

# Report on the national archaeobotanical dataset

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## Introduction

This report provides a quantified description of the national archaeobotanical dataset held within the Haystack database (Digital Archive Document A02). It includes references to SQL queries contained within the FeedSax Digital Archive which can be run against Haystack to reproduce the results presented in this report. In order to run these queries, one must first run a ‘foundation’ script (Digital Archive Document B18) which creates temporary tables to support the subsequent analyses.<sup>1</sup>

This foundation script ends with a select query which returns summary attribute data for all samples from a customisable selection of sites or regions. In the present report, the script has been run against the entire dataset, and the results of the terminal select query have been exported and included as Digital Archive Document B08. Note that all of the results and descriptions in this report are based on data belonging to the core periods of the FeedSax project, phases A1–G2 (c. AD 420–1400) (i.e. excluding anything from phases A0 or H), and across all regions unless otherwise stated.

The foundation query incorporates the taxonomic amalgamations listed in the plant taxon metadata (Digital Archive Document B12, third worksheet). The metadata table includes a column, *amalgamateWith*, that determines which other taxon (if any) a given plant identification should be amalgamated with for analytical purposes; ‘umbrella’ taxa (which incorporate other, amalgamated taxa) are sometimes given a name in the *gloss* column which is applied to the collectively amalgamated records. Amalgamations have been applied in three circumstances:

1. For taxa which are typically indistinguishable on the basis of their charred remains, such as *Bromus hordeaceus* and *Bromus secalinus*, or *Euphrasia* and *Odontites*.
2. For families or genera which typically have only one species in the dataset: for example, Malvaceae and *Malva* records have all been amalgamated with *Malva sylvestris*, because there are almost no other *Malva* species identifications in the dataset.
3. For the purposes of specific analyses: for example, amalgamating all barley taxa under *Hordeum* to facilitate analysis of barley crops in general.

These amalgamations are applied in the foundation query and can be altered as necessary. The default amalgamations in the foundation query, as preserved in the archive (Digital Archive Document B18), are the same as those listed in the metadata (Digital Archive Document B12), and notably include ‘convenient’ simplifications of cereal taxa. So, for example, *Avena sativa* and *Avena strigosa* are amalgamated with *Avena* (thus presuming that generic *Avena* identifications most likely represent cultivars), while *Triticum spelta* and *Triticum dicoccum* are amalgamated with ‘*Triticum* sp. hulled’. Of course, these amalgamations should always be configured to best suit the purposes of a given analysis.

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<sup>1</sup> B18\_foundation01\_samples.sql

As detailed further below, there are two more foundation queries which provide the bases for quantitative and semi-quantitative (presence) analyses respectively:

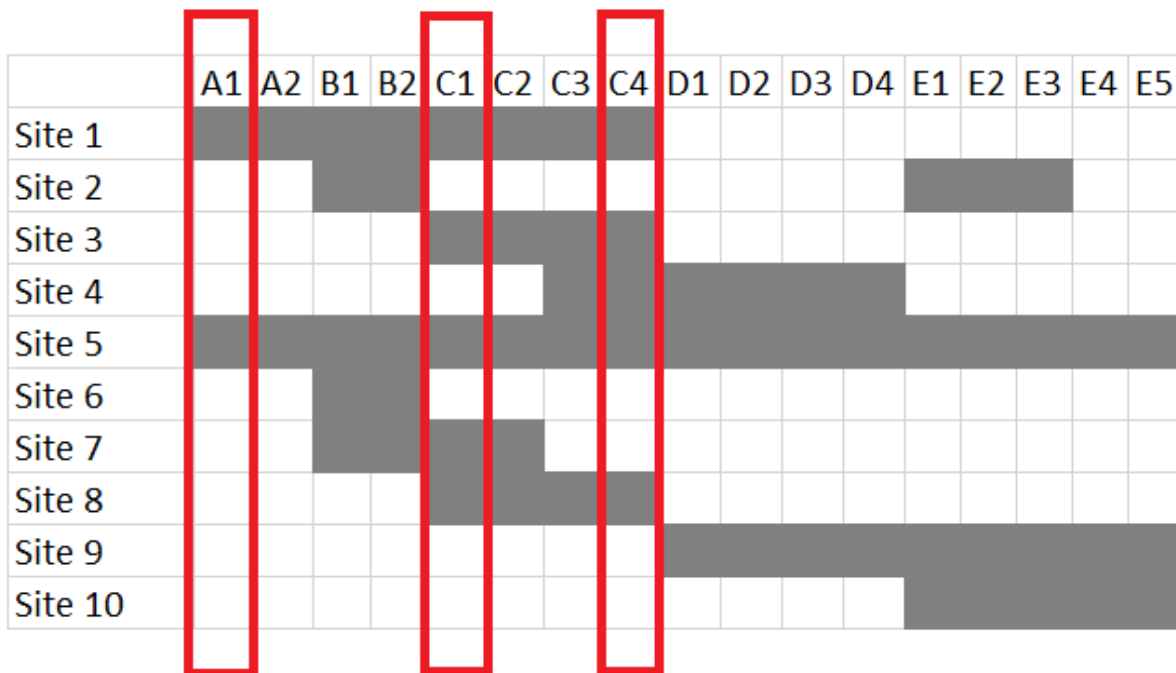
- B19\_foundation02\_quantities.sql
- B20\_foundation03\_presence.sql

