

# Paleo-archives for informing conservation under climate change

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To show that paleorecords from the late Quaternary can be used to infer climate-driven biodiversity change and inform metrics for contemporary conservation policies, we aligned temporal inferences of population-, species-, community- and ecosystem-level changes from 50 k BP to 0 k BP. All biological trends were plotted in calendar years.

## Population- and Species-level data

Time series of mammal fossil abundances are often used to identify biotic changes in response to late Quaternary climatic shifts and they are frequently published in the scientific literature (1). To illustrate population level changes in abundance for mammals we plotted relative abundance through time for three representative rodent taxa, which could be identified at the species level (*Pseudomys australis*, *Rattus fuscipes*, *Pseudomys apodemoides*) from the Naracoorte cave in Australia (2, 3). For each sampled time period (42.9, 39.3, 26.2, 20.1, 16.7, 16.3, 15.1, 13.9, 10.6, and 5.4 k BP) we calculated percent change in relative abundance across the three species.

We used plant relative abundance estimates from pollen counts at Monticchio lake

(Southern Italy) (4) to calculate percent change in relative abundance for three representative taxa, which could be identified either at (i) the species level (*Carpinus betulus*); or (ii) at the genus level, where we knew a priori that the genus was represented by a single species through time (*Abies alba*, *Fagus sylvatica*). We calculated the pollen counts for each selected taxon in each millennial time bin by multiplying the relative abundance of each taxon with the total sum of pollen counts across all taxa (5). We then summed the pollen counts for each selected taxon within each millennial time interval. Lastly, we recalculated the relative abundance for each taxon within each time interval as the percentage of the taxon pollen count relative to the sum of pollen counts across the three taxa.

Changes in the area of a species geographical range can be inferred from georeferenced and dated fossil records, paleoclimatic simulations and species distribution models (6). To show this, we extracted published maps of inferred distribution for muskox (*Ovibos moschatus*) at four different periods (42, 30, 21, and 6 k BP; Fig. 4 E) from Lorenzen et al. (6).

Ancient DNA (aDNA) from fossil remains can be used to estimate population size dynamics over time with Bayesian Skyline plots. To show this we plotted the effective population size ( $N_e$ ) of the muskox for the last 50,000 years using a previously compiled dataset containing 266 radiocarbon-dated fossil records (7, 8). From these, 138 records have associated aDNA sequences (9), which are available in GenBank (10). These have been aligned using Geneious v1.9.8 (11) and the MUSCLE algorithm (12), using default settings. Radiocarbon dates were calibrated using OxCal and the IntCal13 calibration curve (13). We reconstructed the genealogy using BEAUti v1.10.4 and BEAST v1.10.4 (14). We used the calibrated date of each fossil record as prior information for the tip-dates, and the standard deviation surrounding these dates to derive uncertainty in the tip-dates.

We selected a GTR + Gamma + Invariant Sites substitution model, based on Akaike Information Criterion (AIC), done in jModelTest v2.1.10 (15). We used a strict molecular clock, a Coalescent Bayesian Skyline Tree Prior, a constant Skyline Model and the UPGMA starting tree. The Markov Chain Monte Carlo was set with a chain length of 100,000,000 and to log parameters every 10,000 simulations to avoid possible autocorrelation during the MCMC analysis. We then analyzed the output, generated the data for the plot, and visualized it using Tracer v1.7.1 (16). A similar approach has been used previously on changes in mammal population sizes estimated from aDNA and contemporary sequences (17).

Since changes in morphological traits can provide a deeper understanding of phenotypic responses of populations and species to global change (See Main text), we retrieved and plotted estimates of Woodrat (*Neotoma cinerea*) body mass through time, based on paleo-middens (18). Here Smith et al. (18) generated a chronosequence over the last thirty thousand years using 94 paleo-middens from Titus Canyon, Death Valley (US), with body mass being inferred from fossil fecal pellets measured in each midden.

## Community-level data

Changes in plant diversity through time can be estimated using pollen fossil data(19). To show this we estimated plant taxonomic richness at the genus level using data from Monticchio lake (4) and Peten Itza lake (Guatemala) (20). We did this using relative abundances and raw pollen counts, respectively. To transform relative abundance data into presence/absence type data we considered genera to be present when relative abundance values were  $>$  zero. While there are different thresholding approaches for calculating community metrics using pollen data, which include both fixed thresholds and taxa specific thresholds, we followed the approach used by Nieto-Lugilde et al. (21) to convert pollen abundance into presences based on fossil pollen. Importantly Nieto-Lugilde showed that different thresholding techniques do not significantly affect the trend and strength of vegetation change estimated over time (21). We binned the data into thousand-year bins and counted the number of present genera in each millennial time bin.

