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Data

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J.J.C. and S.T.T. designed the research and coordinated data collection; J.J.C. and B.C. analysed the data; and J.J.C. and S.T.T. wrote the manuscript.

2 3	1	Bias, incompleteness, and the "known unknowns" in the Holocene faunal record
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Long-term faunal data are needed to track biodiversity change and extinction over wide spatiotemporal scales. The Holocene record is a particularly rich and well-resolved resource for this purpose but nonetheless represents a biased subset of the original faunal composition, both at the site-level assemblage and when data are pooled for wider-scale analysis. We investigated patterns and potential sources of taxonomic, spatial and temporal bias in two Holocene datasets of mammalian occurrence and abundance, one at the global species-level and one at the continental population-level. Larger-bodied species are disproportionately abundant in the Holocene fossil record, but this varies according to trophic level, probably due to past patterns of human subsistence and exploitation. Despite uneven spatial distribution of mammalian occurrence records, we found no specific source of sampling bias, suggesting that this error-type can be avoided by intensive data collection protocols. Faunal assemblages are more abundant and precisely dated nearer to the present as a consequence of taphonomy, past human demography, and dating methods. Our study represents one of the first attempts to quantify incompleteness and bias in the Holocene mammal record, and failing to critically assess quality of long-term faunal datasets has major implications for understanding species decline and extinction risk.

30 Keywords: bias; Holocene; mammals; extinction; zooarchaeology; fossil record

1. Introduction

In order to respond to the ongoing biodiversity extinction crisis [1,2], it is imperative to understand patterns and drivers of species and population losses across taxonomy, time and space. For example, the disappearance of large-bodied mammals across the late Quaternary is known to have reshaped current-day patterns of mammalian diversity [3] and extinction risk [4,5]. Additional vertebrate species extinctions, range contractions and population losses have been documented in the fossil and historical record across continental and insular regions throughout the late Quaternary up to the present day as a result of climatic changes and anthropogenic impacts [6,7]. Long-term archival data are therefore needed to provide context for measuring changes in biodiversity over wide temporal and spatial scales.

The faunal record of the Holocene Epoch, from $\sim 11,700$ yr BP to present, is particularly well-suited for this purpose. As the most recent geological epoch, it has a rich and well-resolved record documenting vertebrate occurrences over wide spatiotemporal scales [8] and includes extinct and extant species, permitting analysis of factors that influence both extinction and survival. Furthermore, the relative stability of Holocene climate in comparison with the preceding Late Pleistocene means that anthropogenic drivers of biodiversity loss are generally more straightforward to identify and interpret [7], in comparison to the ongoing debate around human versus climatic drivers of late Quaternary megafaunal extinctions [9,10]. As the time period during which major human demographic, subsistence and technological transitions occurred [11], the Holocene is well suited to track faunal responses to a wide variety of human pressures, from low-density hunter-gatherers to settled farming communities and more recent industrial and urbanised societies.

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However, faunal records in long-term environmental archives only ever represent a biased subsample of an ecosystem or community [12], due to multiple processes that influence patterns of taxonomic composition and abundance during the deposition and excavation of faunal assemblages. First-order (pre-excavation) taphonomic modifications of fossil assemblages can include biotic disturbances from other organisms (e.g. trampling, scavenging and burrowing animals, or plant root growth), and abiotic disturbances such as wind, rain, floods and heat [13]. Intrinsic qualities of the faunal deposition can also affect its survival; for example, the largest, hardest, densest bones and teeth generally survive best in response to weathering, burial and decomposition [14,15], potentially biasing the relative representation of different-sized species or individuals (e.g. ontogenetic stages) in the faunal record. Other ecological traits are less well understood in terms of their role in controlling relative patterns of preservation in bone deposits, but factors such as trophic guild [16] and habitat [17] can also affect the frequency with which different species are represented in faunal archives.

It is also important to distinguish between faunal assemblages from natural fossil (palaeontological) sites and those from archaeological sites. In general, fossil sites have been deposited by 'natural' (non-anthropogenic) means, for example from animals dying, decomposing, and being buried and preserved by natural sedimentological processes, or through accumulation of prey species by non-human predators such as raptors. By contrast, faunal remains from archaeological sites (hereafter 'zooarchaeological' assemblages) are by definition found in human contexts such as killing sites, refuse pits or deliberate burials, which reflect prehistoric or historical processes of animal exploitation such as hunting, herding or domestication. A human selection filter reflecting subsistence, social and cultural preferences (both positive and

negative) towards certain species has therefore further influenced the composition of zooarchaeological assemblages in addition to non-anthropogenic first-order taphonomic modifications, and it may not be easy to disentangle these biases from an understanding of which species were formerly present and/or abundant in the local environment [15]. As human populations rapidly expanded during the Holocene from the Neolithic agricultural revolution onwards, zooarchaeological assemblages are by far the most abundant source of faunal records for this time period [8,18]. Most second-order (post-excavation) changes arise from sampling strategy and can therefore be partly controlled for by standardised excavation methods on a site-by-site basis, although the extent to which standardised methods are used is not necessarily reported [19]. Indeed, there has been a notable recorded bias in historical excavations, which often focused primarily on the discovery and description of larger fossil specimens and associated skeletal elements, meaning that large-bodied species have been relatively well-documented whereas many smaller-bodied species remain poorly known from environmental archives [20]. Furthermore, when records are pooled into larger datasets, uneven patterns of site distribution across landscapes can be problematic for spatial analysis. Whilst the discovery and location of palaeontological and archaeological sites is always partly opportunistic and random, spatial bias in the spread of sites can further distort our understanding of underlying natural faunal distributions. For example, sites can be actively searched for in areas of cultural interest, or where archaeological or fossil material is known to survive well. Countries also differ greatly both physically (e.g. topography, underlying geology, extent of urban versus rural areas) and in their political and economic histories, all of which can affect the amount of excavation, i.e. sampling, that has been undertaken.