### **Sites, samples and chronologies**

The descriptions below refer to archaeobotanical data at site- and sample-level, but not assemblage-level (following the definitions of McKerracher 2019, 15). The latter work defined *assemblages* as collections of samples from a site which belong to the same phase (Early, Intermediate, or Mid Saxon), and used them accordingly as units of analysis. That approach is not so readily applicable to the FeedSax dataset, however, because of its more complex, varied and sometimes overlapping chronologies – all based upon the FeedSax universal chronology (see Hamerow *et al.* forthcoming, Chapter 2).

Given a set of site assemblages phased (for example) ‘C2–C3’, ‘C1–C4’, ‘C3–D4’ and ‘B1–E5’, we could perhaps treat each of these as a separate chronological category, and only compare ‘C2–C3’ assemblages with each other. Such an approach could be misleading, however, as all of the other phase-spans mentioned here could also contain information *potentially* pertaining to C2 and/or C3. Phase-spans like ‘C2–C3’ are thus non-exclusive, unlike the Early, Intermediate and Mid Saxon phases employed by McKerracher (2019). In addition, restricting chronological categories in this rigid way can result in very small – and therefore statistically less useful – sets of assemblages.

The alternative method adopted in the FeedSax analyses is here termed the ‘moving window’ approach, and is intended to maximise the usable data available in Haystack for presence analyses. Figure 1 illustrates the phase-spans represented by a (fictitious but realistic) set of site assemblages: some are short (B1–B2), some are very long (A1–E5), many are overlapping, but none are identical. The red boxes represent examples of the analytical ‘moving windows’ applied in the FeedSax presence analyses. Thus, the analysis for phase A1 here uses data from two site assemblages; but those assemblages have such long chronologies that their data can be used again, independently, in analyses of phases C1, C4, and many others.



**Figure 1 – Illustration of the ‘moving window’ approach to chronological comparison.**

This kind of maximising approach nevertheless has drawbacks. In particular, it is prone to overrepresenting taxa in presence analyses, because a taxon present in a deposit phased A1–E5 will effectively be counted 17 times (i.e. once in each of 17 single-phase analyses), even though the plant remains in question can only truly date from one phase. It must be born in mind, therefore, that the FeedSax presence analyses are biased towards overrepresentation.

In the sections below, it will be made clear whether or not the ‘moving window’ approach is applicable in a given analysis – typically in summarising analyses which necessarily aggregate data from a set of sites/samples with a complex array of phases. Where data are not being aggregated in this way (for instance, where average densities or percentages of wheat grain are being calculated on a sample-by-sample basis), a different reductive approach has sometimes been taken: the application of ‘simple’ phases, to reduce the multitude of different phases which inhibits chronological grouping. Thus, the foundation query (B18\_foundation01\_samples.sql) assigns each sample a fsSimpleSpan value which simply removes the numerals from the normal phase span: so C1–D1 becomes ‘CD’, for example, and C4–E5 becomes ‘CE’. Again, this is not a perfect approach and inevitably involves some loss or simplification of information, but some degree of summarisation is necessary to provide more readable results.

## Outline description

Charred plant remains occur in 4,182 samples at 301 sites.<sup>2</sup> Calculated on a ‘moving window’ basis (see above), and therefore of particular relevance to presence analyses, these sites and samples are distributed chronologically as follows (Table 1).<sup>3</sup> The nature of the ‘moving window’ approach means that the sums of sites/samples in this table far exceed the actual totals of 301 and 4,182 for the dataset as a whole. These results show that the charred plant dataset is biased towards phases C, D and (especially) E.

