Nowhere to run, nowhere to hide: carnivoran extinction in the Holocene

INTRO:

Material and Methods

**Sample:**

We collated a sample of 114 species of carnivorans from the Ecoregister (REF). 5 variables of interest were obtained by averaging the observed values per species for 934 observations over 195 sites from all continents (Body mass, Home range, BMR, Diet, Extinction status). The sites were dated from Xya to Xya (covering the late Pleistocene and Holocene) and the final sample contained 19 species or 16.7% extinct, and 95 species or 83.3% extant carnivorans – a coverage of ~32% of all extant species in the order.

Additionally, we collated data on brain size, EQ, locomotor type and litter size from literature sources (see TABLE X for details and sources) and calculated abundance, Shannon, and Simpson indices of diet diversity based on primary data (scat and camera-traps) from the Ecoregister. Diet was categorized using data from scat samples, obtained from the Ecoregister. Scat categories in the Ecoregister include: vertebrates (mammal, bird, reptile), invertebrates (arthropod, arachnid, insect), fruit, plant, aquatic (annelid, mollusc) and fungi. They were obtained from 134 observations from 103 different sites, based on the composition of between 12 and 3878 scats per site. Scat composition was subsequently recategorized using k-means clustering, resulting in 6 different diet categories: 1-6…[describe]

Shannon and Simpson indices of diet (diversity of diet) were calculated using the package vegan (see Table X). Species’ abundance was calculated using data from camera-traps available in the Ecoregister using the following formula:

(count - number) / (count/ count per day) [CHECK THIS]

Furthermore, we obtained a PC derived as the first principal component from a PCA based on the following variables obtained from Noonan (2015): Social Class, Natal Den, Hibernaculum, Predation, Food Storage, Residence, Fossorial Propensity, Primary, Secondary, Occupant, and Burrowing Class (for detailed description of these variables see (Noonan et al., 2015)). This PC is related to burrowing and fossoriality as indicated by the highest positively loaded variables - Fossorial propensity (0.68) and Burrowing class (0.53)). We chose only the first PC, explaining ~53% of the variance, as there was a steep decline in variance explained into the subsequent PCs (PC2 – 23% proportion of variance, PC3 12%, and PC4 – 5%).

All continuous variables (despite abundance) were log scaled (abundance was Yeo-Johnson transformed due to many 0 values) and min-max normalised before imputation.

Detailed description of all variables used, including source, distribution (along with distribution of the imputed datasets) is available in Table X.

Table X – data sources and detailed description of variables, including histograms of the distribution of the original dataset, and density plots of the 20 imputed datasets (red lines) and the observed original data (blue line). NM = number of missing species (out of 114)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Variable | Units | Description | Distribution | Imputation | Source | NM |
|  |  |  |  |  |  |  |
| Body mass | kg | Body mass |  |  | Ecoregister | 10 |
| Home Range | km2 | ? |  |  | Ecoregister | 45 |
| Brain | mm3 | Endocranial volume |  |  | (Michaud et al., 2022) | 28 |
| EQ | Index | Derived using CEQ formula |  |  | (Chambers et al., 2021) | 49 |
| PC | PC score | See methods for details |  |  | (Noonan et al., 2015) | 46 |
| BMR | ml O2 hr-1 |  |  |  | Ecoregister | 0 |
| Litter size | number | Number of offspring per litter |  |  | (Noonan et al., 2015) | 34 |
| Shannon index of diet | Index |  |  |  |  | 46 |
| Simpson index of diet | Index |  |  |  |  | 46 |
| Abundance | Frequency of camera trap observation | See methods for details |  |  |  | 34 |
| Longevity | years | Maximal longevity |  |  | (Noonan et al., 2015) | 49 |
|  |  |  |  |  |  |  |
| **CATEGORICAL** |  |  |  |  |  |  |
| Extinct or Extant | 0 – extinct, 1 - extant |  |  |  | Ecoregister | 0 |
| Locomotor mode | 6 categoris | A – arboreal  R – semiarboreal  SA – semiaquatic  SC – scansorial  SF – semifossorial  T - terrestrial |  |  | Galvez-Lopez | 0 |
| Diet | 6 Categories | Based on k-means clustering of scat data |  |  | Ecoregister | 46 |

**Imputation:**

We imputed 20 datasets as the original dataset contained ~20% missing values (White et al., 2011). The variable with the highest number of missing values was longevity (43% or 49 missing species) while Locomotor type and BMR had no missing values. Detailed description of the missingness pattern and imputation analyses in Supplement. All continuous variables (log scaled and min-max normalised) were imputed using Predictive Means Matching (PMM), and all categorical variables were imputed using Polytomous logistic regression (polyreg). Imputation was run over 100 iterations using the package mice.

**Phylogeny:**

We used the latest PHYLACINE phylogeny (Faurby et al., 2018) providing 1000 trees of 111 of the 114 carnivoran species in our sample. We manually added the 3 missing species as follows: *Martes caurina* as sister species to *Martes americana*, *Conepatus robustus* as sister to both *Conepatus chinga* *and Conepatus leuconotus*, and *Felis lybica* as sister to *Felis silvestris*.

**Statistical analysis:**

All statistical analyses were performed in R 4.2.1 (R Core Team, 2021) using RStudio 2022.07.1 Build 554. All packages used are listed in TABLE X. All phylogenetic analyses were conducted on the 20 imputed datasets and were run across all 1000 trees. The MCMCglmm results (20 datasets, 100 trees, N chains) were pooled used Rubin’s rule (Barnard & Rubin, 1999).

Table X Packages used in the analyses and data processing.

|  |  |  |
| --- | --- | --- |
| **Package name** | **Version** | **Used for** |
| ape | 5.6.2 | Phylogenetic analyses |
| BAMMtools | 2.1.10 | Tree manipulation |
| dplyr | 1.0.10 | Various data manipulation |
| easystats | 0.5.2 | Descriptive statistics |
| ggplot2 | 3.3.6 | Plotting |
| ggtree | 3.4.4 | Phylogenetic tree visualisations |
| lattice | 0.20.45 | Plotting |
| lavaan | 0.6.12 | Structural Equation Modelling |
| mice | 3.14.0 | Multiple imputation |
| MCMCglmm | 2.34 | MCMCglmm |
| mulTree | 1.3.7 | Incorporating multiple trees in MCMCglmm |
| naniar | 0.6 | Analyses of missing data |
| phylolm | 2.6.2 | Phylogenetic logistic regressions |
| phytools | 1.2.0 | Various phylogenetic data manipulation |
| psych | 2.2.9 | Descriptive statistics and plotting |
| see | 0.7.3 | Plotting |
| semTools | 0.5.6 | Plotting SEM |
| vegan | 2.6.4 | Calculating of Shannon and Simpson index |

MCMCglmm

Priors, parameters etc etc

SEM

RESULTS:

DISCUSSION:

References:

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