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The variety of dating methods used for zooarchaeological analysis also means that the precision and accuracy of dating may vary across time. Direct dating methods such as radiocarbon dating have been widely used in an effort to establish reliable megafaunal extinction chronologies and modern human arrival dates during important periods of late Quaternary environmental change, in order to disentangle potential extinction drivers [21,22]. However, for the more climatically stable and human-dominated Holocene, research has instead tended to focus on how faunal assemblages reflect past human society and culture [23] rather than on composition and dynamics of the faunal communities themselves. As a consequence there is often little incentive to date individual bones, and zooarchaeological assemblages are often simply associated with the age of their associated archaeological site. Reported dating of faunal material can thus vary from broad temporal categories such as 'Late Mesolithic', a period potentially spanning a couple of thousand years, to a specific cultural period defined to a couple of hundred years. The extent of this disparity in dating methods, and any associated bias that it may place on the precision and resolution of available faunal records over time, should therefore also be carefully considered where records have been combined into large datasets. In summary, it cannot be assumed that even the recent faunal record faithfully reflects source communities either at the site- or landscape-level, and the potential extent to which pre- and post-excavation biases may actively distort interpretation of underlying patterns of species distributions, range shifts and extinctions should be

critically assessed. To address this substantial but often overlooked concern, we

two Holocene mammal datasets, and investigated how potential sources of bias

influence our understanding of: (i) species-level extinction at the global scale; (ii)

therefore quantified taxonomic, spatial and temporal incompleteness/unevenness in

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population-level change for individual species at the regional scale. These complementary analyses into the quality of the recent faunal record provide important implications for the use of Holocene and older datasets in informing ecological baselines, reconstructing extinction processes, and assessing extinction risk. 2. Materials and methods (a) Global faunal record We compiled a global dataset of 255 mammal species that are known to have become globally extinct during the postglacial period (from the Holocene to the recent historical period), together with their recorded country-level geographic occurrences, description dates (or date of first publication if the taxon has remained formally undescribed beyond initial identification as a new species), and estimated body mass [7] (see electronic supplementary material, table S1). This comprehensive dataset includes both species that were originally described from extant populations that have subsequently become extinct ('modern', e.g. thylacine *Thylacinus cynocephalus*), and species that have only been recorded from the Holocene fossil and/or zooarchaeological records and never observed alive in recent times by scientists ('fossil', e.g. woolly mammoth *Mammuthus primigenius*). Body mass data for a small number of extinct mammals were taken from the PanTHERIA database [24], whilst data for remaining species were taken from previously published body mass estimates for Holocene extinct mammals derived from regression equations based on extant congeners or skeletal measurement parameters [5]. In order to investigate whether pre- and post-excavation modifications to fossil

assemblages are potentially biasing the taxonomic composition of the Holocene faunal

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record, we first investigated whether there was a relationship between species body mass and description date in the overall dataset. We then investigated this relationship in a more nuanced way, by assessing whether the relationship between body mass and description date was modified by whether extinct species were modern or fossil, and whether species inhabited continental or insular regions or both. We conducted analyses using phylogenetic generalised least squares (PGLS), which fits a linear model controlling for the non-independence between species resulting from phylogenetic structure in the data. Although species description date is not itself a heritable trait, it may correlate with traits such as body mass. Following refs [25, 26], we arbitrarily selected the first phylogenetic tree from 1000 available trees in ref. [27]. We used the pgls function in the R package 'caper' [28], with taxonomy standardised between datasets where possible. In total, 89 extinct mammal species in our dataset were absent from the phylogeny (electronic supplementary material, table S2), so this analysis was undertaken with a reduced dataset of 166 species.

- (b) Continental zooarchaeological record

We used an extensive dataset of 18,588 zooarchaeological records for 23 large mammal species (>2kg) in Europe spanning the Holocene, which has previously been used to reconstruct long-term processes of mammalian range decline and extinction [29] (electronic supplementary material, table S3). These data also represent a subset of a larger Holocene vertebrate database that has been widely used to investigate regional faunal turnover, refugia and extinction across various vertebrate taxa [8].

(i) Taxonomic bias

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178	We converted the number of zooarchaeological records for each species into the
179	proportion of sites occupied across its extent of occurrence (defined as a minimum
180	convex polygon enclosing all sites). This was to account for: (i) species' differing range
181	sizes (which might skew the overall abundance of each species), and (ii) areas of Europe
182	with low densities of zooarchaeological sites, which might artificially lower estimated
183	abundance for species' ranges that fell within these areas (electronic supplementary
184	material, table S3). As a proxy measure for zooarchaeological abundance, 'proportion of
185	occupied sites' will hereafter be referred to as 'abundance'. We excluded two species
186	from analyses: (i) wild horse (<i>Equus ferus</i>), because accurate records for this species
187	only cover the first half of the Holocene due to identification problems with domestic
188	horses in the later Holocene [30]; (ii) fallow deer (<i>Dama dama</i>), because its abundance
189	and distribution were heavily affected by human-mediated introduction beyond its
190	natural European range [31].
190 191	natural European range [31]. We compared observed zooarchaeological abundance with ecological variables that
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191 192 193 194 195 196	We compared observed zooarchaeological abundance with ecological variables that could potentially influence whether a species might be recorded in the zooarchaeological record. Due to the small size of the response variable (<i>n</i> =21) we selected only two predictor variables, body mass and trophic level (herbivore/carnivore), on the basis that body mass represents a useful proxy for a range of other life-history variables (e.g. reproductive output) [32], and that humans are
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202 (GLMs) with quasibinomial errors to account for the response variable being a