**Table 1 – Chronological distribution of sites and samples with charred plant remains.**

phase	# sites	# samples
A	27	203
B	35	252
C	126	1215
D	136	1316
E	210	2250
F	121	848
G	51	271
A1	24	197
A2	26	201
B1	30	198
B2	35	252
C1	85	713
C2	103	899
C3	106	880
C4	117	962
D1	116	1005
D2	114	1079
D3	117	1100
D4	114	1056
E1	143	1243
E2	141	1281
E3	175	1617
E4	168	1573
E5	166	1360
F1	120	807
F2	108	722
G1	51	271
G2	34	146

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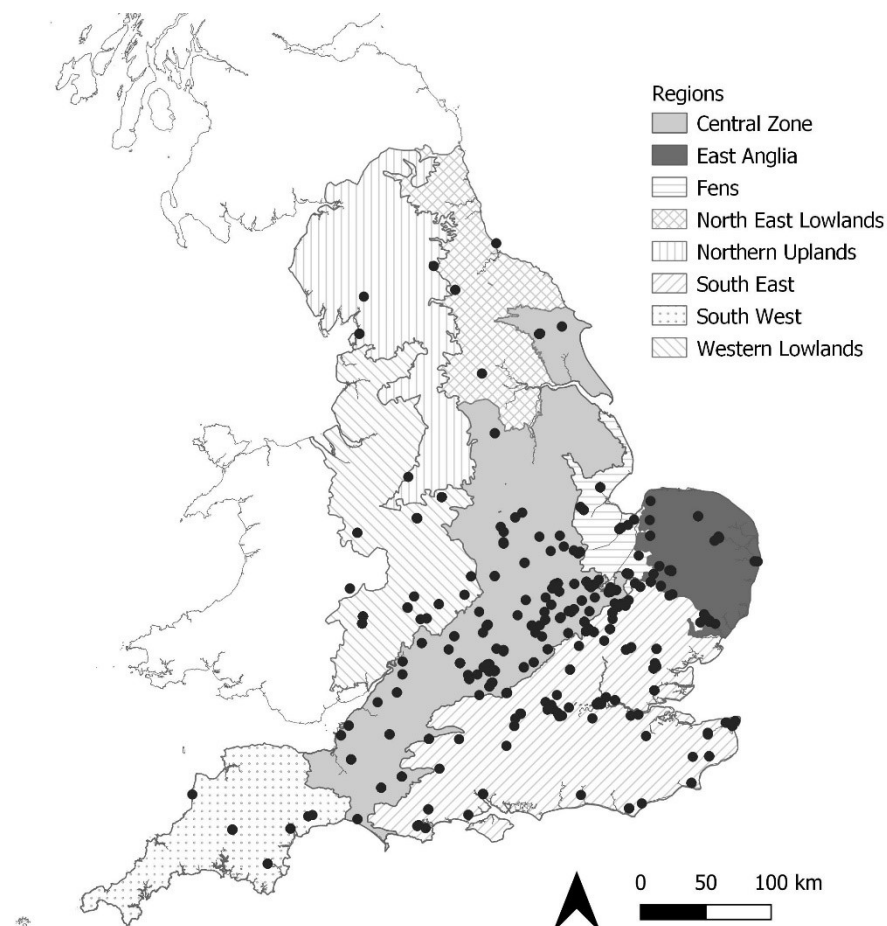
<sup>2</sup> B21\_sitesWithCPR.sql; B22\_samplesWithCPR.sql

<sup>3</sup> B27\_sitesWithCPR\_phase.sql; B28\_samplesWithCPR\_phase.sql

The geographical distributions of the sites and samples, in terms of the regions defined by Rippon *et al.* (2015) and employed by FeedSax, are given in Table 2.<sup>4</sup> The data are also mapped in Figure 2.<sup>5</sup>

**Table 2 – Regional distribution of sites and samples with charred plant remains.**

region	# sites	# samples
Central Zone	122	1286
East Anglia	44	739
Fens	13	304
North East Lowlands	4	44
Northern Uplands	3	20
South East	90	1508
South West	6	95
Western Lowlands	19	186



**Figure 2 – Distribution of sites with charred plant remains.**

<sup>4</sup> B29\_sitesWithCPR\_region.sql; B30\_samplesWithCPR\_region.sql

<sup>5</sup> B31\_sitesWithCPR\_coords.sql

## Quantification and crop dominance

Semi-quantified (presence/abundance) archaeobotanical data – which are usable only in the presence analyses – are available for 23.9% (72) of the sites, and 11.3% (472) of the samples.<sup>6</sup>

Fully quantified archaeobotanical data – which are usable in both semi-quantitative (presence) and quantitative analyses – are available for 85.1% (256) of the sites, and 88.7% (3,710) of the samples.<sup>7</sup> For these fully quantified samples, it is possible to calculate principal means of preservation and dominant crop types (as per McKerracher 2019).

