missing keratin preservation in bog and other anaerobic environments, simply because we do not alert the excavators to the possibility of hair, hoof and horn at some sites. This fact has been driven home to me recently, not only by the bog body experience, but also by an Orkney peat cutter noting hair and indeed handing over to Keith Dobney parts of a sheep (leg pieces only). As aspects of the chemistry of nutrition are locked up in keratin as well as bone, we may thus be missing out on valuable analytical material.

The second taphonomic topic I want briefly to mention is that of insect damage to bone. My previous experience of this has been limited to damage on bones from Nubia and the island of Socotra, the latter case apparently being the result of ants. Others have been aware of potential insect damage, but there is still not enough recognition of the fact that such species might differentially eliminate bone. But this isn't the only problem. The question I want to ask here is, can we yet recognize different kinds of insect damage? The example I want to give is of Roman chicken bones from Uley, Somerset, U.K. Of the large sample of *Gallus*, many displayed well defined tracking across the bones (Fig. 9) and in some instances this had led to fragility, breakage or collapse of the bone.

Because initially I had suspected root damage as the cause, a simple experiment was carried out with the body of a dead cat which I had just buried. Directly over and onto the corpse, I seeded various plants with a view to encouraging roots to 'etch' into the bone. While such experimenting is limited and inadequate, it was not possible to set up a more rigorous experiment at the time with multiple chicken corpses seeded with a wide range of plant species! On excavation, the cat skeleton was found to be covered in large and fine-meshed roots. While the bone surface was damaged and eroded, the destruction did not simulate the distinctive narrow channelling as on the Roman bones. In form (Fig. 10), the damage to Roman bone is remarkably similar to that caused to wood by engraver and bark beetles (Scolytidae). So could it be beetle damage, say by dermestids? As far as I can ascertain, dermestids remove un-mineralised tissue but do not damage bone? Do any of my colleagues know otherwise?

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On using *Bonerec*: Bruce Levitan's computer recording program

Summary

Bonerec is a bone recording program based on dBASE III PLUS. It is easy to set up and use, and has a manual. Records are made onto four, linked files: the main record (context, species, etc.), measurements, age data and comments. There is validation, a supporting macro, and a method for ordering the records. Analytical programs have been written for listing by species and by context, and for summarising.

Introduction

When Bruce Levitan worked at Bristol City Museum, he used the Ancient Monuments Laboratory bone recording system. When he moved to Oxford University Museum and had access to an IBM-compatible PC, he decided to write his own recording system based on the most widely used commercial database program, which at that time was dBASE III PLUS. Bonerec was developed during his time at Oxford. Bruce having now left archaeology (to work with computers in the Health Service), it seemed important that information about the program be presented; it is a large piece of work, with a manual of 82 pages and a program and related files of similar length. There are aspects which could be altered and improved, but this author has found it easy and reliable to use, and it has many useful, time-saving and well-thought-out features. Others may want to use it, or use parts of it (for example, the species and anatomy codes) or ideas from it.

Getting started

The program requires dBASE III PLUS to run it (it is not compatible with dBASE IV), and a computer with a hard disk and at least 640K RAM. Help is given in the manual about how to set up the dBASE and Bonerec directories, and the DOS AUTOEXEC.BAT file. The user then types 'bones', and the setting up is done through a series of questions:

'Are you using a colour monitor?'

'Do you wish to read the directory set-up and information screens?'

'Do you wish to use a new sub-directory?' (If so, there are questions and information about doing so, and if not there is a prompt for entering the sub-directory needed, and if you've forgotten its name, a listing may be requested.)

'Do you wish to use the validation procedure?' (If used, only valid entries for species, anatomy and zone will be accepted; if 'No' is answered, you are free to use these three fields as you like).

This is followed by a menu screen, with the choices:

1 - CREATE NEW SITE FILE (see below)

2 - USE EXISTING SITE FILE (You will be given a modified version of 1, including a list of existing files.)

3 - BACKUP SITE FILES (You are talked through copying files, in dBASE or comma delimited format.)

4 - PROGRAM INFORMATION (The information screens are useful both for bone recording and for computer learning.)