3 4	203	proportion and displaying overdispersion. We calculated "quasi-AICs" (QAICs) using the
5 6 7	204	R package AICcmodavg [34] for model comparison, with the model with the lowest
7 8 9	205	QAIC value interpreted as having the best explanatory power for explaining the
10 11	206	influence of body mass and trophic level on zooarchaeological abundance. We also re-
12 13 14	207	ran the analysis including species as a random effect.
14 15 16	208	In order to assess whether any observed relationship between zooarchaeological
17 18	209	abundance and body mass or trophic level could either be attributed to taphonomic bias
19 20 21	210	or instead reflected natural patterns, we compared our analysis of zooarchaeological
21 22 23	211	abundance with regressions of population density and body mass from an ecological
24 25	212	dataset of global mammal populations [35]. We selected species with a mean body mass
26 27 28	213	between 0.5kg and 700kg and within the orders Artiodactyla, Carnivora and
29 30	214	Perissodactyla, representing the body size distribution and orders that were also
31 32	215	present in the Holocene dataset in order to ensure the two datasets were comparable.
33 34 35	216	This mass range also covered an order of magnitude, considered sufficient to overcome
36 37	217	any potential biasing effects on body size-abundance relationships [36]. We compared
38 39	218	our Holocene dataset with two different ecological datasets: (i) one from North America
40 41 42	219	only (as the most faunally intact and environmentally analogous present-day ecosystem
43 44	220	to compare with the Holocene of northern Eurasia); and (ii) all continents pooled
45 46	221	together. We also conducted separate regressions for all three datasets by trophic level
47 48 49	222	(herbivore/carnivore). As an additional method of comparison, we calculated
50 51	223	confidence intervals for all model slopes (all data, herbivore only and carnivore only)
52 53	224	for the three datasets, with significant differences in abundance-body mass
54 55 56	225	distributions interpreted if 95% confidence intervals did not overlap. All analyses were
57 58	226	conducted using the glm and glmer packages 'MASS' [37] and 'lme4' [38] in R3.5.0 [39].
59 60	227	

(ii) Spatiotemporal bias

The spatial spread of Holocene faunal data across Europe (electronic supplementary material, figure S1) indicated that numbers of zooarchaeological records differed substantially between countries, with higher representation of records in central and western Europe. We investigated alternative possible explanations for this pattern by calculating the total number of zooarchaeological records (interpreted as a proxy for research output) for each country. To determine whether number of zooarchaeological records per country reflected high output from a few sites rather than wider research effort across multiple sites, we tested the relationship between numbers of zooarchaeological records and zooarchaeological sites per country using Pearson's correlation coefficient. Numbers of records and sites were extremely highly positively correlated (r = 0.91, p < 0.05, d.f. = 38), so we retained number of zooarchaeological records as the chosen metric for further analysis. One possible explanation for variation in the number of zooarchaeological records across Europe is variation in country wealth and resources available for zooarchaeological research. Gross domestic product (GDP), a country's total economic activity based on market value of all goods and services, is a widely-used appropriate proxy measurement of a country's wealth [40]. However, it has been demonstrated that a country's land area, GDP and population size are all positively correlated [40], meaning that raw data on numbers of zooarchaeological records and GDP might not be appropriate for analysis as both values might show collinearity with land area. Regression analysis confirmed that country land area and GDP across Europe were positively correlated (r = 0.35, p < 0.05, d.f. = 38). Therefore, (i) we corrected total number of zooarchaeological records by land area into a measure of density of records for each country; and (ii) we used GDP per capita rather than GDP, with data obtained

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from the World Bank website [41]. We analysed the relationship between the density of
zooarchaeological records and GDP per capita for each country using a GLM with
quasipoisson errors to account for overdispersion. GDP per capita was logarithmically
transformed for analysis.

We also investigated whether the spatially uneven spread of zooarchaeological data 257 could instead be related to variable topography across Europe, which might for example 258 affect landscape accessibility for research. We calculated the average elevation for each 259 country using a high-resolution 30-arc seconds (c.1km) elevation map from the 260 WorldClim database [42]. We analysed the relationship between the number of 261 zooarchaeological records and average elevation for each country using a negative 262 binomial GLM to account for count data with considerable overdispersion. Average 263 elevation was logarithmically transformed for analysis. We also compared the elevation 264 profile for the zooarchaeological dataset to that of Europe to assess whether there were 265 differences in the overall range of values, and to check that the average elevation was 266 not being biased by widely outlying values. We calculated the elevation of each 267 zooarchaeological data point at a 30-arc raster square resolution and then randomly 268 269 sampled the same number of points from an ArcMap layer of European elevation and plotted both datasets as histograms. 270

In order to examine any changes or patterns in dating precision over time, we plotted the lower and upper date range by midpoint for each zooarchaeological record. We also plotted all dated Holocene records against a theoretical linear increase in the number of zooarchaeological records, in order to identify changes in the rate of accumulation of records through time.