This study is particularly concerned with *charred samples*, meaning those with charring as a principal means of preservation (as opposed to waterlogging or mineral-replacement, for example), i.e. where at least 70% of the quantified botanical items in a sample are preserved by charring. By this definition, there are 2,289 samples, at 223 sites, with charring as a principal means of preservation.<sup>8</sup>

The chronological distribution of these samples is shown in Table 3, using the fsSimpleSpan values rather than the ‘moving window’ approach: a bias towards simple phases C, D, DE, E and EF is revealed. These data can be obtained from Digital Archive Document B08 (representing the results of the foundation query run against the entire dataset, as discussed above). The regional distribution of these *charred samples* is shown in Table 4, revealing a strong bias towards the Central Zone and South East.<sup>9</sup> The sites are mapped in Figure 3.<sup>10</sup>

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<sup>6</sup> B25\_sitesWithCPR\_semiquant.sql; B26\_samplesWithCPR\_semiquant.sql

<sup>7</sup> B23\_sitesWithCPR\_quantitative.sql; B24\_samplesWithCPR\_quantitative.sql

<sup>8</sup> B32\_sitesWithCharredPMP.sql; B33\_samplesWithCharredPMP.sql

<sup>9</sup> B34\_sitesWithCharredPMP\_region.sql; B35\_samplesWithCharredPMP\_region.sql

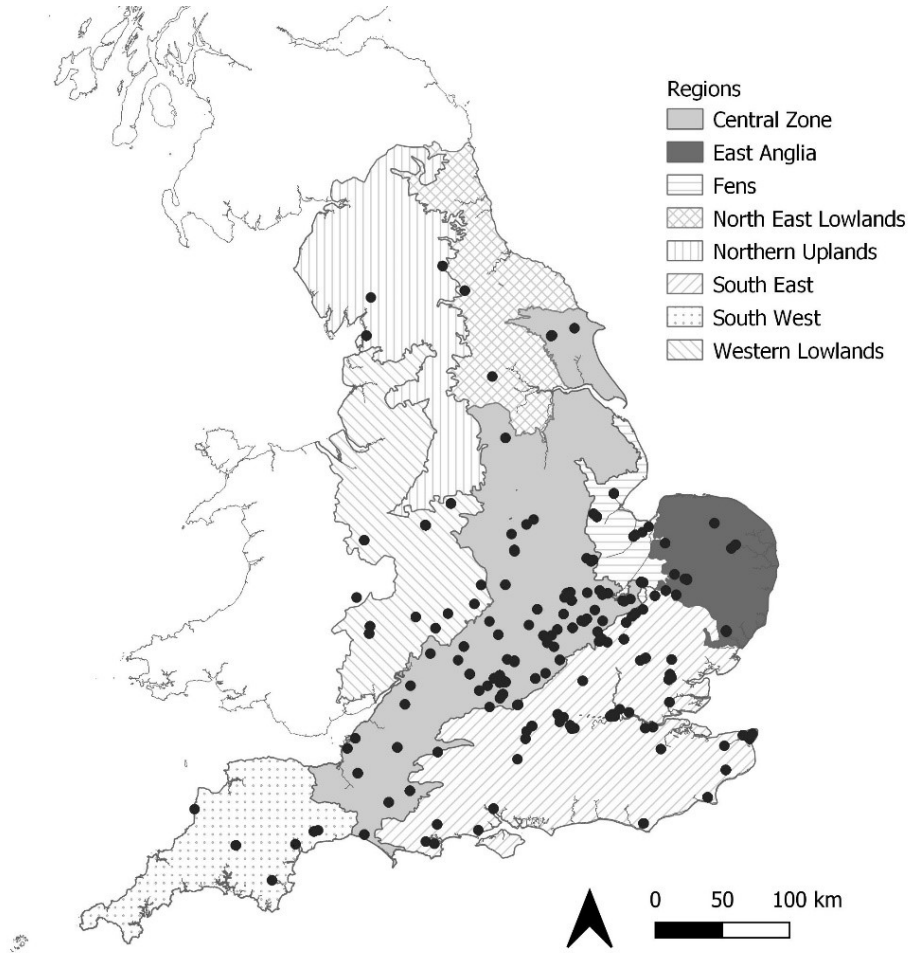
<sup>10</sup> B36\_sitesWithCharredPMP\_coords.sql

**Table 3 – Chronological distribution of charred samples (i.e. where charring is the principal means of preservation), using simplified FeedSax phases.**

<b>fsSimpleSpan</b>	<b># samples</b>
A	34
AB	3
AC	49
AD	8
AE	4
B	4
BC	42
BD	7
BE	2
C	450
CD	14
CE	18
D	295
DE	330
DF	3
DG	8
E	571
EF	220
EG	72
F	88
FG	39
G	28
<b>total</b>	<b>2289</b>