0 - EXIT

Assuming you have chosen 1 above, you will be given help in naming the four files needed, a list of existing files (if any) and will be asked:

'Which main file do you wish to use?'

'Which measurement file do you wish to use?'

'Which ageing file do you wish to use?'

'Which comments file do you wish to use?'

and then, 'Do you wish to modify number sequencing?' (of which, more later).

This is followed by the main BONE RECORDS MENU:

1 - Information about the system

2 - Append records to existing file

3 - Edit records (This uses dBASE's EDIT function with a screen form which shows all the fields on one screen.)

4 - Renumber records

5 - Display records on screen (dBASE BROWSE)

6 - Locate for specified characters (a search facility)

7 - Add new taxon/anatomy codes

0 - Exit

Of these, the user will usually want to choose **2**: append new records.

Bone recording

Having chosen **2** above, the Context screen will appear, in which the context number should be entered and four other references may be entered, e.g. feature, feature type, phase, small find number. On pressing the key <PgDn> (page down), the main Bone Recording Form will appear (Fig. 11). Here, it is filled in to show the context information already entered, and one, complete, left sheep or goat radius. In the lower half of the screen, 'Yes' has been entered for 'Measured', 'Age', 'Butchery' and 'Comment'.

On pressing <PgDn>, the program will check that the entries for species, anatomy and zone are valid ones (if not, help may be requested). It will note whether 'Yes' has been answered to any or all of 'Measured', 'Age' or 'Comments'. In this case (Fig. 11), all three have been flagged, and the following screens will be shown: a measurements information screen giving a suggested measurement list for the common species; a measurement entry screen (up to 14 measurements per bone); an epiphysial fusion screen (if a long bone; or, if

