00	0.01	0.00	3.00	0.00	0.00	0.00	0.00	5.00	1.00	2.00	0.00
1971335	0.01	2.00	0.00	4.00	4.00	0.01	0.00	0.00	3.00	0.00	0.00	1.00
1972214	1.00	2.00	0.01	4.00	4.00	0.01	0.00	0.00	3.00	0.00	0.00	0.00

FILENAME	UI2	SHOVEL	UP1	UC	UC	MESRIDG	UC	UM2	UM2	CUSP5	CARABL	PARAST	UM1	LP2	LCUSPS	PSTYLD	LM2	LM2	CUSP5	LM2	LP1	TOMESR
1970182	2.00		2.00	2.00	1.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
196864	1.00		2.00	0.00	4.00		4.00	4.00	0.01	0.00	0.00	0.00	0.00	3.00	3.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01
1971196	1.00		1.00	2.00	4.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.01	0.01	0.01	0.01	1.00	0.00
196847	0.00		1.00	0.00	0.00		0.00	0.00	0.00	0.00	0.00	1.00	1.00	3.00	3.00	0.01	0.00	0.00	0.01	0.01	0.00	0.00
1971309	0.00		0.00	0.00	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	4.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
1969130	0.00		1.00	0.00	3.00		4.00	4.00	0.01	0.01	1.00	1.00	1.00	3.00	3.00	0.01	0.01	0.01	0.01	0.01	0.00	0.00
196875	0.01		1.00	3.00	4.00		3.00	3.00	1.00	2.00	2.00	0.01	0.01	2.00	2.00	1.00	0.01	0.01	0.01	0.01	0.00	0.00
196846	3.00		0.00	3.00	0.00		4.00	4.00	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
196867	0.00		2.00	0.00	0.00		4.00	4.00	0.01	0.00	0.00	0.00	0.00	3.00	3.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
1971204	0.01		1.00	4.00	4.00		4.00	4.00	0.01	0.00	0.00	0.01	0.01	8.00	8.00	0.01	0.01	0.01	0.01	0.01	0.00	0.00
196855	0.00		0.00	0.00	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
196889	2.00		1.00	3.00	0.00		4.00	4.00	0.01	0.01	0.01	0.01	0.01	3.00	3.00	0.01	0.01	0.01	0.01	0.01	0.00	0.00
196739	3.00		2.00	3.00	2.00		5.00	5.00	0.01	0.00	0.00	0.00	0.00	3.00	3.00	1.00	0.01	0.01	0.01	0.01	0.00	0.00
1970192	0.00		2.00	0.00	5.00		5.00	5.00	0.01	0.01	0.01	0.01	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	1.00	0.00
196888	0.01		2.00	4.00	5.00		5.00	5.00	5.00	0.01	0.01	0.01	0.00	4.00	4.00	1.00	0.01	0.01	0.01	0.01	0.00	0.00
1971319	0.00		3.00	4.00	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00	1.00	1.00	3.00	0.00	0.00
1971308-A	3.00		0.00	0.00	4.00		3.00	3.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00
196876	0.00		0.01	0.00	0.00		4.00	4.00	0.00	0.00	0.00	0.00	0.00	4.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01
196721	0.01		1.00	4.00	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.01	3.00	3.00	1.00	1.00	1.00	1.00	0.01	0.01	0.01
1969104	0.01		0.01	4.00	2.00		4.00	4.00	0.01	0.01	0.01	0.01	0.01	3.00	3.00	1.00	1.00	3.00	3.00	0.01	0.01	0.01
1971297-B	0.01		0.01	3.00	4.00		5.00	5.00	1.00	4.00	4.00	0.01	0.01	6.00	6.00	1.00	1.00	0.01	0.01	0.00	0.00	0.00
1971297-A	0.00		0.01	0.00	3.00		4.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00
1972219	0.00		0.01	1.00	3.00		4.00	4.00	0.01	0.01	0.01	0.01	0.01	3.00	3.00	5.00	5.00	0.01	0.01	2.00	0.00	0.00
1971305	0.00		0.00	0.00	5.00		3.00	3.00	0.01	0.00	0.00	0.00	0.00	2.00	2.00	1.00	1.00	0.01	0.01	0.01	0.01	0.01
1972357	0.00		2.00	0.00	0.00		3.00	3.00	0.01	0.01	0.01	0.01	0.01	6.00	6.00	1.00	1.00	0.01	0.01	3.00	0.00	0.00
1971347	0.00		0.00	0.00	0.01		4.00	4.00	0.01	0.01	0.01	0.01	0.01	3.00	3.00	7.00	7.00	3.00	3.00	0.00	0.00	0.00
1972355	0.00		0.01	0.00	0.00		4.00	4.00	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
1971340	1.00		2.00	1.00	0.01		3.00	3.00	0.01	0.01	0.01	0.01	2.00	7.00	7.00	0.01	0.01	0.01	0.01	0.01	3.00	0.00
1972287	0.00		0.01	0.00	0.00		4.00	4.00	0.01	0.01	0.01	0.01	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.01
1971328	0.00		1.00	0.00	0.00		4.00	4.00	0.01	0.01	0.01	0.01	0.01	3.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01
1971343	0.01		2.00	0.01	3.00		4.00	4.00	0.01	0.01	0.01	0.01	0.01	4.00	4.00	3.00	3.00	4.00	4.00	0.01	0.01	2.00
1970225	0.00		2.00	0.00	0.00		4.00	4.00	0.01	0.00	0.00	0.00	0.00	3.00	3.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01

FILENAME	UI2	UP1	UC	UC	UM2	UM2	UM2	UM2	UM2	UM1	LP2	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR			
1971150	0.00	2.00	4.00	0.00	4.00	0.01	0.00	0.00	3.00	0.00	3.00	0.00	0.00	0.00	2.00
1970227	0.00	0.00	0.00	4.00	4.00	0.01	0.00	0.00	3.00	0.00	3.00	0.01	0.01	0.01	0.01
1970273	3.00	2.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	3.00	0.00	0.00	0.00	0.00
1970233	0.00	0.00	0.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
1971296	0.00	0.00	0.00	0.00	4.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
196890	2.00	0.00	2.00	0.00	5.00	0.01	3.00	2.00	4.00	2.00	4.00	7.00	3.00	0.00	0.00
1971308-B	0.00	2.00	2.00	0.00	0.00	0.00	0.00	0.00	6.00	0.00	6.00	0.00	0.00	0.01	0.01
196711	0.00	0.01	1.00	0.01	0.00	0.00	0.00	0.01	3.00	0.01	3.00	0.01	0.01	1.00	1.00
1969114	1.00	1.00	0.01	3.00	4.00	0.01	1.00	0.01	3.00	0.01	3.00	1.00	3.00	1.00	1.00
196735	1.00	2.00	3.00	0.00	4.00	0.01	0.01	0.01	3.00	0.01	3.00	0.01	0.00	2.00	2.00
196872	0.00	0.01	0.00	0.00	3.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
1971218	0.00	0.00	0.00	0.00	4.00	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00
1971331	0.00	0.01	0.00	0.00	0.00	0.00	0.00	1.00	0.00	1.00	0.00	0.01	0.01	0.00	0.00
1971306	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	1.00	0.00	1.00	0.01	0.00	0.00
196848	1.00	4.00	3.00	4.00	4.00	0.01	0.01	1.00	0.00	1.00	0.00	5.00	0.01	0.01	0.01
1971193-B	4.00	0.01	4.00	4.00	4.00	0.01	0.00	0.01	3.00	0.01	3.00	0.01	0.01	1.00	1.00
1971193-A	0.00	3.00	3.00	5.00	0.00	0.00	0.00	0.00	3.00	3.00	3.00	4.00	0.01	0.01	0.01
1970272	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01
1971304-B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.01	0.01	0.00	0.00
1971304-A	0.00	1.00	4.00	4.00	4.00	0.01	0.00	1.00	6.00	1.00	6.00	0.01	0.01	1.00	1.00
196857	3.00	2.00	4.00	4.00	4.00	0.01	6.00	1.00	6.00	1.00	6.00	1.00	3.00	0.00	0.00
1971277	0.00	2.00	0.00	0.00	4.00	0.01	0.00	0.00	3.00	0.00	3.00	0.00	0.00	2.00	2.00
1971456	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	3.00	0.00	0.00	4.00	4.00
1972295	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	1.00	3.00	1.00	0.01	5.00	5.00
196853	0.00	1.00	4.00	0.00	4.00	0.01	4.00	1.00	4.00	1.00	4.00	0.01	0.01	0.01	0.01
1970191	0.01	4.00	4.00	4.00	4.00	0.01	0.01	0.01	3.00	0.01	3.00	0.01	0.01	0.01	0.01
196716	1.00	2.00	4.00	0.00	4.00	0.01	0.01	0.00	2.00	0.01	2.00	0.01	0.01	1.00	1.00
1972278	0.00	2.00	0.00	4.00	0.00	0.00	0.00	0.00	6.00	1.00	6.00	1.00	0.01	0.00	0.00
196717	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	7.00	4.00	7.00	0.01	0.01	0.01
196874	0.00	2.00	0.00	0.01	3.00	0.01	0.01	0.01	0.01	4.00	0.01	4.00	0.01	0.01	0.01
1971208	2.00	3.00	2.00	5.00	4.00	0.01	0.00	0.00	3.00	0.00	3.00	0.00	0.00	0.01	0.01
196731	0.00	0.01	0.00	4.00	0.00	0.00	0.00	0.00	5.00	0.00	5.00	0.00	0.00	0.00	0.00