60 277 **3. Results**

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5	279	(a) Global faunal record
3	280	The number of extinct species known from Holocene and historical contexts has
, 0 1	281	increased over time since the mid-eighteenth century, with peaks of new species
2 3	282	descriptions in the early twentieth century and again close to the present (figure 1).
4 5	283	This pattern has primarily been driven by description of 'fossil' species (n=199), with
6 7 8	284	description of 'modern' (historically extant) species ($n=56$) largely concluded by the
9 20	285	1950s. Nearly four times as many recently extinct mammal species have been described
21 22	286	from islands ($n=196$) compared to continental regions ($n=55$), with four species having
22 23 24 25 26 27	287	past geographic ranges that included both continents and islands. We found a
26 27	288	significant negative relationship between description date and body mass across the
28 29	289	'fossil' data subset, with larger-bodied species generally described earlier than smaller-
80 81 82	290	bodied species (est=-0.0030, S.E.=0.0013, t-value=-2.000, <i>p</i> <0.05; d.f.=109, R ² =0.048,
52 33 34	291	lambda=1.00), but not for the 'modern' data subset (est=-0.00025, S.E.=0.00057, t-
85 86	292	value=-0.43, <i>p</i> >0.05; d.f.=53, R ² =0.0035, lambda=1.00) (figure 2). For the combined
87 88	293	fossil and modern dataset, we found a significant negative relationship between
89 10	255	tossit and model it dataset, we found a significant negative relationship between
11 12	294	description date and body mass on continental regions, with larger-bodied species
3 4	295	again generally described earlier (est=-0.0031, S.E.=0.0014, t-value=-2.141, <i>p</i> =<0.05;
15 16	296	d.f.=41, R ² =0.10, lambda=1.00), and a non-significant relationship on islands (est=-
17 18	297	0.00021, S.E.=0.00050, t-value=-0.410, <i>p</i> =>0.05; d.f.=103, R ² =0.00163, lambda=0.973)
19 50 51	298	(figure 2). Reanalysis following removal of major outliers did not change the results
52 53	299	(electronic supplementary material, table S5).
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301 (b) Continental zooarchaeological record

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- 3 1	302	The number of zooarchaeological records varied hugely between species in our dataset,
5	303	from nearly 4000 records for red deer (<i>Cervus elaphus</i>) to fewer than 20 records for
7 3 2	304	wolverine (<i>Gulo gulo</i>) (electronic supplementary material, table S3). We found a
, 0 1	305	positive but non-significant relationship between zooarchaeological abundance and
2 3	306	body mass (0.21 \pm 0.11, p = 0.07), and a significant relationship between abundance and
4 5 6	307	trophic level (1.45 \pm 0.39, p < 0.01), with herbivores having a higher number of records
7 8	308	than carnivores. Models with trophic level as the single explanatory variable had the
9 20	309	highest explanatory power, both in our original models and in models that included
21 22 23	310	species as a random factor (figure 3a, electronic supplementary material, table S4).
23 24 25	311	Modern mammalian population density was significantly negatively associated with
26 27	312	body mass in the global dataset (-0.27 \pm 0.09, p < 0.01) (figure 3c), and was negatively
28 29 30	313	but not quite significantly associated with body mass in the North American data subset
81 82	314	(-0.32 \pm 0.16, <i>p</i> = 0.054) (figure 3b). Confidence intervals of slopes for the Holocene
83 84	315	zooarchaeological and North American datasets overlapped, but did not overlap
85 86 87	316	between the Holocene zooarchaeological and global datasets (electronic supplementary
88 89	317	material, table S4), indicating that these two datasets were significantly different. When
10 11 12	318	the data were subdivided by trophic guild, we found a significant negative body mass-
12 13 14	319	abundance relationship across all modern mammal population density datasets (figure
15 16	320	3b-c, electronic supplementary material, table S4).
17 18 19	321	We found no significant body-mass abundance relationships across either trophic
50 51	322	level subset of Holocene data. However, for herbivores the slope was negative and 95%
52 53	323	confidence intervals overlapped with modern herbivore datasets, indicating that it was
54 55 56	324	not significantly different. In contrast, for carnivores the slope was positive and did not
57 58	325	overlap with modern carnivore datasets, indicating that it had a significantly different
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relationship (figure 3a-c, electronic supplementary material, table S4). 326

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42 43 44	344	4. Discussion
45 46	345	
47 48	346	(a) Bias in Ho
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58 59 60	351	Indeed, the dis

er of zooarchaeological records varied considerably between countries wever, when country size was controlled for, we found no association ensity of zooarchaeological records and a country's GDP per capita (0.37) 4) or average elevation (-0.20 \pm 0.16, *p* = 0.21). Elevation profiles showed eological records were present up to 2000 metres above sea level (m.a.s.l.) erally absent at higher elevations (electronic supplementary material, ilst the overall elevation profile for Europe reaches 3000 m.a.s.l., over ntinent is below 2000 m.a.s.l., indicating that the two datasets were not lifferent. sion of dating for records across the Holocene was also temporally Ill, the average date range for each zooarchaeological record became er to the present, with this shift becoming particularly marked around 0 5). Accumulation of successive records across the Holocene was not ne, showing a low rate of accumulation during the early Holocene, dy accumulation for much of the mid-Holocene, and accelerating in the e close to the present. olocene mammal baselines and extinction risk

f description dates for globally extinct mammals demonstrates that we complete and biased understanding of mammalian extinctions and past versity even for the Holocene, the most recent interval of geological time, of ongoing new species descriptions continuing to increase over time. scovery curve of recently extinct mammals shows a nearly exponential