**Table 4 – Regional distribution of charred samples, and sites with charred samples.**

<b>region</b>	<b># sites</b>	<b># samples</b>
Central Zone	94	796
East Anglia	25	300
Fens	12	197
North East Lowlands	3	6
Northern Uplands	2	17
South East	67	788
South West	6	68
Western Lowlands	14	117



**Figure 3 – Distribution of sites with charred samples.**



Crop dominance can also be assessed for the fully quantified samples, where the threshold for ‘dominance’ is set at  $\geq 80\%$  of relevant items (as per McKerracher 2019), using the results of the foundation query as contained within Digital Archive Document B08. These results show that, of the 2,289 charred samples, 86.7% (1,984) have crop components dominated by cereal remains, as opposed to legumes or other crops. Of these cereal-dominated samples, 73.3% (1,454) have cereal components dominated specifically by free-threshing cereals.

Of these *charred free-threshing cereal samples*, 97.3% (1,414 at 191 sites) have  $\geq 30$  free-threshing cereal grains and are therefore eligible for the calculation of percentages of wheat, barley, oat and rye grains. Note that, in these calculations, ‘wheat’ represents an amalgamation of positively identified free-threshing wheat grains with indeterminate ‘*Triticum* sp.’ grains – on the grounds that the latter, in free-threshing cereal-dominated samples, are inherently more likely to represent free-threshing varieties. In addition, charring experiments have found that free-threshing wheat grains are more vulnerable than their hulled counterparts to distortion during charring, and therefore perhaps more likely to be rendered indeterminate (Boardman and Jones 1990).

Table 5 and 6 below give the regional and chronological distributions of these 1,414 samples, and show how this most informative part of the dataset is heavily dominated by samples from the Central Zone and South East, biased towards (simple) phases C, D, DE, E and EF – but E above all.<sup>11</sup> Figure 4 maps these sites, clearly illustrating this geographical pattern.<sup>12</sup>

**Table 5 – Regional distribution of charred free-threshing cereal samples.**

region	# samples
Central Zone	505
East Anglia	178
Fens	82
North East Lowlands	4
Northern Uplands	13
South East	482
South West	54
Western Lowlands	96

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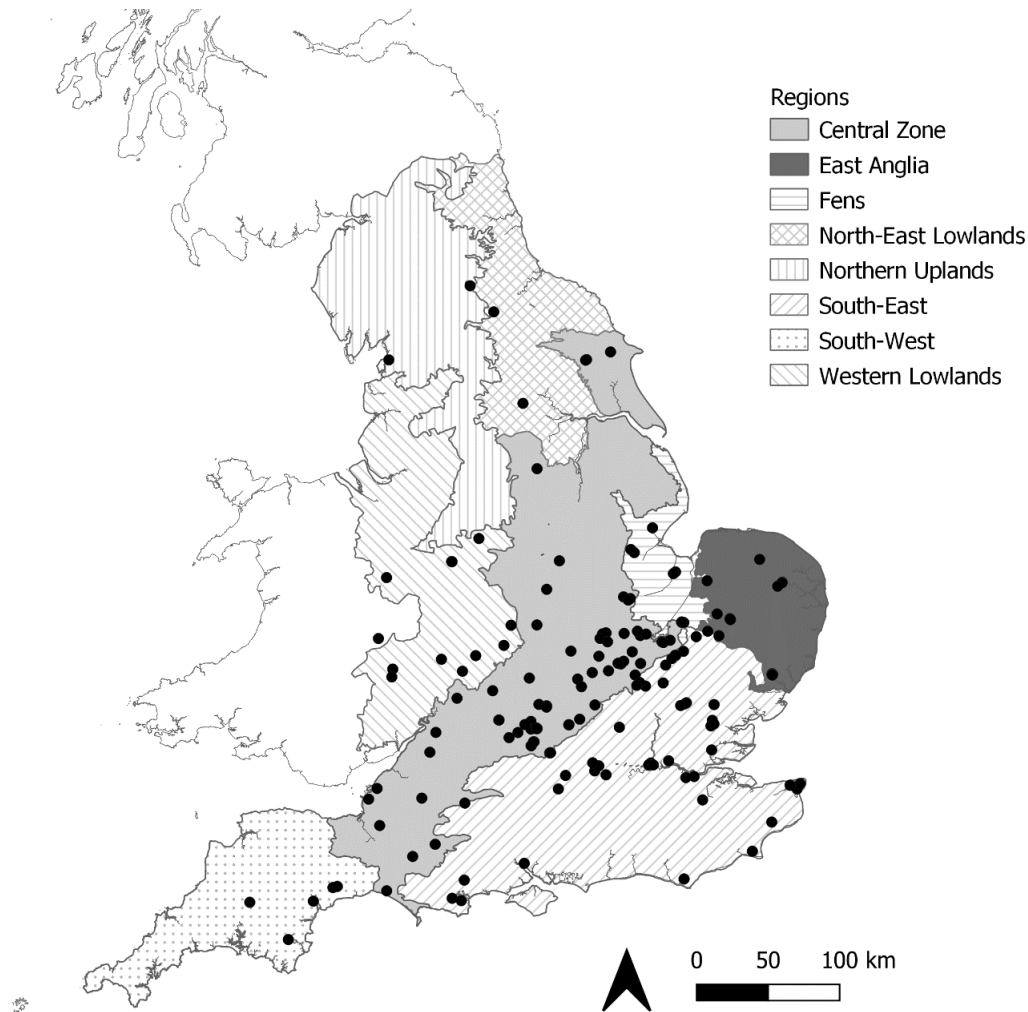
<sup>11</sup> B37\_ftcSamples\_region.sql; B38\_ftcSamples\_phase.sql