FILENAME	UI2	UP1	UC	UC	UM2	UM2	UM2	UM2	UM2	UM1	LP2	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR			
1969111	0.00	0.00	0.00	4.00	5.00	0.01	0.01	0.00	0.00	0.00	0.00	1.00	0.01	0.01	0.00
196896	0.00	2.00	0.00	0.00	4.00	0.00	0.00	0.00	8.00	0.01	0.01	0.01	0.01	0.01	0.01
196720	2.00	0.01	4.00	4.00	4.00	0.01	0.01	1.00	3.00	0.01	0.01	1.00	0.01	0.01	2.00
196886	0.00	2.00	0.00	1.00	4.00	0.01	0.01	0.00	0.01	0.00	0.01	0.00	0.01	0.01	0.00
196850	2.00	2.00	2.00	3.00	4.00	0.01	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
196894	0.00	3.00	0.00	5.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01
196724	0.00	0.00	0.00	0.00	5.00	0.01	0.01	0.00	3.00	0.00	0.01	0.00	0.00	0.01	0.01
196861	1.00	0.01	4.00	5.00	4.00	0.01	0.00	0.00	6.00	0.00	0.01	4.00	0.01	0.01	1.00
1970194	2.00	3.00	2.00	4.00	4.00	0.01	0.01	0.01	3.00	0.01	0.01	0.00	0.00	0.01	0.01
1969107	0.00	3.00	0.00	0.00	4.00	2.00	0.01	1.00	3.00	1.00	3.00	1.00	4.00	0.00	0.00
196881	0.00	2.00	0.00	4.00	4.00	0.01	0.00	0.00	0.01	0.00	0.01	0.00	0.01	0.00	0.00
196858	0.00	4.00	0.00	4.00	5.00	0.01	3.00	5.00	7.00	0.01	0.01	4.00	0.01	0.01	0.00
196878	0.00	2.00	0.00	5.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	2.00	0.00	0.00
196736	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.01	1.00	0.01	0.01	0.01
1971308-BI	1.00	3.00	4.00	4.00	3.00	0.01	0.01	0.01	3.00	0.01	0.01	0.01	0.01	0.01	1.00
1970254	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.01	0.00	0.01	0.01	3.00
196897	0.01	3.00	4.00	4.00	0.00	0.00	0.00	0.01	3.00	0.01	0.01	0.01	0.01	0.01	3.00
196887	1.00	0.01	1.00	4.00	3.00	0.01	0.01	0.01	3.00	0.01	0.01	0.01	0.01	0.01	0.00
1971201	1.00	3.00	1.00	4.00	4.00	0.01	1.00	0.01	3.00	0.01	0.01	2.00	0.01	0.01	1.00
196738	2.00	3.00	3.00	4.00	4.00	0.01	0.00	0.00	3.00	0.00	0.01	0.01	0.01	0.01	0.00
196713	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.00	0.00	0.00	0.00	0.00	0.01	0.01
196898	0.00	2.00	0.00	0.01	4.00	4.00	0.01	0.00	0.00	0.00	0.00	3.00	4.00	0.01	0.01
196854	0.00	0.00	0.00	4.00	4.00	1.00	0.01	0.00	4.00	0.00	0.01	3.00	0.01	0.01	3.00
196845	0.00	0.01	0.00	0.00	4.00	0.01	0.01	0.00	4.00	0.00	0.00	0.00	0.00	0.01	0.01
1969110	3.00	2.00	0.01	3.00	4.00	0.01	0.01	0.00	3.00	0.00	0.01	0.01	0.01	0.01	1.00
1969112	1.00	4.00	5.00	4.00	4.00	0.01	4.00	1.00	3.00	1.00	0.01	0.01	0.01	0.01	0.01
196719	0.00	0.01	0.00	0.01	4.00	0.01	0.01	0.00	0.01	0.00	0.01	0.01	0.01	0.01	0.01
1969109	0.00	3.00	0.00	4.00	4.00	0.01	0.01	3.00	5.00	0.01	0.01	0.01	0.01	0.01	1.00
196852	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00
1971291	0.00	0.01	0.00	4.00	4.00	0.01	0.01	0.00	2.00	0.00	0.01	3.00	0.01	0.01	1.00
196851	3.00	4.00	4.00	4.00	4.00	2.00	0.01	0.01	0.00	0.01	0.00	0.00	0.01	0.00	1.00
196737	2.00	4.00	4.00	5.00	4.00	0.01	1.00	4.00	3.00	0.01	0.01	0.01	0.01	0.01	0.00

FILENAME	UI2	UP1	UC	UC	UM2	UM2	UM2	UM2	UM2	UM2	UM1	LP2	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR				
1972381	0.01	2.00	2.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
1972384	2.00	3.00	5.00	5.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00
1970413	2.00	2.00	0.01	0.01	5.00	0.01	0.01	0.00	5.00	0.01	0.00	5.00	0.00	0.00	0.00	0.00
1972248	0.01	2.00	2.00	5.00	4.00	2.00	0.01	1.00	4.00	0.01	1.00	4.00	0.00	0.00	0.01	0.01
1970250	2.00	1.00	5.00	5.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	1.00	0.01	0.01	1.00
1971171	5.00	0.00	4.00	4.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	1.00
1972377	4.00	1.00	4.00	5.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	2.00	0.01	0.01	0.00
1972438	1.00	3.00	4.00	4.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	1.00
1969119	3.00	2.00	5.00	0.01	4.00	0.01	0.01	0.01	0.01	0.01	0.01	6.00	1.00	0.01	0.01	3.00
1972399	0.00	3.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00
1972444	3.00	1.00	4.00	4.00	3.00	0.01	0.00	0.00	0.00	0.01	0.00	3.00	0.00	0.01	0.01	3.00
1972367	2.00	0.00	4.00	4.00	0.00	0.00	0.00	0.01	0.01	0.00	0.01	6.00	0.00	0.00	0.00	1.00
1972368	3.00	2.00	4.00	4.00	4.00	0.01	0.00	1.00	0.00	0.01	1.00	6.00	1.00	0.01	0.00	0.00
1970168	0.00	0.00	4.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	0.01	0.01
1972399-A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
1972388-B	0.00	0.00	0.00	0.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00
1972388-A	0.00	1.00	4.00	4.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
1972447	2.00	0.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	3.00
1972430	3.00	3.00	3.00	4.00	4.00	0.01	0.01	0.00	0.01	0.01	0.00	3.00	0.01	0.01	0.01	0.01
1969126	1.00	3.00	3.00	4.00	5.00	0.01	0.01	0.01	0.01	0.01	0.01	2.00	0.01	0.01	0.01	0.01
1972428	1.00	2.00	4.00	4.00	4.00	0.01	2.00	2.00	0.01	0.01	2.00	5.00	0.01	0.01	0.00	0.00
1971337	1.00	2.00	4.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00
1969123	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	3.00	0.01	0.01	1.00	0.01
1970266	0.00	2.00	0.00	4.00	4.00	0.01	0.01	0.00	0.01	0.01	0.00	3.00	0.01	0.01	0.01	0.00
1969125	1.00	2.00	4.00	2.00	4.00	0.01	0.00	0.01	0.01	0.01	0.01	6.00	0.00	0.00	0.00	0.00
1969117	2.00	2.00	5.00	4.00	4.00	0.01	2.00	1.00	0.01	0.01	1.00	4.00	0.01	0.01	0.01	0.01
1969141	0.00	0.01	0.00	0.00	4.00	0.01	0.00	0.00	0.00	0.01	0.00	4.00	0.01	0.01	3.00	0.00
1972415	1.00	1.00	4.00	4.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	4.00	1.00	0.01	3.00	3.00
1972412	2.00	0.01	3.00	5.00	5.00	0.01	0.00	0.00	0.01	0.01	0.00	0.01	0.01	0.01	4.00	4.00
1972379	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
1969152	0.00	0.01	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	1.00	3.00	1.00	2.00	0.01	0.01
1972427	2.00	3.00	4.00	5.00	5.00	0.01	0.01	0.01	0.01	0.01	0.01	2.00	1.00	0.01	0.01	0.01