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increase from the 1950s onwards, rather than any signs of levelling off close to the present. This pattern contrasts markedly with the global trajectory of species descriptions for extant mammals over recent decades, which continue to increase but at a relatively reduced rate compared to the total number of extant species already known [43]. Estimating the number of recently extinct mammal species that remain to be discovered and described is therefore an important research goal. However, extrapolating the number of undescribed species from a temporal pattern of past species descriptions is associated with large margins of error unless the inventory of a group is largely complete and beginning to level off over time, which is demonstrably not the case for recently extinct mammals [44,45]. Rapid advancements in ancient DNA and genomics have also facilitated the identification of new species based on fossil material and museum specimens in recent years, and these techniques will doubtless only increase our ability to describe new species into the future [46]. Overall, it therefore remains surprisingly challenging to make even basic assumptions about past patterns of diversity, biogeography, community composition, and severity and dynamics of past human impacts for one of the most-studied and ecologically significant animal groups. Our analysis also highlights that we have a poorer understanding of past diversity of recently extinct small-bodied mammals, notably rodents and bats, compared to

larger-bodied species (e.g. carnivores, artiodactyls, perissodactyls, proboscideans). Small mammals continue to be described regularly from the Holocene palaeontological and zooarchaeological records, whilst the largest species were mostly described by AD 1900. The earlier discovery of larger-bodied mammals in the Holocene record is associated in part with taphonomic processes that preferentially select for the deposition and survival of larger skeletal elements [15]. It also probably reflects the

common historical preference for taxonomists to describe larger, 'charismatic' species first for scientific kudos [7,20]. Even without explicit size-based biases in fossil preservation or description, specific targeted sampling strategies such as fine-mesh sieving are needed to recover remains of smaller vertebrates and invertebrates, and these were not widely employed until the latter half of the twentieth century [47]. Once recovered, smaller bones and teeth can also be more difficult to identify to species level [48], so that the quality of described data can easily be biased towards larger species in Holocene faunal assemblages.

The extinct Holocene mammal fauna currently consists largely of insular species, with geographic hotspots of known global Holocene species extinctions including the Caribbean, Madagascar and insular Mediterranean, and with the vast majority of insular species (nearly 82%) only described during the last 100 years. However, we only found a significant relationship between body mass and description date for continental regions, and not for insular regions. On islands, this lack of significance is at least partly attributable to the general pattern of reduced body masses observed in extinct and extant insular mammals, associated with ecological resource limitation driving dwarfing of large-bodied lineages under the 'island rule' [49]. By contrast, continental regions harboured a wider range of body masses, with the largest generally being found and described first. Many species may also have been described later from insular regions due to their increased geographic remoteness and inaccessibility, and because many major island systems are located in the tropics where preservation of long-term environmental archives is generally poorer and more recently developed techniques can be required to identify and date regional faunal remains [50,51]. Tropical species also tend to exhibit smaller geographic range sizes, which has also been shown to be a negative correlate of description date in mammals [52].

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Small body size has been associated with an overall lower risk of extinction for 402 mammals in both the past [5] and the present [53,54], principally because smaller-403 bodied species have higher reproductive rates that enable faster population growth and 404 recovery [53]. However, this pattern may be more complicated within specific 405 geographical areas and ecoregions, with higher levels of recent extinction and current 406 risk observed in the smallest-bodied species for some regional faunas (e.g. Australia, 407 Caribbean) [53–55], and it has been recognised that the very smallest species in some 408 vertebrate groups may be at higher risk of extinction due to small geographic range 409 sizes [58]. Our analyses indicate that our baseline understanding of mammalian 410 diversity remains incomplete at both global and regional levels, with our knowledge of 411 the extent of recent small mammal extinctions in particular likely to be underestimated 412 due to incomplete and biased sampling. This bias in our baseline hinders our ability to 413 compare recent levels of species losses and assess relative patterns of extinction risk 414 across fundamental gradients of mammalian diversity and ecology. 415

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417 **(b)** Bias in zooarchaeological data through space and time

418 Bias in species occurrence data has been studied extensively in ecological [59], historical [60,61] and palaeontological [62,63] datasets; however, our analysis 419 represents, to our knowledge, the first attempt to directly quantify multiple sources of 420 421 bias in a large zooarchaeological dataset. Due to the fact that patterns of human influence may differ between zooarchaeological deposits, we note that our analysis 422 423 relates specifically to large mammals for the European Holocene, and may not necessarily reflect patterns of bias in other zooarchaeological datasets. 424 Our results show that body mass scales inversely to population density in natural 425 populations of large mammals, a relationship that has also been demonstrated 426

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3 4	427	elsewhere [64,65]. We would therefore expect fewer large-bodied species to be present
5 6 7	428	in the zooarchaeological record if zooarchaeological abundance reflected underlying
7 8 9	429	patterns of ecological abundance and rarity in sampled source communities. By
10 11	430	contrast, abundance increases with higher body mass in our zooarchaeological dataset;
12 13 14	431	although this relationship was not significant, its slope did differ significantly from that
14 15 16	432	of the global ecological mammal dataset. The power of body mass-abundance
17 18	433	relationships in the North American and zooarchaeological datasets may have been
19 20 21	434	reduced by the small sample sizes and smaller range of body masses available for
21 22 23	435	analysis, with paucity of data points leading to a Type 2 error, a problem that has also
24 25	436	been noted in previous large-scale analyses of fossil mammal assemblages [66]. The
26 27 28	437	disproportionately higher abundance of large-bodied mammals in the
28 29 30	438	zooarchaeological record probably reflects preferential human hunting of these species.
31 32	439	The likelihood that larger-bodied vertebrates have been a primary focus of prehistoric
33 34 35	440	human hunting effort is supported by the pattern of terrestrial and insular extinctions
36 37	441	following human arrival or technological change across the globe during the late
38 39	442	Quaternary [7,67], and wild megafaunal vertebrates continue to be overharvested for
40 41 42	443	consumption in many regions today [68]. Whilst the increased vulnerability of large-
42 43 44	444	bodied mammals to humans is also strongly related to their slower reproductive life
45 46	445	histories, these species are highly detectable and non-arboreal and tend to be diurnal,
47 48 49	446	and so are likely to have come into contact with humans relatively frequently [17].
50 51	447	However, the abundance-body mass relationship observed in our zooarchaeological
52 53	448	dataset was also confounded by trophic level, which was the only consistently
54 55 56	449	significant predictor of zooarchaeological abundance across all models, with herbivores
56 57 58	450	more abundant than carnivores. This almost certainly reflects the increased likelihood
59 60	451	of prehistoric humans to hunt herbivores for subsistence, as well as the higher available

