Haystack: the FeedSax database

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The datasets compiled and produced by the FeedSax project are contained within a relational database called Haystack. The digital archive contains both a SQL script to recreate the original database (Digital Archive Document A02) and a set of tables exported from Haystack in CSV format (Digital Archive Documents A05–A44, so that they can be consulted by readers unfamiliar with SQL. This document describes each table's structure, contents, and relationships, to aid the reader's use of either the SQL database or the set of CSV files. The sections below describe each table's structure, content and relationships with other tables, and should be read in conjunction with the Entity Relationship Diagram, produced with Lucidchart and provided in Digital Archive Document A03.[1]

The Haystack database was developed during 2017–22 with MySQL/MariaDB, run on Windows 10, with character sets as defined in Digital Archive Document A02. The database server was 10.4.14-MariaDB. Haystack can be recreated by running A02 in a MySQL/MariaDB relational database management system, and then queried with the scripts provided in the FeedSax Digital Archive (see Digital Archive Document B07 for commentary on the archaeobotany scripts) or with custom queries. The database creation script in Digital Archive Document A02 was created by exporting the database to SQL in the HeidiSQL application.[2]

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[1] https://www.lucidchart.com (accessed August 2022).
[2] https://www.heidisql.com (accessed August 2022).

animalElement

field	note
ID	primary key (unique identifier)
name	e.g. 'humerus', 'pelvis', etc.

animalFusion

field	note
ID	primary key (unique identifier)
name	e.g. 'fused', 'unfused', 'fusing', etc.

animalPosition

field	note
ID	primary key (unique identifier)
name	'anterior', 'posterior', or 'indeterminate'

animalSex

field	note
ID	primary key (unique identifier)
name	'male', 'female', or 'indeterminate'

animalSide

field	note
ID	primary key (unique identifier)
name	'left', 'right', or 'indeterminate'

animalTaxon

field	note
ID	primary key (unique identifier)
name	'cattle', 'sheep', or 'pig'

animalToothAlveolar

field	note
ID	primary key (unique identifier)
levelNo	from 0 to 5
name	from 'no recession' to 'new bone formation nearly complete'

context

A **site** may have one or more **contexts** associated with it; a context may have one or more **samples**, **faunaBones** records, or **faunaDental** records associated with it.

field	note
ID	primary key (unique identifier)
name	context name/number given in original archaeobotanical report/table; where only a sample name/number was available, this has been used in brackets as the context name
siteID	foreign key to **site**
featureName	as given in original report
featureTypeID	foreign key to **featureType**
sitePhaseID	foreign key to **sitePhase**

county

field	note
ID	primary key (unique identifier)
name	post-1974 county names

event

An 'event' here refers to an archaeobotanical or zooarchaeological assessment/analysis.

field	note
ID	primary key (unique identifier)
siteID	foreign key to **site**
workerID	foreign key to **worker**
eventTypeID	foreign key to **eventType**
reference	bibliographical reference for this specific analysis

eventType

field	note
ID	primary key (unique identifier)
name	'archaeobotanical', 'zooarchaeological' or 'palynological'

faunaBones

field	note
ID	primary key (unique identifier)
contextID	foreign key to **context**
box	archive box where located
condition	description of condition/preservation quality
boneCode	code for internal FeedSax use, to facilitate matching of bones to stable isotope **labSample** records; this relationship is properly encoded in **labSample.faunaBonesID**
animalTaxonID	foreign key to **animalTaxon**
animalElementID	foreign key to **animalElement**
animalSideID	foreign key to **animalSide**
animalPositionID	foreign key to **animalPosition**
zone_1	Bone zones present/absent (following Serjeantson 1996)
zone_2	
zone_3	
zone_4	
zone_5	
zone_6	
zone_7	
zone_8	
proximal_animalFusionID	foreign key to **animalFusion**, for proximal end
distal_animalFusionID	foreign key to **animalFusion**, for distal end
pelvisMorphology_animalSexID	foreign key to **animalSex**, according to pelvis morphology
osteophyte	number of osteophytes present
eburnation	present/absent
articularContourChange	present/absent
PEX	new bone formation near the proximal articulation. This encompasses entheseal as well as osteophytic changes 1–4
DEX	new bone formation near the distal articulation. This encompasses entheseal as well as osteophytic changes 1–4
PLIP	functional extension of the proximal articular surface due to new bone formation, 1–4
PEB	eburnation on the proximal articular surface, pathognomonic of osteoarthritis 1–2
DEB	eburnation on the distal articular surface, pathognomonic of osteoarthritis 1–2
STR	transverse striations on the medio-proximal surface of metatarsals near the attachment site for the musculus extensor digitorum brevis 1–2
BRD	broadening of the distal (primarily medial) condyle of the metapodial, likely as an adaptation to loading 1–4
DEPR	depressions on the palmar/plantar surface of the distal shaft of metapodials 1–3
FUS	ankylosis of the vestigial second metacarpal with the medial side of the third metacarpal 1–2
FAC	striations on the triangular facet for the attachment of the ligamentum accessorium 1–2
GL	greatest length (millimetres)