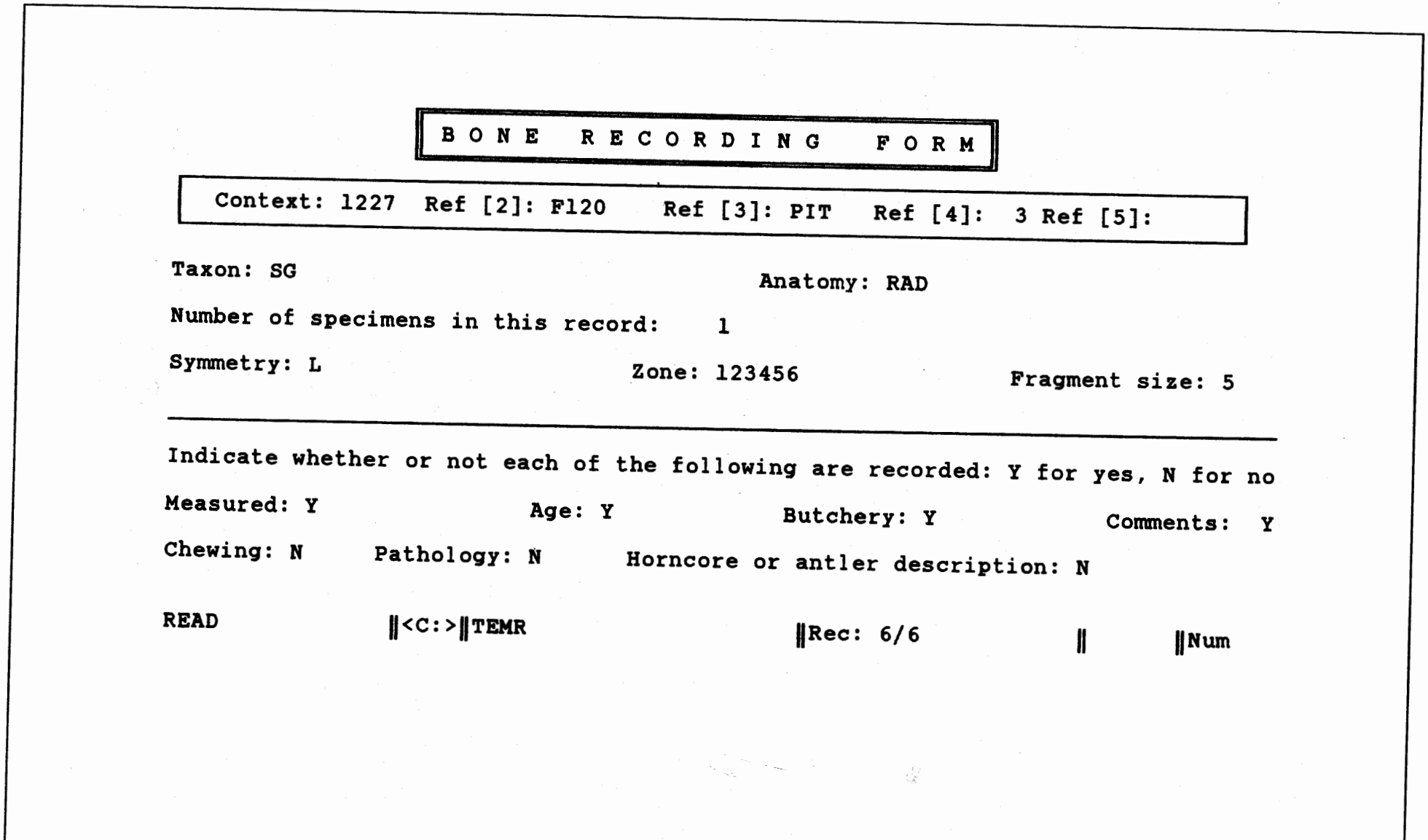

Figure 11. The main bone recording form for Bonerec.

a tooth or mandible, two screens, for recording teeth using Payne's (1973; 1987) and/or Grant's (1982) method(s)); and a comments screen, which will take up to three lines, each of 60 characters. This is followed by:

'Do you wish to keep the same context?'

If so, there is no need to repeat the context entries, and a new Bone Recording Form is presented.

Species and anatomy are recorded using abbreviations. The recording method for the zone field is defined in the manual, but can be changed to suit the user (the field is seven characters wide). The fragment size field is a modified Ancient Monuments Laboratory coding (1: <25% complete; 2: 25–49%; 3: 50–74%; 4: 75–99%; 5: 100% complete). This field is not validated and any four characters could be entered.

The program is supported by a macro (Superkey, a commercial macro program), so that, for example, in normal use the entries needed in the above 'Getting started' section will all be done by pressing F1 and then F2; and the common species and parts of the anatomy will be entered using 'hot keys', the control key for species and the alt key for anatomy, e.g. <Ctrl>p for PIG and <Alt>f for FEM (femur). The macro does not have to be used, but it saves time.

Editing is straightforward for most fields, but where a species, anatomy or zone is changed, some knowledge of the system is required since the species, anatomy and zone order numbers will also require editing (see below). And where 'No' has been incorrectly recorded for 'Measured', 'Age' or 'Comments', as the program stands at present some knowledge of dBASE is necessary: the record file has to altered to 'Yes' (easy); and, using dBASE III PLUS, a record needs to be appended in the Measurement, Ageing or Comments file showing the specimen number and data required. In practice, I chose to do most editing using dBASE rather than Bonerec's edit options, but this was out of an intention to maintain and extend my familiarity with dBASE. It is possible to use Bonerec with only a limited knowledge of dBASE itself, but clearly the greater one's knowledge, the more one is in control.

Structure

The program was designed to be easy to use and to be as flexible as possible within the limitations of a very structured database. The use of four files saves space: where no measurements are taken, no empty fields are stored; and-similarly—for the age data and comments. Conversely, where there is a comment to make there is sufficient space. The file structure is shown in Appendix 1. The fields in the Main Record File are identical with those seen in Fig. 11, with the exception of no. 18, SPEC_NO, and nos. 20–22, SPORDER, ANORDER and ZORDER.

The SPEC_NO (specimen number) is added by the program to the Main Record file. When 'Yes' has been entered for 'Measured', this number will also be written to the Measurements file, thus providing a link between the files. The SPEC_NO can be started at any numeral. The question 'Do you wish to modify number sequencing?' when setting up a new set of files, allows the user to start the new set at a higher number than the last number of the previous set. This will prevent duplication of specimen numbers when, for example, a new set of files are used for a new phase—a useful feature.