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biomass of large herbivores in ecosystems compared to carnivore biomass. Interestingly, the scaling of abundance and body mass in the zooarchaeological record also differs between trophic groups; small herbivores were more abundant than larger herbivores, a pattern shown in natural populations, whereas large carnivores were more abundant than smaller carnivores, which is significantly different from the pattern seen in natural populations [35]. This unexpected finding may reflect the fact that because herbivores were more heavily exploited overall for subsistence, humans were less discriminate and hunted all body size classes opportunistically, leading natural patterns of relative abundance to be reflected in the zooarchaeological record. The particular dominance of species such as red deer and wild boar (Sus scrofa) in Europe's zooarchaeological record may also be partly due to forest laws that afforded protection to these 'noble game' species for recreational hunting, e.g. in medieval Britain [69]. By contrast, humans were less likely to come into contact with smaller carnivores and more likely to see large carnivores as competitors for both wild prey and domestic livestock, and so might have disproportionately targeted these species. Indeed, large carnivores are more likely to be involved in human-wildlife conflict than smaller carnivores for these reasons today [70]. Large carnivores such as wolf (*Canis lupus*) and brown bear (Ursus arctos) were also the focus of recreational hunting in medieval Europe [69]. Although the spatial spread of zooarchaeological data was uneven across Europe,

we found that the relative wealth of a country did not influence research output across European countries once geographic size was taken into account. This pattern may partly reflect the fact that archaeology is a fairly international endeavour and therefore academics will often fund, carry out, or collaborate on excavations in countries other than their own. For example, within our study area there is a strong international

academic presence in Anatolian archaeology [71] and parts of the Caucasus [72]. Furthermore, even where research funds are reduced, countries can nonetheless have strong traditions of academic research and achieve relatively high research outputs through the efforts of only a few researchers. A final reason may be that the literature searches carried out to compile the database included grey literature in numerous European languages as well as research published in international journals, and therefore reached a range of research repositories beyond those dependent on or linked to higher levels of funding [29,73]. This finding is therefore a strong argument for employing exhaustive and thorough data collection protocols when compiling species occurrence datasets based on zooarchaeological assemblages in order to minimise sources of researcher bias. There is also increasing availability of large, open-access databases of zooarchaeological and palaeontological records that will continue to facilitate the incorporation of long-term archives into biodiversity assessments [74]. However, as these datasets are usually derived from multiple and often secondary sources, great care is needed in auditing and curating in order to minimise the use of erroneous or poor-quality data [75]. We also found no elevational bias in the spatial spread of zooarchaeological data across Europe. This may be due to the fact that many prehistoric human populations are known to have lived at high altitudes in Europe (and elsewhere globally), and that archaeological research is increasingly conducted in remote and hard-to-access landscapes including at higher elevations [76]. The precision of dating for zooarchaeological records, represented by the length of available date ranges, also varied across the Holocene, providing a further source of bias in our zooarchaeological dataset and influencing its ability to make inferences about past biodiversity baselines and human impacts. This temporal variation partly reflects the mix of absolute and relative methods used to date records; whereas the majority of

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502	our zooarchaeological records were indirectly dated, direct radiocarbon dates are
503	generally associated with shorter ranges. However, in general we found that
504	zooarchaeological records were assigned increasingly specific dates nearer to the
505	present. This finding probably reflects the fact that archaeologically-defined time
506	periods (e.g. Mesolithic, Neolithic, Bronze Age) tend to denote changes in human
507	technology and subsistence, and so become narrower towards the present due to the
508	general acceleration of technological change through time, with archaeologists
509	increasingly confident in constructing chronologies and assigning dates to
510	archaeological material nearer the present. Ideally zooarchaeological records would be
511	directly radiocarbon dated to ensure that chronologies for investigating faunal turnover
512	and extinction were comparably accurate and consistent across datasets. However,
513	given the sheer quantity of data generated from archaeological sites and the costs
514	involved in absolute dating, this is unfortunately still rarely a realistic option.
515	Our results also reveal periods of increased accumulation of Holocene
516	zooarchaeological records over time. This pattern might reflect periods of prehistoric
517	human population increase. For example, there is a notable increase in our
518	accumulation curve from ~AD 500 to AD 1200, coincident with the Medieval period,
519	during which there was an estimated six-fold increase in human population in Europe
520	and evidence for associated large-scale forest clearance [77]. Increased pressure on
521	wildlife populations could therefore potentially have led to increased numbers of
522	zooarchaeological records found within these sites. Conversely, it has been
523	demonstrated that younger components will always be more abundant than older
524	components in the archaeological record, due to increased taphonomic destruction of
525	older faunal remains and greater detectability of stratigraphically higher samples [78].
526	These temporal trends therefore indicate that we have more abundant and precise

records of faunal occurrence nearer the present, with important implications for using
zooarchaeological datasets of faunal records through time to reconstruct biodiversity
change.