Bp	breadth proximal end (millimetres)
Dp	depth proximal end (millimetres)
SD	shaft diameter (millimetres)
BT	breadth of trochlea (millimetres)
HTC	height of trochlear constriction (millimetres)
Bd	breadth distal end (millimetres)
BdF	breadth of distal fusion (millimetres)
a	breadth medial condyle (millimetres)
b	breadth lateral condyle (millimetres)
3	depth medial condyle (millimetres)
BCR	distance between the two metapodial condyle ridges (millimetres)
DCM	distance from medial metapodial condyle ridge to the medial margin (millimetres)
SDPu	smallest diameter pubis (millimetres)
MDRA	minimum diameter rim of acetabulum (millimetres)
sampledC14	true, if sampled for radiocarbon dating
sampleIsotopes	true, if sampled for stable isotope analysis
comments	free text

faunaDental

field	note
ID	primary key (unique identifier)
contextID	foreign key to **context**
box	i.e. archive box where located
animalTaxonID	foreign key to **animalTaxon**
animalSideID	foreign key to **animalSide**
P2	presence/ ante-mortem loss (P / am)
P2_calculus	calculus accumulation, from 0 (absent) to 3 (considerable)
P2_animalToothAlveolarID	foreign key to **animalToothAlveolar**
P2_periostealNewBone	present/absent
P3	presence/ ante-mortem loss (P / am)
P3_calculus	calculus accumulation, from 0 (absent) to 3 (considerable)
P3_animalToothAlveolarID	foreign key to **animalToothAlveolar**
P3_periostealNewBone	present/absent
P4	wear stage (C, V, E, H, U, a–l)
P4_calculus	calculus accumulation, from 0 (absent) to 3 (considerable)
P4_animalToothAlveolarID	foreign key to **animalToothAlveolar**
dP4W	width (millimetres)
P4_periostealNewBone	present/absent
dP2	presence/ ante-mortem loss (P / am)
dP3	presence/ ante-mortem loss (P / am)
dP4	wear stage (C, V, E, H, U, a–m)
M1W	width (millimetres)
M1	wear stage (C, V, E, H, U, a–m)
M1_calculus	calculus accumulation, from 0 (absent) to 3 (considerable)
M1_animalToothAlveolarID	foreign key to **animalToothAlveolar**
M1_periostealNewBone	present/absent
M2	wear stage (C, V, E, H, U, a–m)
M2W	width (millimetres)
M2_calculus	calculus accumulation, from 0 (absent) to 3 (considerable)
M2_animalToothAlveolarID	foreign key to **animalToothAlveolar**
M2_periostealNewBone	present/absent
M3	wear stage (C, V, E, H, U, a–m)
M3W	width (millimetres)
M3_calculus	calculus accumulation, from 0 (absent) to 3 (considerable)
M3_animalToothAlveolarID	foreign key to **animalToothAlveolar**
M3_periostealNewBone	present/absent
comments	free text

faunaNISP

Representation in this table is the principal indication that a site has any zooarchaeological data in Haystack.

field	note
ID	primary key (unique identifier)
siteID	foreign key to **site**
sitePhaseID	foreign key to **sitePhase**
cattle	number of cattle elements in assemblage (NISP)
sheepGoat	number of sheep/goat elements in assemblage (NISP)
pig	number of pig elements in assemblage (NISP)
CA	
CB	
CC	
CD	
CE	number of cattle specimens at each mandibular wear stage (Grant 1982)
CF	
CG	
CH	
CI	
SA	
SB	
SC	
SD	
SE	number of sheep/goat specimens at each mandibular wear stage (Grant 1982)
SF	
SG	
SH	
SI	
cattleAgeSummary	free text commentary on the cattle ageing data
sheepGoatAgeSummary	free text commentary on the sheep/goat ageing data
comments	free text

featureType

field	note
ID	primary key (unique identifier)
name	as given in original reports

ftirReading

field	note
ID	primary key (unique identifier)
ftirRunID	foreign key to **ftirRun**
ftirWavelengthID	foreign key to **ftirWavelength**
reading	

ftirRun

One **FTIR run** may have one or more **FTIR readings**.

field	note
ID	primary key (unique identifier)
labSampleID	foreign key to **labSample**
name	

ftirWavelength

To ensure consistency in **ftirReading**.