FILENAME	UI2	UP1	UC	UC	UC	UM2	UM2	UM2	UM2	UM2	UM1	LP2	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR				
1969159	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	3.00	0.01	0.01	0.01	0.01	0.01	0.01
1969161	0.00	2.00	0.00	5.00	4.00	0.01	0.01	0.01	0.01	3.00	1.00	0.01	0.01	0.01	0.01	0.00
1972445	0.00	0.00	0.00	4.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
1972441	0.00	0.01	0.00	0.00	4.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00
1972397	0.00	0.01	0.00	4.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00
1972395	1.00	2.00	3.00	4.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00
1972423	1.00	1.00	4.00	0.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00
1970LOST	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	1.00
1971166	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	5.00
1972436	1.00	1.00	4.00	4.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	0.00	0.00	0.00	4.00
1972379-B	0.00	0.00	0.00	4.00	4.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	0.00	0.00	0.00	0.01
1972442	1.00	2.00	0.01	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
1969158	0.00	2.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	0.00	0.00	0.01	0.00
1969129	0.00	0.01	0.00	4.00	4.00	0.01	0.01	0.01	0.01	3.00	0.01	0.01	0.01	0.01	0.01	0.01
1972443	2.00	1.00	5.00	5.00	3.00	0.01	0.01	0.01	0.01	3.00	1.00	4.00	0.01	0.01	3.00	3.00
1972451	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	1.00	0.01	0.01	0.01	0.01	0.01
1969156	0.00	0.00	0.00	5.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.00
1969161-B	0.00	2.00	4.00	5.00	4.00	0.01	0.01	0.01	0.01	3.00	1.00	0.01	0.01	0.01	1.00	1.00
1972374	0.01	2.00	4.00	4.00	4.00	0.01	0.01	0.01	0.01	0.01	1.00	0.01	0.01	0.01	0.01	0.00
1972380	0.00	0.01	0.00	5.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	1.00	1.00
1970270	0.01	2.00	2.00	4.00	4.00	0.01	0.01	0.01	0.01	3.00	1.00	0.01	0.01	0.01	1.00	1.00
1972365	0.01	3.00	3.00	4.00	4.00	0.01	0.01	0.01	0.01	6.00	0.01	0.01	0.01	0.01	2.00	2.00
1970175	0.00	2.00	0.00	5.00	4.00	0.01	0.01	0.01	0.01	6.00	3.00	0.01	0.01	0.01	3.00	3.00
1970264	0.00	3.00	0.00	5.00	4.00	0.01	0.01	0.01	0.01	0.00	1.00	0.01	0.01	0.01	0.00	0.00
1972410	0.00	0.00	0.00	5.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
1972408	1.00	0.01	4.00	5.00	0.00	0.00	0.00	0.00	0.00	3.00	0.01	0.01	0.01	0.01	0.01	0.00
1970164	0.00	1.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
1972398	0.00	0.00	0.00	4.00	4.00	0.01	0.01	0.01	0.01	6.00	2.00	4.00	0.00	0.00	3.00	3.00
1972414	3.00	2.00	4.00	4.00	5.00	2.00	0.00	0.00	0.00	3.00	3.00	0.01	0.01	0.01	0.01	0.01
1969131	0.00	0.00	0.00	4.00	3.00	0.01	1.00	1.00	1.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01
1970249	0.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	1.00	0.01	1.00	0.01	0.00	0.00
1970256	1.00	3.00	3.00	4.00	0.00	0.00	0.00	0.01	0.01	3.00	1.00	1.00	1.00	1.00	0.01	0.01

FILENAME	UI2	UP1	UC	UC	UM2	UM2	UM2	UM2	UM2	UM1	LP2	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR			
1970260	2.00	2.00	2.00	5.00	4.00	1.00	0.01	0.01	3.00	0.01	3.00	0.01	0.01	0.01	0.01
1970155	4.00	0.00	5.00	0.00	0.00	0.00	0.00	2.00	0.00	0.01	0.00	0.01	0.01	3.00	0.00
1972411	4.00	1.00	4.00	5.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00
1969137	0.00	0.01	0.00	4.00	3.00	0.01	0.01	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00
1967133	1.00	3.00	4.00	4.00	4.00	1.00	0.01	0.01	0.01	0.01	0.01	2.00	2.00	2.00	0.00
1969163	0.00	2.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	0.01	0.00
1969140	2.00	0.01	4.00	3.00	4.00	0.01	0.00	1.00	0.00	1.00	0.00	0.00	0.00	0.01	1.00
196718	0.01	1.00	2.00	3.00	4.00	0.01	2.00	0.01	3.00	0.01	3.00	0.01	0.01	0.01	2.00

6.9.5 THE DATA FOR LECHLADE, BUTLER'S FIELD, GLOUCESTER

FILENAME	UI2	UP1	UC	UC	UM2	UM2	UM2	UM2	UM2	UM2	UM1	LP2	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR				
LBF852	0.00	0.01	3.00	0.01	3.00	0.01	0.01	0.00	0.01	0.00	0.01	0.01	0.00	0.01	0.01	0.01
LBF8557	1.00	2.00	2.00	2.00	4.00	0.01	0.00	0.01	2.00	1.00	0.01	2.00	1.00	0.01	0.01	0.01
LBF851/1	0.01	0.01	3.00	1.00	4.00	1.00	2.00	0.01	4.00	0.01	0.01	4.00	0.01	0.01	0.01	0.01
LBF8510	0.00	0.01	3.00	1.00	3.00	0.01	0.00	1.00	0.00	0.01	1.00	0.00	0.01	0.01	0.01	0.01
LBF851161	4.00	1.00	3.00	0.01	3.00	0.01	0.01	0.01	2.00	0.01	0.01	2.00	0.01	0.01	0.01	3.00
LBF851118	0.00	1.00	0.00	0.00	3.00	0.01	0.01	0.01	0.00	0.00	0.01	0.00	0.00	0.00	1.00	1.00
LBF8511081	4.00	2.00	0.01	4.00	4.00	0.01	2.00	0.01	5.00	0.01	2.00	5.00	0.01	0.01	0.01	0.01
LBF851086	1.00	1.00	2.00	3.00	3.00	3.00	1.00	0.00	2.00	0.00	0.00	2.00	0.00	0.01	0.00	0.00
LBF851035	0.01	0.01	0.01	1.00	3.00	0.01	0.01	0.01	2.00	0.01	0.01	2.00	0.01	0.01	4.00	0.00
LBF8596	5.00	0.00	5.00	0.00	3.00	3.00	0.00	1.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00
LBF851054	3.00	0.01	4.00	5.00	4.00	0.01	1.00	0.01	2.00	0.01	0.01	2.00	0.01	0.01	0.01	1.00
LBF851213	0.00	1.00	4.00	2.00	4.00	0.00	0.00	0.01	2.00	0.01	0.01	2.00	0.01	0.01	0.01	0.01
LBF851207	0.00	0.01	0.00	0.00	4.00	3.00	1.00	0.01	8.00	0.01	0.01	8.00	0.01	0.01	0.01	0.01
LBF851184	1.00	0.01	2.00	4.00	4.00	0.01	5.00	0.01	4.00	1.00	0.01	4.00	1.00	0.01	0.01	3.00
LBF851197	3.00	0.01	4.00	3.00	3.00	0.01	3.00	0.01	2.00	1.00	0.01	2.00	1.00	0.01	0.01	1.00
LBF851194	0.01	0.01	2.00	4.00	0.00	0.00	0.00	0.00	4.00	0.00	0.00	4.00	0.00	0.00	0.00	2.00
LBF851189	0.01	1.00	0.01	5.00	4.00	1.00	0.01	1.00	2.00	1.00	1.00	2.00	1.00	0.01	1.00	1.00
LBF851180	0.01	1.00	2.00	0.00	3.00	0.01	1.00	0.01	0.00	0.00	0.01	0.00	0.00	0.00	3.00	3.00
LBF851182	1.00	0.01	0.01	3.00	4.00	3.00	0.00	0.00	2.00	0.01	0.00	2.00	0.01	0.01	1.00	1.00
LBF851177	0.00	1.00	4.00	5.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	3.00	3.00
LBF851178	0.01	1.00	0.01	0.01	4.00	0.01	0.00	0.00	2.00	1.00	1.00	2.00	1.00	0.01	0.00	0.00
LBF851175	0.00	0.00	0.00	0.00	4.00	0.01	0.00	0.00	5.00	0.00	1.00	5.00	0.00	0.00	0.00	0.00
LBF851162	0.00	1.00	0.00	0.00	4.00	0.01	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.01	0.01
LBF851168	3.00	0.01	4.00	2.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
LBF851167	0.00	0.01	3.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01
LBF851166	0.01	1.00	0.01	2.00	4.00	0.01	0.00	0.01	3.00	0.01	0.00	3.00	0.01	0.01	0.01	0.01
LBF851159	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	1.00	1.00	0.00	0.00	0.00	0.01	0.01
LBF851133	0.01	0.01	0.01	1.00	3.00	2.00	0.01	0.01	2.00	0.01	0.01	2.00	2.00	0.01	3.00	3.00
LBF851130	0.01	0.01	3.00	5.00	4.00	0.01	0.01	0.01	2.00	0.01	1.00	2.00	1.00	0.01	0.01	3.00

