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Contrasting evidence of phylogenetic trophic niche conservatism in mammals worldwide

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Abstract

Aim Phylogenetic niche conservatism (PNC), a pattern of closely related species retaining ancestral niche-related traits over evolutionary time, is well documented for abiotic (Grinnellian) dimensions of the ecological niche. However, it remains unclear whether biotic niche (Eltonian) axes are also phylogenetically conserved, even though knowledge of biotic niches is essential to an understanding of the spatiotemporal dynamics of ecological communities. We conduct the first analysis of biotic PNC by evaluating dietary specialization in a vertebrate class.

Location Global

Methods We analysed two global compilations of diets of living mammals and a more detailed database for large carnivores together with a species-level phylogeny to evaluate trophic PNC. We searched for evidence of PNC by estimating the phylogenetic signal in distinct descriptors of dietary niche.

Results Trophic niches were generally similar among related species but not strongly conserved under a niche-drift macroevolutionary model (Brownian Motion). The degree of similarity in trophic niche varied among different taxonomic groups and was, importantly, even within the same group, contingent on the metric of dietary preferences used and the quality of information on the database.

Main conclusions Overall, our results showed limited support for PNC in the trophic niche of mammals. However, different data sources and metrics of dietary preferences sometimes offered different conclusions, highlighting the importance of gathering high-quality quantitative data and considering multiple metrics to describe dietary niche breadth and to assess PNC. The fully quantitative database for large carnivores provided some interesting evidence of PNC that could not be detected with semi-quantitative or presence/absence descriptors. Subsequent assessments of phylogenetic imprints on dietary specialization would benefit from considering different metrics and using well-resolved phylogenies jointly with detailed quantitative diet information. While Eltonian trophic niches did not show the same high levels of evolutionary conservatism often

displayed by Grinnellian niches, both niche components should be considered to understand range limits of species and clades at biogeographic scales.

Introduction

In 1957, Hutchinson formalized the concept of ecological niche as a multidimensional hypervolume that describes the set of biotic and abiotic conditions where a species can persist. Traditionally, ecological niches have been conceptually divided into two main classes: Grinnellian and Eltonian (Soberón, 2007). While the former can be defined by broad scale non-interactive environmental variables, the Eltonian niche (also named functional or trophic niche) focuses on biotic interactions and resource–consumer dynamics. Certain axes of the ecological niche change slowly and closely related species tend to retain their ancestral niche-related traits over evolutionary time, resulting in a pattern known as “phylogenetic niche conservatism” (PNC, Wiens & Graham, 2005; Wiens *et al.*, 2010). Phylogenetic niche conservatism is usually assessed estimating phylogenetic signal which is a measure of the statistical dependence among species' trait values due to their phylogenetic relationships (Revell *et al.*, 2008). Most research on PNC has centred in evaluating the extent to which realized Grinnellian niches are phylogenetically conserved, whereas much less effort has been directed at examining conservatism in Eltonian aspects of the niche (Soberón, 2007). Beyond their relevance for a number of basic and applied questions in ecology and conservation biology (Wiens & Graham, 2005), realized climatic niches can be readily characterized from geographic distribution ranges (Olalla-Tárraga *et al.*, 2011). However, the data that define Eltonian niches are more difficult to obtain (Cooper *et al.*, 2010). This may explain why PNC in Grinnellian traits (e.g. those determining abiotic niche axes) has been studied at a variety of spatial and temporal scales (Pearman *et al.*, 2008; Peterson, 2011), but PNC in Eltonian traits (e.g. those determining resource utilization and biotic interactions) remains largely unexplored.

Phylogenetic niche conservatism is not ubiquitous and the extent to which many niche-related ecological traits are conserved or labile over evolutionary time still remains unclear. Considering that the detection of PNC depends on the trait and spatiotemporal scales of analysis, its existence should not be *a priori* assumed but needs to be tested (Losos, 2008; Wiens, 2008). With some exceptions (e.g. Pearman *et al.*, 2014), there is overall growing evidence for PNC in climatic niche dimensions such that closely related species occupy similar, albeit not necessarily identical, environments (Wiens & Graham, 2005; Wiens *et al.*, 2010; Olalla-Tárraga *et al.*, 2011). Regrettably, even for mammals and birds that have typically received most of the attention in the macroecological and macroevolutionary literature, empirical evidence of PNC in Eltonian traits is more limited and equivocal. In two seminal papers, Böhning-Gaese & Oberrath (1999) and Brändle *et al.* (2002) found patterns consistent with PNC in the diets of bird species in central Europe. In contrast, Pearman *et al.* (2014) could not find evidence for PNC in the trophic niches of 405 species of breeding birds in Europe. With the exception of Kamilar & Cooper (2013), who found a weak phylogenetic signal in the diets of 213 primate species worldwide, there are no studies of PNC in mammal dietary specialization at any spatial or phylogenetic scale. In primates, the consumption of leaves, fruits and animal matter was largely disconnected from phylogenetic relatedness and diet was identified as one of the most evolutionary labile traits among the set of morphological, behavioural, life-history, ecological and climatic niche variables that were examined by Kamilar & Cooper (2013).