At the point where <PgDn> is pressed on completing the Bone Recording Form, the species, anatomy and zone entries are checked against three databases. At the same time, three numerical codes for the entries are written to the SPORDER (species order), ANORDER (anatomy order) and ZORDER (zone order) fields, which allow the records to be put in order. Extracts from the three databases are shown in Appendix 2. The lists probably cover most of the species and anatomical parts needed; 254 species of mammals, birds and fish, and 219 anatomical parts (for mammals, birds and fish) are listed. Where new species, bones or zones are required, this is easily done by altering the relevant databases, which are independant of the program itself. A likely situation for wishing to add new codes is for either/or categories, e.g. RED/FAL could be added, with a number between Fallow deer and Deer. [These databases could be used as adjuncts to other computer recording systems].

This author has not so far altered BL's program. Several improvements could be made, and this is not in principle difficult. The

program is not compiled, and is clearly set out, with titles and explanations.

Listing and summarising

Bonerec is a bone recording and not an analytical program. (BL intended to tackle the analytical side at a later date.) Records made using Bonerec are ordinary dBASE files, which can be manipulated in dBASE III PLUS or dBASE IV, or read by other programs, e.g. Paradox, SuperCalc5. BL wrote some programs, for example, a search facility (see **6** of the Bone Records Menu) and a program for totalling species and showing percentages.

This author's first requirement, on having recorded a bone assemblage, was to have a sensible, ordered copy of everything which had been entered, on A4/21 cm-wide paper, both to browse through and to be the bone archive. This necessitated learning some dBASE programming, and BL's help in doing this is acknowledged. (De Pace's 'dBASE III PLUS' (1987) has proved useful). A brief description of the work done is given. At present these programs are not user friendly, but the variables (path, file names, titles) are clearly marked in the programs.

List by species. The records are ordered by species, anatomy, symmetry and zone. The site name, phase and column headings are shown at the top of each page; the species sub-titles are shown in full ('Horse' not 'HOR', 'Large unidentified mammal' not 'LAR') and the total for each species is given. It proved possible to get most of the information recorded onto a single line per record: context, other references, specimen number, N, anatomy, zone, fragment state, fusion (from the Age file), an abbreviation (M A B Ch P) where 'Yes' had been flagged (to Measured, Ageing, Butchery, Chewing or Pathology) and the Comments (running onto a second or third line where necessary). There is an option to start each new species on a new page.

List by context: a similar list of all the records, but by context, and showing totals for each context and sub-totals for each species within the context. This could be used to print out particular context(s), for example at the end of a recording session. (It had been decided that computer recording should replace not duplicate a manuscript record).

Measurements and tooth data. These are shown separately, but repeat relevant data, e.g. the measurements list shows the context, specimen number, fusion and zone data, and a 'c' if a comment was made.

Anatomical analysis. This is a detailed anatomical analysis showing for each bone of each species: total number of bones, number classed as fragments, the total for each individual zone for the left, right and left+right sides, the total number of zones per bone and the average number of zones present.

Any of the above can be used to show particular groups, e.g. the pathological bones, a given area, building, type of feature, or group of contexts. It has been useful, while writing up a site, to be able quickly to print out a detailed anatomical analysis of, for example, an important group of post-holes, and see species and anatomy totals, minimum numbers, zone totals and numbers classed as fragments; and to be able to refer to the context printout for the primary record and comments made.

A number of other programs have been written, for example: to remind me how to index the main record file; to test whether the species, anatomy and zone entries match correctly their respective numerical codes (a mismatch can occur for example where the species has been edited but the SPORDER field left unchanged); and to join two sets of files.

Access

The Bonerec program is available free from the author (address below) at the time of publication. Users should send a formatted 5¼" or 3½" disk (IBM-compatible, with at least 650k space) which will be returned with BL's Bonerec and GJ's Boneanal files loaded. A copy of the manual can be supplied on disk or a paper copy may be borrowed and freely photocopied. A copy of dBASE III PLUS is essential (current price *c.* £395 + VAT) and a copy of Superkey is recommended (current price *c.* £65 + VAT).