FILENAME	UI2	UP1	UC	UC	UM2	UM2	UM2	UM2	UM2	UM1	LP2	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR			
LBF851134	0.01	1.00	4.00	5.00	3.00	0.01	1.00	0.01	4.00	0.01	4.00	0.01	0.01	0.01	1.00
LBF8511322	1.00	1.00	2.00	4.00	4.00	1.00	1.00	0.01	0.01	0.01	0.01	1.00	1.00	0.01	0.01
LBF851135	1.00	1.00	4.00	0.01	4.00	0.01	1.00	0.01	0.00	0.01	0.00	2.00	0.01	2.00	1.00
LBF8511401	0.01	1.00	2.00	0.01	4.00	1.00	0.01	0.01	2.00	0.01	2.00	1.00	1.00	3.00	0.01
LBF851127	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00	0.01	0.01
LBF851129	4.00	0.01	0.01	4.00	4.00	3.00	2.00	1.00	3.00	1.00	3.00	0.01	1.00	0.01	1.00
LBF851128	1.00	0.01	1.00	0.01	3.00	0.01	0.01	2.00	6.00	2.00	0.00	0.01	0.01	0.01	0.01
LBF851179	0.00	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01
LBF851121	1.00	0.01	1.00	0.00	4.00	0.01	0.01	1.00	2.00	1.00	2.00	0.01	0.01	0.01	1.00
LBF8511252	0.01	0.01	0.01	4.00	0.00	0.00	0.00	0.01	2.00	0.01	2.00	0.01	0.01	2.00	0.01
LBF851125	1.00	0.01	3.00	0.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
LBF851115	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
LBF851110	2.00	0.01	4.00	3.00	3.00	3.00	0.01	1.00	5.00	1.00	0.00	0.01	0.01	3.00	1.00
LBF851123	0.00	1.00	0.00	0.00	3.00	0.01	1.00	0.01	0.00	0.01	0.00	0.01	0.01	0.01	0.01
LBF851122	1.00	0.01	0.01	0.01	0.00	0.00	0.00	1.00	2.00	1.00	2.00	0.01	0.01	0.01	0.00
LBF851119	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00
LBF851117	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF851120	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.00
LBF8511082	1.00	2.00	4.00	4.00	0.00	0.00	0.00	0.01	2.00	0.01	2.00	0.00	0.00	0.00	0.01
LBF851113	0.00	0.00	0.00	0.00	3.00	0.01	0.01	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00
LBF851109	1.00	1.00	1.00	2.00	3.00	2.00	2.00	0.01	9.00	0.01	0.00	1.00	1.00	3.00	0.01
LBF851092	4.00	1.00	2.00	1.00	3.00	0.01	0.01	1.00	3.00	1.00	3.00	1.00	1.00	0.01	0.00
LBF851090	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00
LBF851103	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	0.00	4.00	0.00	0.00	0.00	0.01
LBF851099	1.00	0.01	3.00	3.00	3.00	2.00	0.01	2.00	9.00	2.00	0.00	1.00	1.00	0.01	1.00
LBF851067	1.00	1.00	3.00	2.00	3.00	2.00	0.01	2.00	5.00	2.00	2.00	1.00	1.00	2.00	0.01
LBF851072	2.00	1.00	0.01	5.00	4.00	0.01	1.00	0.01	2.00	1.00	0.00	1.00	1.00	0.01	0.00
LBF851087	1.00	0.00	2.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
LBF851088	1.00	0.01	0.01	0.00	3.00	1.00	1.00	0.01	3.00	0.01	3.00	0.01	0.01	0.01	1.00
LBF851082	2.00	1.00	5.00	2.00	4.00	0.01	0.01	0.01	2.00	0.01	2.00	1.00	1.00	0.01	1.00
LBF851085	2.00	2.00	2.00	5.00	4.00	2.00	1.00	0.01	2.00	1.00	2.00	0.01	0.01	4.00	3.00
LBF851059	1.00	1.00	0.01	0.01	4.00	2.00	0.01	0.00	2.00	0.01	2.00	0.01	0.01	0.01	1.00

FILENAME	UI2	SHOVEL	UP1	UC	UC	MESRIDG	UC	UM2	UM2	CUSP5	UM2	CARABL	PARAST	UM1	LCUSPS	LP2	PSTYLD	UM2	CUSP5	LM2	LP1	TOMESR
LBF8510621	0.01		0.01	3.00	0.00	4.00	0.01	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF851077	0.01		0.01	2.00	4.00	4.00	0.01	4.00	0.01	0.01	0.00	0.00	2.00	2.00	3.00	3.00	0.01	0.01	4.00	4.00	2.00	2.00
LBF851076	1.00		0.01	1.00	4.00	3.00	0.01	3.00	0.01	0.01	0.01	0.01	0.00	0.00	2.00	2.00	3.00	0.01	0.01	0.01	3.00	3.00
LBF851060	0.01		0.01	3.00	1.00	4.00	0.01	4.00	0.01	0.01	0.01	0.01	0.01	0.01	2.00	2.00	0.01	0.01	0.01	0.01	1.00	1.00
LBF851061	0.01		0.01	0.01	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	1.00	0.01	0.01	0.01	0.00	0.00
LBF8510631	1.00		1.00	3.00	5.00	3.00	0.01	3.00	0.01	0.01	0.01	0.00	1.00	1.00	3.00	3.00	1.00	0.01	0.01	0.01	3.00	3.00
LBF851047	0.00		1.00	2.00	2.00	4.00	0.01	4.00	0.01	0.01	0.01	0.00	0.01	0.01	5.00	5.00	0.01	0.01	4.00	4.00	0.00	0.00
LBF8510482	1.00		1.00	0.01	4.00	3.00	0.01	3.00	0.01	0.01	0.01	1.00	0.01	0.01	2.00	2.00	1.00	0.01	0.01	0.01	2.00	2.00
LBF851041	0.00		1.00	0.00	0.00	3.00	0.00	3.00	1.00	0.01	0.01	0.01	0.01	0.01	7.00	7.00	0.01	0.01	0.01	0.01	0.01	0.01
LBF851023	1.00		0.01	2.00	3.00	3.00	0.01	3.00	2.00	0.01	2.00	2.00	0.01	0.01	2.00	2.00	0.01	0.01	2.00	2.00	2.00	2.00
LBF851037	0.01		1.00	3.00	0.01	3.00	0.01	3.00	0.01	0.01	0.01	0.01	0.00	0.00	9.00	9.00	1.00	0.01	2.00	2.00	2.00	2.00
LBF851026	0.01		0.01	1.00	0.00	4.00	0.01	4.00	0.01	0.01	0.01	0.00	0.00	0.00	7.00	7.00	0.01	0.01	0.01	0.01	0.01	0.01
LBF851046	1.00		0.01	0.01	0.01	3.00	0.01	3.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	2.00	2.00
LBF851011	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
LBF851008	1.00		1.00	4.00	4.00	4.00	0.00	4.00	2.00	2.00	2.00	0.00	0.01	0.01	2.00	2.00	1.00	0.00	3.00	3.00	0.00	0.00
LBF851104	2.00		1.00	3.00	0.00	4.00	0.00	4.00	2.00	2.00	0.01	0.01	1.00	1.00	4.00	4.00	0.01	0.01	0.01	0.01	1.00	1.00
LBF851039	0.01		1.00	0.01	2.00	3.00	0.01	3.00	0.01	0.00	0.00	0.00	0.00	0.00	4.00	4.00	0.00	0.00	0.00	0.00	0.01	0.01
LBF8510171	1.00		0.01	0.01	1.00	4.00	0.01	4.00	0.00	0.00	0.00	0.00	0.01	0.01	3.00	3.00	0.00	0.00	0.00	0.00	0.01	0.01
LBF851016	1.00		1.00	5.00	3.00	3.00	0.01	3.00	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	1.00	1.00	2.00	2.00	1.00	1.00
LBF851012	0.01		1.00	2.00	1.00	4.00	0.01	4.00	0.01	0.01	0.01	0.00	0.00	0.00	4.00	4.00	0.00	0.00	0.00	0.00	0.01	0.01
LBF851018	0.01		0.01	2.00	0.00	4.00	0.01	4.00	0.01	0.01	0.01	0.01	0.01	0.01	2.00	2.00	1.00	0.01	4.00	4.00	1.00	1.00
LBF851020	0.01		1.00	4.00	3.00	3.00	0.01	3.00	0.01	0.01	0.01	0.01	2.00	2.00	2.00	2.00	0.01	0.01	0.01	0.01	0.00	0.00
LBF8510062	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF8510061	0.00		0.01	0.00	0.00	4.00	0.01	4.00	0.01	0.01	0.01	0.01	0.01	0.01	4.00	4.00	1.00	0.01	0.01	0.01	0.00	0.00
LBF8510172	0.00		1.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF851007	0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF851001	2.00		1.00	2.00	4.00	4.00	0.01	4.00	0.01	0.01	0.01	2.00	0.00	0.00	4.00	4.00	1.00	0.01	0.01	0.01	3.00	3.00
LBF851002	0.01		1.00	0.01	3.00	4.00	0.01	4.00	2.00	0.01	0.01	0.01	0.00	0.00	3.00	3.00	0.01	0.01	0.01	0.01	1.00	1.00
LBF8510064	2.00		0.01	4.00	3.00	4.00	0.01	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01
LBF851003	0.00		0.00	0.00	0.00	3.00	0.01	3.00	0.01	0.01	0.01	0.01	1.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
LBF85181	1.00		1.00	1.00	2.00	3.00	0.01	3.00	0.01	0.01	0.01	0.01	0.01	0.01	3.00	3.00	1.00	0.01	0.01	0.01	1.00	1.00
LBF85191	1.00		0.01	2.00	2.00	3.00	0.01	3.00	0.01	0.01	0.00	0.00	0.01	0.01	2.00	2.00	0.01	0.01	0.01	0.01	0.01	0.01