## Ecosystem-level data

To illustrate changes in plant biomass since the last deglaciation, we retrieved published estimates of total tree biomass from Blarquez and Aleman (22). Blarquez and Aleman used modern pollen assemblages and remote-sensing data to calculate above ground tree biomass for six tree genera (*Abies*, *Acer*, *Betula*, *Picea*, *Pinus*, and *Populus*) at one-thousand year time intervals (14 ka to 0 ka) across eastern Canada (22). To do this they:

1. Modelled associations between modern pollen assemblages and tree biomass values for each local assemblage using remote sensing data. Estimates were validated against observed values, and model skill assessed using root mean squared error.

2. Used a transfer function (modern analogue technique [MAT]) to assign tree biomass values to past assemblages from their closest modern analogues.

To show changes in net primary productivity (NPP) through time we retrieved annual NPP values at a  $1^\circ \times 1^\circ$  grid cell resolution for land-based areas of the world (23). We then subset the global dataset to estimate NPP for the North American zoogeographic region (24) at 25-year intervals over the last fifty thousand years (50 ka - 0 ka) and plotted the mean and standard deviation calculated for each time interval.

We estimated changes in past Savanna ecosystems in Asia for four time periods (42, 30, 21, and 6 ka), using global paleo vegetation maps that were generated using a simulation approach with three distinct steps, as described by Allen et al. (25):

1. The paleoclimate of each time slice was simulated using the HadCM3 coupled atmosphere-ocean general circulation model, following the approach described by Singarayer and Valdes (26), but with land-surface properties simulated dynamically using revised specifications of Triffid, ice-sheet extent and elevation (27). Anomalies between the paleoclimate of a time slice and the pre-industrial experiment were calculated for the climatic variables required to run the LPJ-GUESS dynamic global vegetation model (DGVM) (28, 29). Following Miller et al. (30), these anomalies were then interpolated to a half-degree grid and used, along with the CRU TS 3.0 climate dataset (31), to drive an LPJ-GUESS simulation of global vegetation. In order to simulate the vegetation of grid cells on shelf areas exposed by lowered glacial sea levels we combined and followed the approaches of Huntley et al. (32, 33).
2. LPJ-GUESS simulations were made without simulating the nitrogen cycle or nitrogen-limitation of growth. We followed Allen et al. (34) and specified the atmospheric CO<sub>2</sub> concentration according to Vostok ice-core data (35, 36), using the EDC3 chronology (37), and obliquity specified following Laskar (38). The plant functional types (PFTs) used followed Forrest et al. (39), but with the addition of seven shrub PFTs, details of the parameterization of which are given by Allen et al. (25). Carbon mass (C-mass) and leaf area index (LAI) of each PFT in each grid cell were computed as the mean of their values for the last 90 years of the simulation and across 25 replicate 0.1 ha plots. The simulation for each plot was run for 590 simulated years with a mean interval of 100 years between stochastic patch-destroying disturbance episodes. For

each time slice, LPJ-GUESS was run for all half-degree grid cells with non-zero extent of ice-free land. For time slices in the range 22 ka - 0 ka, eustatic sea-level followed Lambeck (40); for earlier time slices, eustatic sea level was estimated using a model relating eustatic sea levels reported by Lambeck (40) to millennial marine oxygen isotope data (41) and millennial mean relative sea level for the Red Sea (42). For time slices in the range 26 ka - 0 ka, the fractional ice cover in a grid cell was estimated as the distance-weighted mean of the values given in the ICE-6G dataset (43) for the surrounding nine one-degree grid cells; for earlier time slices, the fractional ice cover was taken as that for the time slice in the range 26 ka - 0 ka with the closest matching eustatic sea level to that estimated for the target time slice. The ice-free land area of the grid cell was then estimated as the product of the land area and the fractional ice cover.

3. Biomes were inferred using a rule-based model, full details of which are given by Allen et al. (25). The Savanna biome mapped here was inferred when, firstly, the simulated total C-mass for the grid cell was above a threshold value equivalent to  $1.0 \times 10^9$  kg for a half-degree grid cell at the equator, area  $3087.57 \text{ km}^2$  (i.e.  $0.324 \text{ kg m}^{-2}$ ), and secondly, LAI of the Tropical Broadleaved Evergreen tree PFT was  $\leq 2.0$  AND LAI of the Tropical Broadleaved Raingreen tree PFT was  $\leq 0.6$  AND LAI of the C4 Grass PFT was  $> 0.3$  and either the combined LAI of Tropical Shrub PFTs was  $> 0.3$  OR the LAI of the Tropical Broadleaved Raingreen tree PFT was  $> 0.3$

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