field	note
ID	primary key (unique identifier)
name	

grainPhoto

A catalogue of the charred grain images contained in the FeedSax photographic archive, corresponding to the index in that collection (https://doi.org/10.25446/oxford.20254137.v1).

field	note
ID	primary key (unique identifier)
title	a descriptive title for the image
filename	
sampleID	foreign key to **sample**
imageFunction	e.g. for morphometric analysis, or as a record prior to destructive analysis
view	view of the grain(s), e.g. dorsal, polar, etc.
plantMasterID	foreign key to **plantMaster**
labSampleID	foreign key to **labSample**
radiocarbonIDs	can contain one or more foreign keys to **radiocarbon**, but as a free text field; one photograph can be associated with more than one date, so a single, straightforward foreign key field is not practical here
authors	the person who took the photograph, and the PI
doi	unique DOI for this image
doiURL	unique DOI for this image, given as an URL

isotopeReading

Here, 'raw' means 'not drift corrected'.

field	note
ID	primary key (unique identifier)
labSampleID	foreign key to **labSample** (if the record is for a sample, not a standard)
isotopeRunID	foreign key to **isotopeRun**
runOrder	
standard	true/false
labStandardID	foreign key to **labStandardID** (if the record is for a standard, not a sample)
Ps	position in stable isotope run
Wt	weight in milligrams
NugR	nitrogen amount (μg) – raw
d15NR	δ^{15}N value – raw
CugR	carbon amount (μg) – raw
d13CR	δ^{13}C value – raw
d18OR	δ^{18}O – raw
Nugdc	nitrogen amount (μg) – drift corrected
d15Ndc	δ^{15}N value – drift corrected
Cugdc	carbon amount (μg) – drift corrected
d13Cdc	δ^{13}C value – drift corrected
d18Odc	δ^{18}O – drift corrected
pcC	%C
pcN	%N
CN	C:N
normd15N	normalised δ^{15}N$_{(AIR)}$
d15Nsd	δ^{15}N standard deviation as per Kragten spreadsheet method
normd13C	normalised δ^{13}C$_{(VPDB)}$
d13Csd	δ^{13}C standard deviation as per Kragten spreadsheet method
comments	

isotopeRun

One **isotope run** may have one or more **isotope readings**.

field	note
ID	primary key (unique identifier)
name	
lab	'Iso-Analytical' or 'RLAHA' (Research Laboratory for Archaeology and the History of Art, University of Oxford)

labSample

field	note
ID	primary key (unique identifier)
name	assigned by FeedSax, e.g. 'STT001'
experimental	true/false (some runs include modern samples for experiments)
nonFeedsax	true/false (some runs include samples from other projects)
siteID	foreign key to **site**
faunaBonesID	foreign key to **faunaBones** (if it is a bone collagen sample)
plantRecordID	foreign key to **plantRecord** (if it is a charred grain sample)
weightPreTreatment	in milligrams
weightPostTreatment	in milligrams
numberOfGrains	if a charred grain sample
notes	including e.g. if a sample's grains were analysed in bulk rather than individually; if a sample was rejected for analysis; or if its analysis was duplicated

labStandard

field	note
ID	primary key (unique identifier)
name	e.g. 'ALANINE', 'COW', etc.

parentType

A 'parent type' is required when a record can be the 'child' of different kinds of parent record, e.g. a radiocarbon date can be the child of a sample, context, or site.

field	note
ID	primary key (unique identifier)
name	can be site, context, sample

plantFamily

Referenced by the **plantMaster** table, which lists all taxa in the dataset.

field	note
ID	primary key (unique identifier)
name	nomenclature following Stace 2010

plantGenus

Referenced by the **plantMaster** table, which lists all taxa in the dataset.

field	note
ID	primary key (unique identifier)
name	nomenclature following Stace 2010

plantIdentification

A **plant record** may have one or more **plant identifications** associated with it.

Used to associate plant taxa with **plantRecord** entries, since a record may contain more than one identification (e.g. '*Secale/Triticum*' contains two identifications).

field	note
ID	primary key (unique identifier)
plantRecordID	foreign key to **plantRecord**
plantMasterID	foreign key to **plantMaster**

plantMaster

A 'master list' of all plant taxa in the dataset.

field	note
ID	primary key (unique identifier)
name	default nomenclature following Stace 2010 for most taxa but conventional archaeobotanical names for cereals (e.g. Cappers and Neef 2012, 15–16)
plantFamilyID	foreign key to **plantFamily**
plantGenusID	foreign key to **plantGenus**

plantMasterAlias

Aliases associated with the plant taxa in **plantMaster**, including both Latin names (from different sources) and English common names.

field	note
ID	primary key (unique identifier)
plantMasterID	foreign key to **plantMaster**
alias	English or Latin name
suffix	if any, e.g. 'L.'
preferred	true/false (whether or not this name should be used in analytical output)

plantPart

Each record in **plantRecord** has an associated plant part.