5. Disentangling bias from reality in the Holocene faunal record

Our combined analyses demonstrate that bias is widespread, with sources and patterns of bias varying across taxonomic, spatial and temporal scales in the Holocene faunal record. Size bias is a particularly complex issue to resolve, especially when using the recent faunal record to investigate species population dynamics and extinctions at both local and global scales. For example, large mammals tend to be well-identified and overrepresented in the Holocene fossil and zooarchaeological records relative to their status in natural source populations, whereas our knowledge of many small mammals is generally more incomplete or even altogether unknown, providing a biased understanding of extinction risk across different taxa. In contrast, modern-day abundance has been shown to be a strong predictor of abundance in the Holocene faunal record for other vertebrate groups [18]. Sources and patterns of bias in Holocene faunal datasets therefore need to be carefully identified and quantified on a case-by-case basis, particularly accounting for potential variation in bias between different taxonomic or ecological groups, and considering appropriate spatial extents, timescales, and types of faunal data that are most relevant to the specific parameters of different research questions.

However, whilst this study has addressed potential limitations associated with the use of recent fossil and zooarchaeological data "at face value", we also recognise that Holocene faunal data can be a reliable and important indicator of biodiversity change when bias is accounted for. Indeed, we have previously used the zooarchaeological

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2 3 4	552	dataset studied above to reconstruct mammalian range change across the Holocene in
5 6 7	553	Europe, and by controlling for sample size variation across time and between different
7 8 9	554	species we were able to reconstruct the dynamics of range declines and identify
10 11	555	taxonomic variation in vulnerability or resilience to human impacts over time [4]. These
12 13 14	556	data provide the only available insights into a wide range of important questions
14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42	557	surrounding past environmental and ecological conditions and how they have changed
	558	through time in response to different stressors or drivers, and so must remain an
	559	essential component of the toolkit available for biodiversity research.
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	561	Data accessibility. The datasets supporting this paper are available in the
	562	supplementary materials.
	563	Authors' contributions. J.J.C. and S.T.T. designed the research and coordinated data
	564	collection; J.J.C. and B.C. analysed the data; and J.J.C. and S.T.T. wrote the manuscript.
	565	Competing interests. We have no competing interests.
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42 43 44	569	Acknowledgments. We are extremely grateful to Dr Robert Sommer and Prof. Norbert
45 46	570	Benecke for providing zooarchaeological data from the 'Holocene History of the
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789	FIGURE LEGENDS
790	
791	Figure 1. Cumulative and decadal descriptions of extinct Holocene mammal species, AD
792	1750 – AD 2012.
793	
794	Figure 2. The relationship between log body mass of extinct Holocene mammal species
795	and description date, modified by whether they were described from modern or fossil
796	specimens (top row) or whether they originated from continental or insular regions
797	(bottom row). Slopes taken from linear regressions; see main text for regression
798	information.
799	
800	Figure 3. Comparison of the abundance-body mass relationship between
801	zooarchaeological and ecological datasets. (a) Relationship between proportion of
802	occupied sites in which a species occurs in the zooarchaeological record and log body
803	mass. (b, c) Relationship between population density and body mass in the orders
804	Artiodactyla, Carnivora and Perissodactyla, within the body size range 0.5-700 kg from

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2 3 4	805	the ecological dataset published by Damuth (1987); data for North America (b) and all
5 6 7	806	continents pooled together (c). Population density and body mass are log transformed.
7 8 9	807	Closed circles represent herbivores, open circles represent carnivores. Dashed lines
10 11	808	represent a simple linear regression for herbivore subsets, solid lines represent a
12 13 14	809	simple linear regression for carnivore subsets; see main text for regression information.
15 16	810	
17 19	811	Figure 4. Map of Europe showing the density of mammalian Holocene zooarchaeological
18 19 20	812	records (Azimuthal Equidistant projection, cell size: 1 x 1 degree).
21 22	813	
23 24	814	Figure 5. Plot showing (i) ranges of estimated dates for all zooarchaeological records
25 26 27	815	through the Holocene (black bars), and (ii) the accumulation of records in the
28 29	816	zooarchaeological record through time (red line). Grey slope denotes a theoretical
30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60	817	linear rate of accumulation.

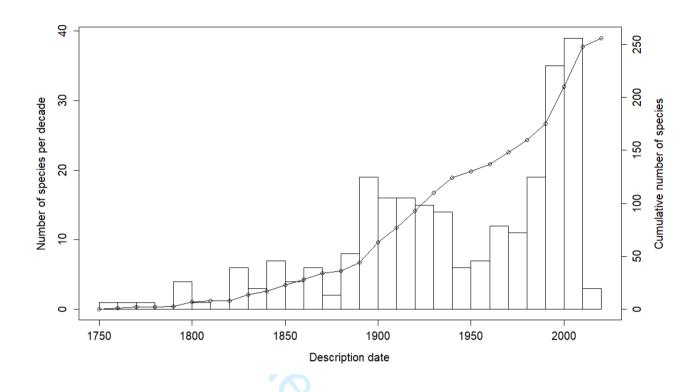


Figure 1. Cumulative and decadal descriptions of extinct Holocene mammal species, AD 1750 – AD 2012.