FILENAME	UI2	UP1	UC	UC	UM2	UM2	UM2	UM2	UM2	UM2	UM1	LP2	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR				
LBF85192	0.00	0.01	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
LBF85158	1.00	1.00	0.01	1.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01	3.00	1.00	4.00	2.00	2.00
LBF85157	0.00	0.00	0.00	0.00	4.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00
LBF85159	1.00	0.00	3.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	0.00	0.00	0.01	0.01
LBF85179	4.00	0.01	0.01	1.00	4.00	0.01	0.00	0.00	0.00	0.00	0.00	6.00	0.01	0.01	0.01	0.01
LBF85182	0.00	0.00	0.00	0.00	4.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
LBF85171	2.00	0.01	2.00	2.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01	3.00	1.00	0.01	1.00	1.00
LBF85143	1.00	0.01	4.00	4.00	3.00	0.01	1.00	0.01	0.01	0.01	0.01	3.00	0.01	3.00	0.01	0.01
LBF85144	0.00	1.00	0.00	2.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00
LBF85149	4.00	0.01	0.01	2.00	4.00	1.00	0.01	0.01	0.01	0.01	0.01	3.00	0.01	4.00	1.00	1.00
LBF85145	0.00	0.01	0.00	4.00	4.00	0.01	1.00	0.01	0.01	0.01	0.01	2.00	1.00	0.01	1.00	1.00
LBF851562	0.01	0.01	1.00	1.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	3.00	0.01	0.01	0.01	0.01
LBF851561	0.01	0.01	0.01	4.00	3.00	4.00	0.01	0.01	0.01	0.01	0.01	2.00	1.00	0.01	2.00	2.00
LBF85142	0.00	0.00	0.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF85141	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
LBF851401	0.00	1.00	1.00	0.00	3.00	0.01	1.00	0.01	0.01	0.01	0.01	4.00	0.01	0.01	0.01	0.01
LBF85140	0.00	1.00	0.00	0.00	4.00	0.01	2.00	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00
LBF85135	0.00	1.00	0.00	0.00	3.00	2.00	2.00	2.00	0.01	0.01	0.01	3.00	1.00	0.01	1.00	1.00
LBF85132	1.00	1.00	2.00	1.00	3.00	0.01	0.00	0.00	0.00	0.00	1.00	0.01	0.01	0.01	1.00	1.00
LBF85139	0.00	1.00	3.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	3.00	1.00	0.01	0.01	0.01
LBF85122	0.00	0.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
LBF85112	1.00	0.01	4.00	4.00	3.00	5.00	0.01	0.01	0.01	0.01	0.01	0.00	1.00	0.01	0.01	0.01
LBF85113	0.01	0.01	3.00	0.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	2.00	0.01	0.01	0.01	0.01
LBF85128	1.00	0.01	4.00	4.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01	3.00	2.00	0.01	2.00	2.00
LBF85126	0.01	0.01	3.00	0.01	3.00	0.01	1.00	0.01	0.01	0.01	0.01	3.00	1.00	0.01	0.01	0.01
LBF85131	1.00	0.01	3.00	1.00	4.00	0.01	2.00	0.01	0.01	0.01	0.01	2.00	0.01	0.01	1.00	1.00
LBF85108	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
LBF85107	0.01	0.01	3.00	2.00	3.00	0.01	0.00	1.00	0.01	0.01	1.00	5.00	1.00	0.01	1.00	1.00
LBF85106	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
LBF85109	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
LBF85110	0.01	0.01	4.00	4.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01	2.00	1.00	0.01	3.00	3.00
LBF8592	1.00	0.01	3.00	1.00	3.00	0.01	0.01	0.00	0.00	0.01	0.00	6.00	1.00	0.01	3.00	3.00

FILENAME	UI2	UP1	UC	UC	UC	UM2	UM2	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	LM2	LM2	CUSP5	TOMESR		
LBF8593	1.00	0.01	4.00	4.00	3.00	0.01	0.01	0.01	3.00	0.01	0.01	0.01	0.01	0.01	0.00	0.00
LBF8586	0.00	1.00	4.00	3.00	4.00	0.01	0.01	0.00	5.00	1.00	3.00	3.00	3.00	3.00	3.00	3.00
LBF8587	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	3.00	3.00
LBF8594E	0.01	0.01	0.01	2.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00
LBF8578	0.01	0.01	4.00	0.01	3.00	0.01	0.01	1.00	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00
LBF8574	1.00	1.00	3.00	5.00	3.00	0.01	0.01	0.01	3.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01
LBF8575	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF8573	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00
LBF8580	0.00	0.01	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF8585	0.01	0.01	2.00	1.00	3.00	3.00	4.00	0.01	6.00	1.00	0.01	1.00	0.01	0.01	2.00	2.00
LBF8584	0.00	0.01	0.00	5.00	0.00	0.00	0.00	0.01	5.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF85591	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
LBF8565	0.00	0.01	0.00	0.00	3.00	3.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF8560	1.00	0.01	1.00	2.00	4.00	0.01	2.00	1.00	3.00	2.00	0.01	2.00	0.01	0.01	1.00	1.00
LBF8566	0.01	0.01	1.00	0.00	0.00	0.00	0.00	0.00	0.01	1.00	0.01	1.00	0.01	0.01	1.00	1.00
LBF8567	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF8576	3.00	0.00	4.00	0.00	3.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF8577	5.00	0.00	4.00	0.00	4.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF8551	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.01	0.01	0.00	0.00
LBF8556	1.00	0.00	4.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LBF8516	0.00	0.00	3.00	1.00	3.00	0.01	0.00	0.01	4.00	0.00	0.01	0.00	0.01	0.01	0.01	0.01
LBF8517	1.00	0.01	3.00	0.01	3.00	0.01	1.00	0.01	2.00	0.01	0.01	0.01	0.01	0.01	1.00	1.00
LBF8519	0.01	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.01	1.00	0.01	0.01	0.00	0.00
LBF8518	1.00	0.01	2.00	2.00	4.00	0.01	0.01	0.00	7.00	1.00	0.01	1.00	0.01	0.01	0.00	0.00
LBF8550	1.00	0.01	0.01	3.00	4.00	2.00	0.01	0.01	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01
LBF853	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	0.01	0.01	0.01	0.01	0.01	2.00	2.00
LBF8515	0.00	1.00	3.00	4.00	0.00	0.00	0.00	0.00	3.00	1.00	0.01	1.00	0.01	0.01	0.01	0.01
LBF85100	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	0.00	0.00	0.00	0.00	0.00	2.00	2.00
LBF851136	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	0.01	0.01	0.01	0.01	0.01	0.00	0.00

FILENAME	UI2	UP1	UC	UC	MESRIDG	METACO	UM2	CUSP5	UM2	CARABL	PARAST	UM1	LP2	LCUSPS	PSTYLD	LM2	CUSP5	LM2	LP1	TOMESR
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	UM2	CUSP5	CARABL	PARAST	UM1	LP2	LCUSPS	PSTYLD	LM2	CUSP5	LM2	LP1	TOMESR		
PWE15	4.00	1.00	5.00	5.00	3.00	0.01	0.01	0.01	0.01	0.01	3.00	3.00	0.01	5.00	0.01	0.01	3.00	0.01	0.01	
PWE14	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	0.01	0.01	0.01	0.01	3.00	0.01	3.00	
PWE12	0.00	0.00	4.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	0.00	0.01	0.01	0.01	4.00	0.01	4.00	
PWE51	1.00	2.00	5.00	4.00	4.00	0.01	0.01	0.00	0.01	0.01	3.00	3.00	1.00	4.00	0.01	0.01	1.00	4.00	0.01	
PWE53	0.00	0.00	5.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	1.00	0.01	0.01	0.01	1.00	0.01	1.00	
PWE52	1.00	2.00	4.00	0.00	4.00	0.01	0.01	0.00	0.01	0.00	3.00	3.00	0.00	0.01	0.01	0.01	2.00	0.01	2.00	
PWW8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	
PWW1	0.00	1.00	0.00	4.00	4.00	1.00	1.00	4.00	4.00	1.00	3.00	3.00	1.00	0.01	0.01	0.01	1.00	0.01	1.00	
PWW2	0.00	1.00	0.00	0.00	3.00	0.01	0.01	0.01	0.01	0.00	3.00	3.00	1.00	0.01	0.01	0.01	1.00	0.01	1.00	
PWE29	1.00	1.00	5.00	4.00	3.00	0.01	0.01	0.00	0.01	0.01	8.00	8.00	1.00	0.01	0.01	0.01	1.00	0.01	1.00	
PWW7	1.00	1.00	4.00	4.00	4.00	0.01	0.01	4.00	4.00	0.01	8.00	8.00	1.00	0.01	0.01	0.01	0.00	0.01	0.00	
PWE9	0.00	0.00	0.00	0.00	4.00	0.01	0.01	0.00	0.00	0.00	4.00	4.00	0.00	0.00	0.00	0.00	1.00	0.00	1.00	
PWE11	0.00	1.00	4.00	4.00	3.00	0.01	0.01	0.00	0.00	0.00	6.00	6.00	0.00	0.00	0.00	0.00	3.00	0.00	3.00	
PWE28	0.00	0.00	3.00	0.00	4.00	0.01	0.01	0.00	0.00	0.00	5.00	5.00	0.00	0.01	0.01	0.01	2.00	0.01	2.00	
PWE55	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	3.00	0.00	0.01	0.01	0.01	1.00	0.01	1.00	
PWE7	0.00	2.00	0.00	4.00	4.00	0.01	0.01	0.00	0.00	0.00	6.00	6.00	0.00	0.01	0.01	0.01	1.00	0.01	1.00	
PWE6	0.00	1.00	1.00	0.00	4.00	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	3.00	
PWE49	1.00	1.00	4.00	4.00	4.00	0.01	0.01	0.01	0.01	1.00	6.00	6.00	1.00	2.00	2.00	2.00	1.00	2.00	1.00	
PWE37	0.00	0.01	0.00	4.00	3.00	0.01	0.01	0.00	0.00	0.00	4.00	4.00	0.00	0.01	0.01	0.01	1.00	0.01	1.00	
PWWF3	2.00	2.00	4.00	4.00	4.00	0.01	0.01	5.00	5.00	0.01	8.00	8.00	2.00	4.00	4.00	4.00	0.00	4.00	0.00	
PWW3	3.00	2.00	4.00	4.00	4.00	0.01	0.01	0.00	0.01	0.01	6.00	6.00	1.00	5.00	5.00	5.00	0.01	5.00	0.01	
PWWF1	0.00	1.00	4.00	4.00	4.00	3.00	3.00	0.01	0.01	0.01	6.00	6.00	0.01	0.01	0.01	0.01	0.00	0.01	0.00	
PWWF7	0.00	2.00	0.00	5.00	4.00	0.01	0.01	4.00	4.00	0.01	4.00	4.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	