Acknowledgement

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Appendix 1. Bonerec files structure

Main record file

	Field name	Type	Width
1	SPECIES	C	6
2	ANATOMY	C	6
3	NO_SPEC	N	4
4	CONTEXT	N	4
5	REF2	C	6
6	REF3	C	4
7	REF4	N	2
8	REF5	N	4
9	SYMMETRY	C	3
10	ZONE	C	7
11	FRAG_STATE	C	4
12	MEASURED	L	1
13	BUTCHERED	L	1
14	PATHOLOGY	L	1
15	CHEWING	L	1
16	AGEING	L	1
17	HC_ANTLERS	L	1
18	SPEC_NO	N	6
19	COMMENT	L	1
20	SPORDER	N	7,3
21	ANORDER	N	7,3
22	ZORDER	N	6,2
Total			84

Measurements file

	Field name	Type	Width
1	SPEC_NO	N	6
2	MEAS1	N	5
3	MEAS2	N	5
and so on to:			
15	MEAS14	N	5
Total			77

Ageing file

	Field name	Type	Width
1	SPEC_NO	N	6
2	PROX	C	2
3	DIST	C	2
4	PDP4 (Payne dp_4)	C	3
5	PP4	C	3
6	PM1	C	3
7	PM2	C	3
8	PM3	C	3
9	GDP4 (Grant dp_4)	C	1
10	GP4	C	1
11	GM1	C	1
12	GM2	C	1
13	GM3	C	1
Total			31

Comments file

	Field name	Type	Width
1	SPEC_NO	N	6
2	COM1	C	60
3	COM2	C	60
4	COM3	C	60
Total			185

Notes: C—character, N—numeric, L—logical; ',3'—to 3 decimal places.

Appendix 2. Examples of the species, anatomy and zone abbreviations and codes used in the bonerec program

Taxon codes and names

Code number	Taxon code	Full name
Common mammalian taxa (archaeological order)		
1.000	COW	Cattle
2.000	SHE	Sheep
2.010	GOA	Goat
2.020	SG	Sheep/Goat
3.000	PIG	Pig
4.000	HOR	Horse
4.010	DON	Donkey
5.000	DOG	Dog
6.000	CAT	Cat
7.000	DRAB	Rabbit (domestic)
10.000	RED	Red deer
10.010	ROE	Roe deer
10.020	FAL	Fallow deer
10.990	DEER	Deer
Other mammalian taxa (taxonomic order)		
100.000	HEDG	Hedgehog
101.000	MOLE	Mole
102.000	CSHREW	Common shrew
102.010	PSHREW	Pygmy shrew
102.030	WSHREW	Water shrew
102.990	SHREW	Shrew

... and so on.

Anatomy codes and names

Code number	Anatomy code	Full name
9.000	ATLAS	atlas
9.100	AXIS	axis
9.200	CERV	cervical vertebra
10.000	THOR	thoracic vertebra
11.000	LUMB	lumbar vertebra
12.000	SAC	sacrum
13.000	CAUD	caudal vertebra
13.500	PGS	pygostyle
14.000	VERT	vertebra
15.000	RIB	rib
15.100	CC	costal cartilage
15.200	RAY	fin-ray bone
15.300	SPN	spine
15.400	BRANCH	branchiostegal ray
16.000	STERN	sternum
16.500	FUR	furcula
16.700	COR	coracoid
16.800	CLV	clavicle
17.000	BAC	baculum (os penis)
17.100	CLT	cleithrum
18.000	SCP	scapula
19.000	HUM	humerus
20.000	RAD	radius
21.000	ULN	ulna
22.000	CAR	carpal
23.000	MC	metacarpal
23.100	MC1	metacarpal I

Key to zone codes

Zone	Zone number
Long bones and mandible:	
123456	6.01
12345-	6.04
-23456	6.05
1234--	6.09
-2345-	6.11
--3456	6.12
123---	6.13
-234--	6.15
--345-	6.16
---456	6.18
12----	6.19
-23---	6.21
--34--	6.22
---45-	6.23
----56	6.25
1-----	6.27
-2----	6.29
--3---	6.30
---4--	6.31
----5-	6.32
-----6	6.35

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