<sup>12</sup> B38\_sitesWithFTCSamples\_coords.sql



**Table 6 – Chronological distribution of charred free-threshing cereal samples.**

<b>simple phase</b>	<b># samples</b>
A	19
AB	1
AC	15
AD	4
AE	2
B	3
BC	24
BD	5
BE	2
C	247
CD	12
CE	14
D	185
DE	206
DF	1
DG	5
E	403
EF	129
EG	56
F	48
FG	27
G	6



**Figure 4 – Distribution of sites with charred free-threshing cereal samples.**

The relative proportions of wheat, barley, oat and rye grains in these 1,414 samples can be used to create bar charts (to show changing percentages over time) or heat maps (to show regional trends in percentages, via Inverse Distance Weighting: McKerracher 2018, 56). The data necessary to create such outputs can be extracted from the terminal query in the foundation script (see above), as exported for the entire dataset in Digital Archive Document B08; these results must be filtered, either within the query or in a spreadsheet, to restrict analysis to charred free-threshing cereal samples with at least 30 free-threshing cereal grains.

### **Standard abundance and average density**

The foundation script calculates for each sample the `totalStandardQuantity` (equivalent to McKerracher 2019's standard abundance) and `avgDensity` (average density: items per litre of soil, rounded to the nearest integer) – the latter only being calculated where soil volume data are available and the standard abundance is greater than or equal to the average density quorum (Parameter 7 in the foundation script: here, set at 30). These calculated values can be found via the terminal select query in the foundation script, and in the exported results in Digital Archive Document B08. All of the 1,454 charred free-threshing cereal samples have a `totalStandardQuantity`  $\geq 30$ , ranging from 33 to

130,921. Of these, avgDensity was calculated (to at least one item per litre, rounded to the nearest integer) for 1,136 samples, ranging from one to 16,384 items per litre.

## Crop processing

The foundation script also assigns each of the 1,454 charred free-threshing cereal samples a crop processing classification, using the basic components or ‘ratio’ method developed by Jones (1990), and including the interpolated ‘USG’ (un-sieved grain) category described by McKerracher (2019).<sup>13</sup> This method assesses the relative proportions of cereal grain, rachis segments and weed seeds in each sample; these percentage values are assigned to the percGrain, percRachis and perWeedSeed fields in the foundation script and, where totalParts  $\geq 30$  (Parameter 7), a classification is assigned to ratioClass. The results are summarised in Table 7, and given in full in the first worksheet in Digital Archive Document B09.<sup>14</sup>

**Table 7 – Summary of crop processing classifications (using ratio method).**

classification	# samples	% samples
CWBP	43	2.9
FSBP	87	5.8
FSP	794	52.8
MS	270	18.0
USG	260	17.3
<b>total</b>	<b>1,454</b>	<b>100.0</b>

Jones devised another, complementary crop processing classification method, based on a discriminant analysis of weed seeds categorised according to their physical characteristics (and thus behaviour under crop processing conditions) (Jones 1987).<sup>15</sup> This analysis, run with SPSS software, requires archaeobotanical data in a specific format, appended to the modern control data assembled by Jones (made available for the present analysis by Amy Bogaard and Michael Charles, with kind permission of Glynis Jones). Each weed taxon included in the FeedSax analyses has been assigned, where possible, a weedSeedClass in the plant taxon metadata (Digital Archive Document B12). These classifications were based upon data from previous analyses, provided by Amy Bogaard, along with first-hand examination of weed seeds in the School of Archaeology’s reference collection in Oxford. Classifications could not be obtained for all taxa, and some taxa had ambiguous classifications, e.g. Poaceae, a family which include species with BFH and SFH seeds. Such identifications were only included in the crop processing analysis if the archaeobotanical record included a ‘qualifier’ which specified whether the seeds in question were ‘big’ (>2mm) or ‘small’ (<2mm). The big/small classifications of qualifiers are provided in the qualifier metadata (Digital Archive Document B12).