6.9.7 THE DATA FOR QUEENFORD MILL, DORCHESTER ON THAMES, OXFORDSHIRE

FILENAME	UI2	UP1	UC	UC	UM2	UM2	UM2	UM2	UM2	UM1	LP2	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR			
QF72F4	4.00	1.00	3.00	5.00	4.00	1.00	2.00	1.00	2.00	1.00	2.00	0.01	0.01	0.01	1.00
QF72F2	1.00	0.01	3.00	4.00	4.00	0.01	0.00	1.00	3.00	4.00	0.01	0.01	0.01	0.01	0.00
QF72F7	0.01	1.00	4.00	4.00	4.00	0.01	0.01	0.01	5.00	0.01	0.01	0.01	0.01	0.01	3.00
QF72F6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8.00	0.00	0.00	0.01	0.01	2.00	0.00
QF72F1	0.00	0.01	0.00	4.00	0.00	0.00	0.00	0.00	6.00	1.00	0.01	0.01	0.01	0.01	4.00
QF72F50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.01	0.01	0.01	0.01	0.01	1.00
QF72F53	5.00	2.00	5.00	5.00	5.00	0.01	2.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
QF72F49	0.00	0.01	0.00	0.01	4.00	0.01	0.00	0.00	3.00	0.01	0.01	0.01	0.01	2.00	0.01
QF72F46	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00	3.00	0.01
QF72F48	2.00	2.00	4.00	0.00	5.00	1.00	3.00	1.00	0.00	1.00	0.00	0.00	0.00	3.00	0.00
QF72U/S-A	0.01	0.01	1.00	4.00	3.00	0.01	0.01	0.01	3.00	0.01	0.01	0.00	0.00	0.00	0.00
QF72U/S-B	0.00	0.01	3.00	0.00	5.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
QF72U/S-C	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
QF72U/S-D	0.00	0.00	0.00	4.00	0.00	0.00	0.00	1.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00
QF72F47	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.01
QF72F39	3.00	0.01	5.00	5.00	5.00	0.01	0.01	0.01	3.00	3.00	3.00	1.00	1.00	4.00	0.00
QF72F36	0.00	0.01	0.00	4.00	0.00	0.00	0.00	0.00	8.00	0.01	8.00	1.00	1.00	0.01	0.00
QF72F45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
QF72F33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
QF72F32	0.00	2.00	4.00	3.00	0.00	0.00	0.00	0.00	8.00	0.00	8.00	0.01	0.01	2.00	0.01
QF72F35	3.00	2.00	4.00	0.00	5.00	2.00	0.01	0.01	6.00	1.00	6.00	1.00	1.00	0.01	0.00
QF72F35-B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	1.00	1.00	0.01	1.00
QF72F43	1.00	1.00	2.00	3.00	4.00	0.01	4.00	0.01	0.00	0.01	0.00	0.01	0.01	2.00	0.00
QF72F30	0.00	0.00	3.00	0.00	4.00	0.00	0.00	1.00	6.00	1.00	6.00	1.00	1.00	4.00	0.00
QF72F38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00
QF72F31	0.00	0.00	0.00	0.00	5.00	0.01	0.01	0.01	0.00	0.01	0.00	1.00	1.00	2.00	0.00
QF72F12	4.00	0.01	4.00	5.00	5.00	0.01	0.01	1.00	3.00	4.00	3.00	4.00	4.00	0.01	0.00
QF72F10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00	0.01	0.00
QF72F17	0.00	1.00	0.00	0.00	5.00	0.01	0.00	0.00	3.00	0.00	3.00	1.00	1.00	3.00	0.01
QF72F12-B	2.00	0.01	4.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

FILENAME	UI2	SHOVEL	UP1	UC	UC	MESRIDG	METACO	UM2	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	LM2	CUSP5	LM2	LP1
		DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	LCUSPS	PSTYLD	LM2	CUSP5	LM2	LP1	TOMESR		
QF72F18	3.00	1.00	3.00	4.00	5.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	1.00	0.01	0.01	0.00	0.00
QF72F14	4.00	0.01	5.00	5.00	5.00	0.01	0.01	1.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01	1.00	1.00
QF72F22	0.00	1.00	0.00	4.00	2.00	0.01	0.00	1.00	0.00	0.00	0.00	0.00	3.00	0.01	0.01	0.01	0.01
QF72F24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
QF72F25	1.00	2.00	3.00	4.00	5.00	0.01	0.01	1.00	8.00	0.01	0.01	0.01	0.01	0.01	0.01	2.00	2.00
QF72F21	0.00	2.00	0.00	0.00	4.00	0.01	0.00	0.00	5.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	2.00
QF72F26	0.00	0.00	0.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.00	0.00
QF72F15	0.00	0.00	0.00	0.00	4.00	0.00	0.00	0.00	3.00	0.00	0.00	0.01	0.00	0.01	0.01	0.01	0.01
QF72F20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
QF72F23	0.01	2.00	4.00	0.01	3.00	0.01	0.01	0.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01	3.00	3.00
QF72F16	2.00	0.01	3.00	5.00	4.00	0.01	0.01	0.01	0.00	0.01	0.01	0.00	0.00	0.00	0.00	1.00	1.00
QF72F151	0.00	1.00	0.00	4.00	4.00	0.01	0.00	0.00	4.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01
QF72F70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
QF72F64	2.00	2.00	3.00	4.00	5.00	1.00	3.00	1.00	3.00	3.00	1.00	0.01	0.01	0.01	0.01	0.01	0.01
QF72F176	0.00	2.00	0.00	0.00	4.00	2.00	2.00	0.01	0.00	2.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
QF72F57	0.00	1.00	0.00	4.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
QF72F58	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	2.00
QF72F63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01
QF72F178	2.00	2.00	3.00	5.00	4.00	1.00	0.01	0.01	0.01	0.01	0.01	3.00	4.00	3.00	3.00	1.00	1.00
QF72F153	2.00	0.01	4.00	5.00	0.00	0.00	0.00	0.00	5.00	0.00	0.00	2.00	1.00	2.00	2.00	0.01	0.01
QF72F65	4.00	1.00	5.00	5.00	5.00	0.01	0.01	0.00	7.00	0.01	0.01	4.00	3.00	4.00	4.00	0.01	0.01
QF72F59	0.00	0.01	0.00	4.00	5.00	0.01	0.00	0.00	4.00	0.00	0.00	0.01	0.01	0.01	0.01	1.00	1.00
QF72F106	0.00	2.00	0.00	4.00	5.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
QF72F175	2.00	2.00	4.00	4.00	4.00	0.01	0.00	0.01	7.00	0.01	0.01	0.01	1.00	0.01	0.01	0.01	0.01
QF72F150	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
QF72F152	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	1.00	0.01	0.01	0.00	0.00
QF72F177	0.00	2.00	4.00	4.00	4.00	3.00	0.00	0.00	3.00	0.00	0.00	0.01	1.00	0.01	5.00	2.00	2.00
QF72F155	4.00	1.00	4.00	4.00	4.00	0.01	0.00	0.01	4.00	0.00	0.01	0.01	1.00	0.01	0.01	3.00	3.00
QF72F179	1.00	1.00	4.00	5.00	5.00	2.00	1.00	0.01	3.00	1.00	0.01	0.01	1.00	0.01	0.01	3.00	3.00
QF72F5171	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
QF72F74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
QF72F3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