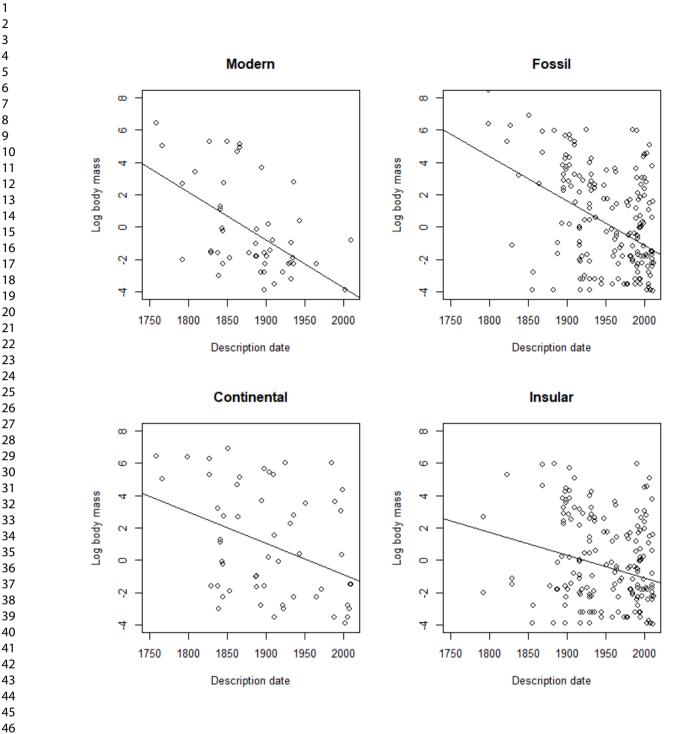


Figure 2. The relationship between log body mass of extinct Holocene mammal species and description date, modified by whether they were described from modern or fossil specimens (top row) or whether they originated from continental or insular regions (bottom row). Slopes taken from linear regressions; see main text for regression information.

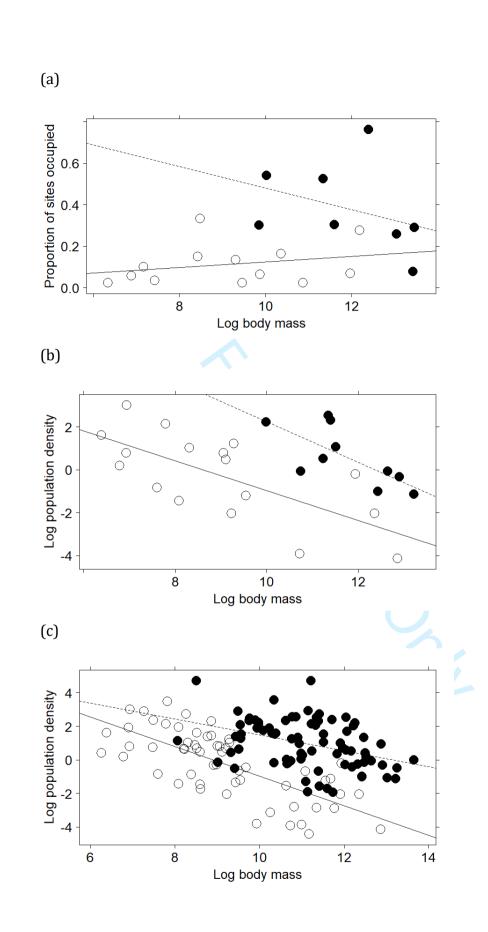


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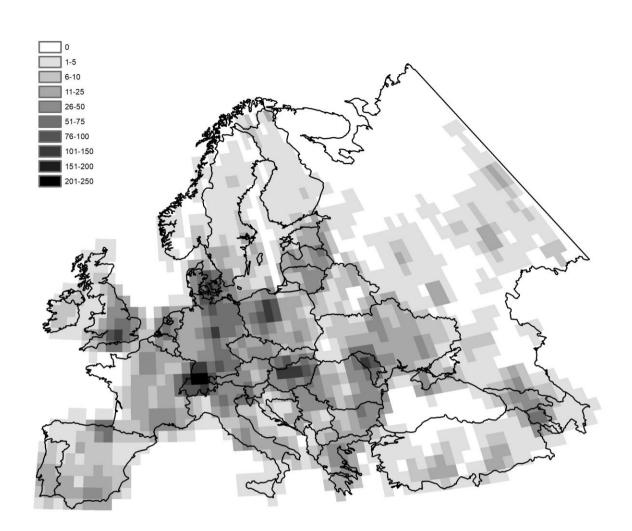


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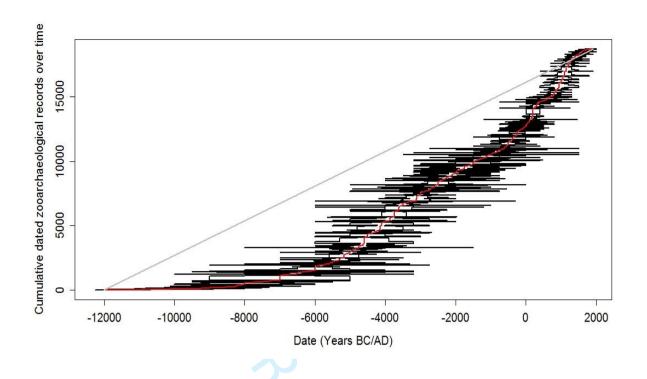


Figure 5. Plot showing (i) ranges of estimated dates for all zooarchaeological records through the Holocene (black bars), and (ii) the accumulation of records in the zooarchaeological record through time (red line). Grey slope denotes a theoretical linear rate of accumulation.