For samples with at least ten classified weed seeds (Parameter 6 in the foundation query), the seed-percentage of each taxon was square-rooted, and these values summed for each of the six weed seed

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<sup>13</sup> Classification are as follows: CWBP = coarse-sieving or winnowing by-product, FSBP = fine-sieving by-product, FSP = fine-sieved product, MS = mixed stages, and USG = un-sieved grain (i.e. prior to fine-sieving).

<sup>14</sup> B40\_ratioClass.sql

<sup>15</sup> The six weed seed types are: BHH (big headed heavy), BFH (big free heavy), SHH (small headed heavy), SHL (small headed light), SFH (small free heavy) and SFL (small free light).

classes, for each sample. The resulting input data for the 1,090 eligible samples are shown in the second worksheet of Digital Archive Document B09.<sup>16</sup> These were appended to Jones' original modern control data for analysis, but the latter data do not belong to this project and are therefore not published here.

The 'casewise' results exported from SPSS are given in the third worksheet, and pared down to the most important fields in the fourth worksheet: the predicted crop processing group,<sup>17</sup> the probability of the prediction, and the two discriminant functions extracted for each sample. Considering all the charred free-threshing cereal samples, the classifications can be summarised as follows in Table 8.<sup>18</sup>

**Table 8 – Summary of crop processing classifications using discriminant analysis method.**

classification	# samples	% samples
WBP (1)	168	11.6
CSBP (2)	6	0.4
FSBP (3)	417	28.7
FSP (4)	499	34.3
n/a	364	25.0
<b>total</b>	<b>1,454</b>	<b>100.0</b>

If, for greater rigour, we apply a minimum probability quorum of 0.8 (i.e. we only accept discriminant analysis results assigned a probability of  $\geq 0.8$ ), the results can be summarised as follows in Table 9.

**Table 9 – Summary of crop processing classifications with probabilities  $\geq 0.8$ , using discriminant analysis method.**

classification	# samples	% samples
WBP (1)	112	13.5
CSBP (2)	4	0.5
FSBP (3)	320	38.7
FSP (4)	392	47.3
<b>total</b>	<b>828</b>	<b>100.0</b>

The fifth worksheet in Digital Archive Document B09 assembles these discriminant analysis results along with those of the ratio-based analysis, and attempts to reconcile the two following the criteria set out by McKerracher (2019, 48). Since the discriminant analysis output is not contained within Haystack, these reconciled results have been compiled 'manually' and cannot be directly replicated in SQL. First, the reconciled results of *all* samples can be summarised as follows in Table 10.

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<sup>16</sup> B41\_weedDiscriminantInput.sql; 'NO' is an arbitrary numbering sequence for the purposes of the discriminant analysis, and 'PROC' is the crop processing classifications – here 0 (undefined) for all samples at input stage.

<sup>17</sup> 1 = winnowing by-product, 2 = coarse-sieving by-product, 3 = fine-sieving by-product, 4 = fine-sieved product.

<sup>18</sup> Unlike the ratio method, the discriminant analysis method distinguishes between winnowing by-products (WBP) and coarse-sieving by-products (CSBP).

**Table 10 – Reconciled crop processing classifications, based on ratio and discriminant analysis methods.**

classification	# samples	% samples
CWBP	17	1.2
FSBP	57	3.9
FSP	269	18.5
USG	222	15.3
none	525	36.1
too small	364	25.0
<b>total</b>	<b>1,454</b>	<b>100.0</b>

If we accept only those discriminant analysis classifications with a probability  $\geq 0.8$ , the reconciled results can be summarised as follows in Table 11.

**Table 11 - Reconciled crop processing classifications, based on ratio and discriminant analysis methods, where the latter are assigned probabilities  $\geq 0.8$ .**

classification	# samples	% samples
CWBP	13	1.6
FSBP	52	6.3
FSP	223	26.9
USG	173	20.9
none	367	44.3
<b>total</b>	<b>828</b>	<b>100.0</b>

In both cases, it is clear that the majority of classifiable samples represent grain-rich FSP or USG samples.