FILENAME	UI2	UP1	UC	UC	MESRIDG	METACO	CUSP5	UM2	CARABL	PARAST	LCUSPS	PSTYLD	LM2	CUSP5	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	UM2	CARABL	PARAST	LCUSPS	PSTYLD	LM2	CUSP5	LM2	LP1	TOMESR
QF72F88	0.01	1.00	0.01	4.00	4.00	0.01	4.00	7.00	0.01	2.00	2.00	2.00	0.01	2.00	1.00	
QF72F55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	0.00	0.00	3.00	
QF72F56	1.00	2.00	4.00	5.00	4.00	0.01	4.00	4.00	1.00	9.00	3.00	3.00	4.00	0.01	0.01	
QF72F78	0.00	0.00	0.00	0.00	4.00	0.01	4.00	0.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	
QF72F73	2.00	2.00	4.00	4.00	4.00	0.01	4.00	0.00	1.00	3.00	0.00	0.00	0.01	0.01	1.00	
QF72F57-B	0.00	1.00	0.00	5.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	
QF72F170	0.00	2.00	0.00	0.00	4.00	2.00	4.00	1.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	
QF72F67	4.00	0.00	5.00	0.00	4.00	0.00	4.00	0.00	0.00	4.00	0.00	0.00	0.00	0.00	3.00	
DBP53	0.00	0.00	0.00	0.00	3.00	0.01	3.00	2.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	
DBP31	3.00	2.00	5.00	2.00	4.00	0.01	4.00	0.00	0.01	7.00	1.00	1.00	0.01	1.00	1.00	
DBP51	3.00	2.00	4.00	2.00	3.00	0.01	3.00	0.01	0.00	0.01	1.00	1.00	5.00	0.01	0.01	
DBP10	0.00	1.00	4.00	0.01	3.00	1.00	3.00	0.01	0.00	3.00	0.01	0.01	0.01	0.01	0.01	
DBP6	3.00	1.00	3.00	2.00	0.00	0.00	0.00	0.00	1.00	4.00	0.00	0.00	0.01	0.01	0.01	
DBP36	0.00	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	0.01	0.01	0.01	
DBP102	0.01	0.00	0.00	0.00	4.00	0.01	4.00	2.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	
DBP107	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	0.00	0.00	0.01	0.01	2.00	
DBP73	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	
DBP64	0.00	1.00	0.00	0.00	4.00	0.01	4.00	0.00	2.00	3.00	1.00	1.00	0.01	0.01	1.00	
DBP106	0.00	1.00	3.00	2.00	3.00	0.01	3.00	0.01	0.01	3.00	0.01	0.01	3.00	0.01	0.01	
DBP59	2.00	2.00	0.00	0.00	4.00	2.00	4.00	3.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
DBP19	1.00	1.00	4.00	2.00	4.00	0.01	4.00	0.01	0.01	3.00	1.00	1.00	2.00	2.00	2.00	
DBP4	3.00	2.00	5.00	0.01	3.00	0.01	3.00	3.00	3.00	6.00	1.00	1.00	4.00	4.00	1.00	
DBP122	0.00	2.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	
DBP11	0.01	2.00	4.00	0.01	4.00	0.01	4.00	0.00	0.00	3.00	0.00	0.00	0.00	0.00	0.00	
DBP110	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.00	0.00	0.00	0.00	0.00	3.00	
DBP95	2.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	0.00	0.00	1.00	
DBP111	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	2.00	2.00	0.01	
DBP108	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	0.00	0.00	0.01	
DBP153	3.00	0.01	4.00	0.01	3.00	0.01	3.00	0.01	0.01	4.00	0.01	0.01	0.01	0.01	0.01	
DBP152	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	
DBP101	0.00	0.01	0.00	0.00	4.00	0.01	4.00	0.01	0.00	0.01	0.00	0.00	0.01	0.01	0.01	
DBP67	1.00	0.00	3.00	0.01	4.00	0.01	4.00	1.00	0.01	0.00	0.00	0.00	0.01	0.01	0.00	

FILENAME	UI2	UP1	UC	UC	UM2	UM2	UM2	UM2	UM2	UM1	LP2	LM2	LM2	LM2	LP1
	SHOVEL	DSHOVE	TDENT	MESRIDG	METACO	CUSP5	CARABL	PARAST	PARAST	LCUSPS	PSTYLD	CUSP5	TOMESR		
DBP32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00
DBP33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00
DBP131	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
DBP22	4.00	2.00	0.01	0.01	5.00	1.00	0.01	0.01	0.01	0.01	0.01	0.01	1.00	0.01	1.00
DBP47	1.00	0.01	4.00	1.00	3.00	0.01	2.00	0.01	0.01	0.00	0.01	0.01	2.00	0.01	0.00
DBP48	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.01	0.01
DBP30	1.00	0.01	5.00	0.01	4.00	3.00	5.00	0.01	0.01	0.01	8.00	2.00	3.00	4.00	4.00
DBP126	0.01	2.00	4.00	0.01	4.00	1.00	0.01	0.01	0.01	0.01	3.00	0.01	3.00	3.00	3.00
DBP18	3.00	1.00	2.00	0.01	4.00	0.01	2.00	0.01	0.01	0.01	4.00	5.00	0.01	0.01	0.01

6.10 APPENDIX X INDIVIDUALS USED IN INDIVIDUAL LEVEL STATISTICS AND SCORES FROM MULTIDIMENSIONAL SCALING (MDS)

individual	dimension1	dimension2	individual	dimension1	dimension2
BERWC61	4.3979	-2.9028	BRD4675	2.7462	-0.4257
BERWC125	-0.7509	-0.0257	BRD3113	-0.7160	0.7410
BERWC5	0.0934	1.9126	IKLA47#22	-2.2027	3.1246
BERWC91	2.3996	2.7497	IKLA42#25	-1.0711	-0.2592
BERWC150/1	-1.0321	3.0175	IKLA117#38	2.4667	-0.0077
BERWC4	-1.1934	0.0130	IKLA13#7	0.8691	2.4155
BERWC147	3.3767	3.2172	IKLA97#1	1.4164	1.6945
BERWC82	0.9768	1.7584	IKLA141#8	1.2079	1.9228
BERWC107-1	-0.5216	0.2138	IKLA75#33	-0.0954	0.2200
BERWC8	0.9706	2.6707	IKLA11#5	0.9403	-0.7077
BERWC127	6.7813	0.8185	IKLA79#35	0.6194	2.2964
BERWC108	0.3116	1.2315	IKL0630672	-1.3285	1.0813
BERWC18	5.1766	0.7367	IKL0630618	5.5201	-2.4649
BERWC73	-1.8971	0.6036	1971293-A	-0.7629	-0.4395
BERWC73-B	-2.6811	1.8859	1970179	-1.8508	-1.0126
BERWC72	-2.3894	3.4396	1970181	-1.8163	-2.0536
BERWC29	2.2632	2.2546	1971212	-1.5696	-0.8052
BERWC141-1	1.5059	1.8005	1970232	-0.0025	0.8557
BERWC102	-0.3572	1.0106	1971349	-2.9264	0.7730
BERWC34	3.3643	0.6037	1970243	1.1534	2.5511
BERWC58	-0.3397	1.9784	1970228	0.6628	0.1377
BERWC35	-1.3703	-0.8480	1971332	0.5599	-0.9471
BERWC152	0.5740	2.9236	1972352	-0.8985	0.1790
BERWC3	1.3890	-1.2438	1972220	0.4421	1.1202
BERWC15	0.9407	1.6169	1972358	-0.1632	1.1729
BERWC57	-0.3270	-0.7249	1971315	0.6402	1.5844
BERWC67	0.3177	3.2514	1971203	-0.9443	-0.5766
BRD3098	2.1485	-0.7100	1970222	-3.7059	1.5100
BRD3073	1.9376	0.9947	1970226	-1.2968	0.2443
BRD3083	-1.5663	-0.2431	1970893	-1.2814	-0.9012
BRD3093	-3.0597	2.4442	1969130	-1.9858	-0.9350
BRD4558	-0.7731	-1.1509	196875	-1.2408	0.7147
BRD4580	-1.8768	0.4429	1971204	3.0860	-2.4696
BRD4587	-1.2994	0.8552	196889	-0.0704	0.3188
BRD1555	-0.2448	1.6516	196739	0.9127	0.4966
BRD0187	-0.8090	0.8365	196888	0.5877	0.2416
BRD1849	-0.0496	0.3668	1969104	-1.1227	-1.2355
BRD1656	3.0502	-3.0606	1971297-B	2.6708	-0.8952
BRD1708	3.3372	-0.7718	1972219	-0.6857	-0.6898
BRD1778	0.8750	2.0710	1971340	0.7860	-5.2251
BRD1816	0.7471	1.9463	1971328	-1.1696	-0.0317
BRD1840	-0.0947	1.7822	1971343	1.5052	-0.9475
BRD1850	0.5038	0.2104	196890	2.9980	1.2312
BRD1897	2.2678	0.4368	1969114	-0.5939	-1.0622
BRD4022	-0.7273	0.3465	196735	-0.7138	0.0921
BRD4021	0.5800	0.4591	196848	-0.0238	1.0592
BRD1406	1.3330	1.3302	1971193-B	-0.1538	1.2724
BRD1497	-0.0923	2.2206	1971304-A	1.8488	-1.0235
BRD1541	7.6079	0.5413	196857	5.1603	1.3376
BRD1553	6.4868	1.6629	196853	1.3584	0.8142
BRD4853	-0.0353	2.3262	1970191	-1.5654	0.2956
BRD3135	0.2612	0.4843	196716	-1.6537	0.9235
BRD3116	-0.9028	1.1937	196874	-3.9003	-0.0984
BRD4738	1.9717	2.1650	196720	-0.4292	0.5919