field	note
ID	primary key (unique identifier)
name	names for parts as entered from original archaeobotanical reports/tables, except for 'caryopsis' which has always been entered as 'grain'

plantPreservation

Each record in **plantRecord** has an associated mode of preservation.

field	note
ID	primary key (unique identifier)
name	as recorded in original reports, e.g. 'charred', 'part-mineralised', etc.

plantRecord

A **sample** may have one or more **plant records** associated with it; a plant record may have one or more **plant identifications** associated with it.

field	note
ID	primary key (unique identifier)
sampleID	foreign key to **sample**
qualifierID	foreign key to **qualifier**
plantPreservationID	foreign key to **plantPreservation**
plantPartID	foreign key to **plantPart**
fragmented	true/false
abundance	i.e. presence/absent, or semi-quantitative scale of abundance (e.g. '++++'); entered here as free text
quantity	
seedCode	free text descriptor (including sample name and cereal-type) for cereal grain records submitted for stable isotope analysis, to facilitate matching of **plantRecord** records with **labSample** records; this relationship is properly encoded in **labSample.plantRecordID**

qualifier

A **plantRecord** may, but need not, have an associated qualifier, e.g. 'hulled', 'germinated', 'cf.', which adds information beyond the purely taxonomic. Where a record has more than one qualifier, e.g. 'cf. … germinated', these have been concatenated such that 'cf., germinated', is a single associated qualifier.

field	note
ID	primary key (unique identifier)
name	as given in original reports

radiocarbon

field	note
ID	primary key (unique identifier)
parentID	foreign key to **site, context** or **sample** – depending upon the value in parentTypeID
parentTypeID	foreign key to **parentType**
labRef	unique laboratory code assigned by the Oxford Radiocarbon Accelerator Unit (ORAU), e.g. OxA-45678
feedsaxCode	arbitrary code for internal FeedSax use, prior to assignment of ORAU codes
datedMaterial	free text descriptor, e.g. '3 x Avena grains'
dateBP	
plusMinus	
calibration notes	representative calibrated date range with high probability, obtained from OxCal with IntCal20 (Bronk Ramsey 2009; Reimer *et al.* 2020); given in form '605-658 @ 95.4% [IntCal20]'

region

field	note
ID	primary key (unique identifier)
name	the regions defined by Rippon *et al.* 2015, plus 'Northumberland' for two sites further north than those regions

sample

A **context** may have one or more **samples** associated with it; a sample may have one or more **plant records** associated with it.

field	note
ID	primary key (unique identifier)
name	the name and/or number of a sample, as given in original archaeobotanical report/table; where only a context name/number was available, this has been used in brackets as a sample name
contextID	foreign key to **context**
percentageSorted	
soilVolume	in litres
soilWeight	in kilograms

site

A **region** or **county** may have one or more **sites** associated with it; a site may have one or more **contexts** associated with it.

field	note
ID	primary key (unique identifier)
name	short name for excavation site, usually as given in report title
longName	extended, more descriptive name for the site, to clarify which site is meant
countyID	foreign key to **county**
regionID	foreign key to **region**
eastings	from National Grid Reference
northings	from National Grid Reference
elevation	in metres above Ordnance Datum
referenceMain	principal bibliographical reference for the excavation, whether published or unpublished; for some sites this reference is to a specialist report (as in **event.reference**) where that report was the principal reference for FeedSax purposes
referenceLink	where available, URL for the relevant report online

sitePhase

field	note
ID	primary key (unique identifier)
name	usually as given in original report but sometimes, where phase definitions have been revised using new dates obtained by FeedSax, phase names have been renamed accordingly, with 'FeedSax' referenced in the name for the avoidance of doubt
fromYear	as given in original report, unless revised by FeedSax (see above)
toYear	as given in original report, unless revised by FeedSax (see above)
siteID	foreign key to **site**
siteTypeID	foreign key to **siteType** (not recorded for all sites)
fsStartYear	given to fit FeedSax universal chronology
fsEndYear	given to fit FeedSax universal chronology
fsStartPhase	given to fit FeedSax universal chronology
fsEndPhase	given to fit FeedSax universal chronology
fsPhaseSpan	i.e. the start and end phases separated with a dash

siteType

field	note
ID	primary key (unique identifier)
name	e.g. 'rural', 'high-status', etc.

worker

A 'worker' here means an analyst of archaeobotanical or zooarchaeological material, as given in the original reports used by FeedSax.

field	note
ID	primary key (unique identifier)
name	mostly comprising surname and initial(s) (or name, if ambiguous), but also records for 'anonymous', 'various', and 'The Environmental Archaeology Consultancy'

References

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