### Input for quantitative analyses

Besides the quantitative analyses listed above – pertaining to cereal percentages, average density, and crop processing, for instance – the FeedSax project also applied more complex, multivariate statistical analyses to the crop and weed data, based on methods in functional weed ecology. These included correspondence analyses to explore seasonal sowing patterns (detailed at length in Digital Archive Document B10), and discriminant analyses to explore soil disturbance and intensity of cultivation (see Hamerow *et al.* forthcoming, and Bogaard *et al.* 2022). These analyses required input data to be extracted from Haystack in a particular format, with a row for each taxon and a column for each sample. For example, each worksheet in Digital Archive Document B11 represents correspondence analysis input data for a different case study site; input data for the discriminant analyses took a comparable form. It is not practical to extract a table compiling such data for all 1,454 charred free-threshing cereal samples, since this would require the creation of an unwieldy table with around 1,455 columns. Rather, the input datasets should be compiled separately for individual sites (or groups of sites, if required). There is no single query in the digital archive that can complete this task; rather, there is a separate ‘mini-script’ for each sample (consisting of two SQL queries), dynamically created in the foundation script, in the field quantitiesQuery. For each required sample, these ‘mini-scripts’

should be copied into the foundation quantities script (Digital Archive Document B19), immediately before the last select query in that script, which will return the results ready for export.<sup>19</sup>

## Multivariate statistics results

The methods and results of the multivariate statistical analyses mentioned above are discussed in detail in the project monograph and other FeedSax publications (Hamerow *et al.* forthcoming; Bogaard *et al.* 2022; McKerracher 2022), but basic results are presented in bulk in the Digital Archive. Hence, Digital Archive Document B10 presents the correspondence analysis results, while results from the discriminant analyses of cultivation intensity and soil disturbance are provided in Digital Archive Documents B46/B48 (for graphs), and B47/B49 (for raw data, including discriminant functions and sample metadata, linking back to sample records in Haystack via the sampleID column).

## Getting presence data

Presence analyses (for both sites and samples) can be conducted using the foundation presence script (Digital Archive Document B20). This script builds directly upon the original foundation script (Digital Archive Document B18), and therefore uses the taxonomic amalgamations incorporated therein. For each taxon in the dataset extracted by the original foundation script, the presence analysis script calculates the numbers and percentages, of both sites and samples, at which its charred remains occur in each phase. The queries apply a ‘moving window’ approach, as defined earlier in this report. Two terminal select queries in the presence analysis script provide summary tables of presence data for sites and samples respectively, including some taxonomic metadata to facilitate further investigation: recordClass (e.g. cereal, pulse, weed, non-arable), recordSubClass (e.g. for weeds, family or genus; for cereals, hulled or free-threshing), and recordCerealGroup (for cereal taxa only: wheat, barley, oat or rye). Since some taxonomic identifications are ambiguous (e.g. ‘*Triticum/Secale*’), these metadata fields can contain more than one value, separated by commas.

It is implicit in the presence script that a taxon need only occur once in a sample, or at a site, to be counted as present (i.e. McKerracher 2019’s Parameter 2 is set at ‘one’, and cannot be changed within this script). It is possible, however, to configure the total number of sites/samples required to support the calculation of percentage presence: this is McKerracher 2019’s Parameter 8, and it is set as a variable at the start of the foundation script – in this case, set as ten. Where a given phase has fewer than ten sites/samples, the percentage presence is recorded as zero.

The results of the presence analyses, run according to the amalgamation data in Digital Archive Document B12, are preserved in Digital Archive Documents B42 (for sites) and B43 (for samples). Each of these Excel workbooks contains six sheets: one for the national dataset as a whole, and then one for each of five regions (Central Zone, East Anglia, Fens, South East, and Western Lowlands). The remaining three regions (North-East Lowlands, Northern Uplands, and South West) have too few sites/samples to support a usable number of presence results on their own, but data from these regions are nonetheless included in the national results in the first sheet. These different regional results were obtained by configuring the sample selection query in the foundation script (Digital Archive Document B18).

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<sup>19</sup> B19\_foundation02\_quantities.sql

## Counting analysts

The diversity of analysts who have produced the data in a given dataset provides some measure of that dataset's internal consistency, or 'inter-worker uniformity' (McKerracher 2019, 19). Accordingly, Haystack can be queried to count how many site analyses have been performed by each archaeobotanist recorded in the worker table.<sup>20</sup> It should be noted that a single site can have more than one 'site analysis' if more than one archaeobotanist has worked on that project; for instance, within Haystack, the site of Lyminge has two site analyses: one by McKerracher and one by Roushannafas. The results of this assessment are provided in Digital Archive Document B45. They show that, although 64 archaeobotanists (including 'anon') are represented in the dataset, the top nine of these (i.e. those who have undertaken at least ten site analyses) account for more than 50% of all analyses – a pattern which lends a reassuring degree of 'inter-worker uniformity' to the dataset.

## References

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<sup>20</sup> B44\_countAnalysts.sql