individual	dimension1	dimension2
196850	-2.3187	2.2911
196861	2.1104	-0.4991
1970194	-0.7199	0.5447
196858	4.7534	0.0407
1971308-BI	-1.0765	0.4658
196887	-2.1404	-1.2363
1971201	-0.6783	0.2131
196738	-0.3147	0.9905
1969110	-1.2338	-0.5870
1969112	1.2418	2.5258
196719	-4.6146	-0.8077
1969109	1.1877	-0.4201
1971291	-2.1959	0.3052
196737	0.4236	2.1215
1970250	0.9335	1.3503
1971171	0.0852	0.6826
1972377	1.0157	2.6120
1972438	-2.8153	2.5367
1969119	1.7608	-2.2438
1972444	-0.7275	0.6303
1972368	2.1812	-0.2964
1972388-A	-3.5270	1.9182
1972430	-0.7870	0.9408
1969126	-0.6479	1.2629
1972428	1.7183	0.0736
1970266	-1.7912	-0.1474
1969125	1.3749	-1.9844
1969117	0.9752	1.1639
1972415	-0.3955	-0.5024
1972412	-2.1412	2.7607
1972427	-0.6453	2.6119
1969161	-0.5653	0.9603
1972397	0.3678	0.9630
1972395	-2.6181	2.2408
1969129	-1.6380	-0.3192
1972443	1.3444	1.8441
1969161-B	-0.4425	1.2717
1972374	-3.2230	2.0256
1970270	-0.9134	-0.1214
1972365	1.9493	-1.2313
1970175	1.3388	-1.1024
1972414	1.0320	1.8220
1969131	-1.1436	0.1598
1970260	-1.2735	0.4693
1967133	-2.2187	2.5675
1969140	-0.0512	0.3406
196718	-1.2814	-0.9012
LBF852	-4.2111	-0.6526
LBF8557	-1.8289	-0.1965
LBF851/1	-0.2321	-1.9990
LBF8510	-1.6681	-1.8870
LBF851161	-2.5174	-1.2175
LBF8511081	1.2821	-0.4000
LBF851086	-1.5044	-0.1773
LBF851035	-2.8579	-2.8686
LBF851054	-1.6485	1.6489
LBF851213	-1.9607	-0.0560
LBF851207	2.3327	-4.1498
LBF851184	1.6750	0.3951
LBF851197	-0.5894	1.4445
LBF851189	-2.1431	-0.0797
LBF851182	-3.1828	-1.6643

individual	dimension1	dimension2
LBF851178	-3.0280	-2.6341
LBF851168	-3.5426	1.2761
LBF851166	-2.3712	-2.3133
LBF851133	-3.0455	-2.7851
LBF851130	-1.8525	0.5163
LBF851134	0.0955	0.1613
LBF8511322	-3.2152	1.6440
LBF851135	-0.5289	-1.5083
LBF8511401	-2.1631	-2.0865
LBF851129	-0.0275	0.2498
LBF851128	-0.1795	-4.8084
LBF851121	-2.6342	-1.1699
LBF851125	-4.6926	0.0908
LBF851110	1.7229	-1.2503
LBF851109	4.3056	-4.5705
LBF851092	-2.1507	-1.6299
LBF851099	3.5663	-4.1468
LBF851067	1.0468	-2.0671
LBF851072	-1.9050	0.6127
LBF851088	-2.0649	-2.1492
LBF851082	-1.8380	0.3743
LBF851085	0.5872	1.7541
LBF851059	-3.3805	-2.8764
LBF851077	-0.7028	-0.8859
LBF851076	-2.0106	-0.2830
LBF851060	-2.6638	-1.5099
LBF8510631	-0.4655	0.6066
LBF851047	1.3868	-2.0534
LBF8510482	-2.0081	-0.2427
LBF851041	1.1103	-3.6666
LBF851023	-0.8104	-0.0898
LBF851037	3.0581	-5.9071
LBF851026	0.1727	-4.6104
LBF851046	-4.9271	-1.8933
LBF851008	0.6907	1.8472
LBF851104	-0.2325	-1.1926
LBF851016	-0.3461	0.0002
LBF851018	-1.2946	-0.7962
LBF851020	-1.7474	0.1249
LBF851001	0.4356	-0.1691
LBF851002	-1.9511	-1.9318
LBF8510064	-0.7211	0.0757
LBF85181	-2.5099	-2.1646
LBF85191	-3.3088	-1.4497
LBF85158	-1.2714	-2.6599
LBF85179	-0.5298	-4.0806
LBF85171	-1.7910	-1.4758
LBF85143	-0.1984	0.3182
LBF85149	-0.6289	-1.3673
LBF85145	-1.5936	0.4954
LBF851562	-3.1418	-3.1501
LBF851561	-2.2757	-1.1431
LBF851401	-0.7047	-1.8233
LBF85135	-0.6006	-0.7022
LBF85132	-4.0694	-0.2980
LBF85112	-0.5588	-0.1588
LBF85113	-2.8825	-0.9559
LBF85128	-0.7854	0.1614
LBF85126	-2.1656	-2.5831
LBF85131	-1.7943	-0.7111
LBF85107	-0.0014	-2.5927
LBF85110	-1.5361	0.4375

individual	dimension1	dimension2	individual	dimension1	dimension2
LBF8592	0.5269	-3.7225	PWWF7	1.6570	1.7514
LBF8593	-0.9678	0.1162	QF72F4	-0.2478	2.5170
LBF8586	1.7216	-1.0818	QF72F2	-0.4032	0.4018
LBF8578	-4.9013	-1.1372	QF72F7	-0.1634	-1.5785
LBF8574	-1.4056	0.2910	QF72F39	1.8270	2.3434
LBF8585	1.5159	-3.5229	QF72F35	2.2098	-0.7938
LBF8560	-0.7195	-1.0815	QF72F43	0.9040	-0.2458
LBF8517	-3.2680	-2.1408	QF72F12	0.5070	2.1688
LBF8518	1.3275	-3.7807	QF72F18	-0.0152	0.3964
LBF8550	-1.2820	-2.4029	QF72F14	-0.2926	1.8452
PWE32	7.3911	1.5796	QF72F25	2.5619	-2.7482
PWE63	2.5625	3.0182	QF72F23	-1.7281	-2.1650
PWE40	1.1360	-1.7932	QF72F64	0.4458	1.4654
PWE60	1.1176	2.9158	QF72F178	-1.4219	3.2195
PWE61	2.5361	0.6124	QF72F65	4.9383	0.6957
PWE62	4.0396	0.4722	QF72F175	3.1576	-0.7813
PWE17	-0.3865	-1.1638	QF72F177	1.8934	1.4387
PWE16	0.8896	2.1671	QF72F155	0.9176	0.8967
PWE19	-1.2252	0.5965	QF72F179	0.5065	1.4200
PWE54	2.2640	1.8540	QF72F88	0.1698	1.3350
PWE56	0.0458	0.8433	QF72F56	6.6609	-0.8400
PWE58	0.0479	-1.6042	QF72F73	-0.0583	1.2403
PWE67	-0.4301	0.7612	DBP31	3.0018	-1.4229
PWE1	-1.2289	-0.9415	DBP51	-1.5103	2.0723
PWE43	-0.5924	1.4415	DBP10	-1.9054	-1.8697
PWE42	2.0666	-0.7065	DBP106	-0.6869	-0.8071
PWE5	0.1413	1.4283	DBP59	-2.3093	2.4452
PWE4	-0.4276	0.8099	DBP19	-0.3587	-0.5126
PWE15	1.1973	2.2142	DBP4	4.1406	-1.1796
PWE51	1.3655	1.7757	DBP153	-0.8318	-2.0916
PWW1	1.0242	1.6220	DBP22	-4.1795	-0.4552
PWE29	4.0281	-1.5113	DBP47	0.1088	-1.4673
PWW7	4.5357	-1.2795	DBP30	5.9645	-2.9112
PWE49	2.3064	-1.0427	DBP126	-0.5257	-1.8290
PWWF3	6.6986	-0.1003	DBP18	0.1139	-1.5663
PWW3	3.9027	0.2881			
PWWF1	1.6956	-1.4262			