Ecological specialization in mammals is strongly linked to a wide array of specialized dentitions and anatomical morphologies and, hence, to dietary niche breadth. In fact, evolutionary transitions in trophic strategy and dietary innovations within lineages have been proposed as critical factors determining mammalian diversification (Price *et al.*, 2012; Cantalapiedra *et al.*, 2014). Here we conducted the first phylogenetically-comprehensive global analysis of PNC in dietary specialization among mammals. If PNC exists, it may be more easily detectable at higher phylogenetic levels (Losos, 2008). We, therefore, used two recently published global datasets of dietary preferences in

living mammals (Kissling *et al.*, 2014; Wilman *et al.*, 2014), together with a nearly complete species-level phylogenetic supertree (Fritz *et al.*, 2009) to explore whether mammalian dietary specialization tends to be conserved over evolutionary time or not. These large databases provide qualitative and semi-quantitative species-specific dietary descriptions for extant mammals (Kissling *et al.*, 2014; Wilman *et al.*, 2014). Complementarily, we compiled from the scientific literature a high resolution dataset, including both qualitative and quantitative diet information, to analyse three families in the order Carnivora (Canidae, Ursidae and Felidae) in more detail and assess the extent to which our inferences regarding PNC were affected by the way niche dimensions were defined and measured. Carnivora is an ideal taxonomic group to investigate the phylogenetic structure in trophic niche specialization as it covers a wide dietary spectrum from hypercarnivory to opportunistic omnivory and even strict herbivory. The majority of felids are active predators with highly carnivorous diets, whereas most ursids are omnivores and canids show an intermediate position across this gradient of dietary specialization. Accordingly, although macroevolutionary patterns in dietary specialization may not be apparent in Carnivora as a whole, trends may emerge within lineages or for different niche dimensions.

There has been much debate in the literature about which is the best definition and method to test for PNC, with some researchers arguing that phylogenetic signal alone can provide evidence of PNC and others insisting that PNC is only present when phylogenetic signal is stronger than expected under Brownian motion (Losos, 2008; Wiens, 2008; Cooper *et al.*, 2010; Wiens *et al.*, 2010). Because there is consensus that evidence of phylogenetic signal is necessary to demonstrate PNC, we first calculated empirical values of Blomberg's K (2003) to evaluate the tendency for related species to resemble each other more than they resemble species drawn by chance in a phylogeny. We then searched for evidence of niche-drift PNC (*sensu* Cooper *et al.*, 2010) evaluating the level of fit in the data to a Brownian motion (BM) model. Under such a scenario, species are viewed as having inherited their niches from their ancestors, after which interspecific differences have accumulated gradually over time following a random walk or BM model. This is a

classic macroevolutionary model to test for PNC although, as mentioned above there is current disagreement as to the thresholds at which we can regard the phylogenetic signal as high enough to be considered evidence of PNC (Losos, 2008; Kamilar & Cooper, 2013). Here, we adopted the view that if niche evolution fits a BM model, it is indicative of PNC (Cooper *et al.*, 2010; Kamilar & Cooper, 2013). Evidence of PNC could also be tested using different evolutionary models, for example assuming stabilizing selection towards one or multiple optima (i.e. Ornstein Uhlenbeck model), particularly if we expect slow evolving traits and phylogenetic inertia (Cooper *et al.*, 2010). However, a recent study (Cooper *et al.*, 2016) has shown that the Ornstein Uhlenbeck model is often incorrectly favoured over simpler models, particularly for data with measurement error and/or intraspecific variability. Given limitations in the data (see results) here we followed a precautionary approach and only tested the simpler drift model (BM).

Beyond the above-mentioned investigations for birds and mammals, there is a striking paucity of work evaluating congruence in PNC between Grinnellian and Eltonian niches. Larson *et al.* (2010) called attention to the possibility that the evolutionary trajectories of Grinnellian and Eltonian niches may be decoupled, as they found for the signal crayfish (*Pacifastacus leniusculus*).

Galapagos finches and African Rift lake cichlids are instances of adaptive radiations in which trophic niches were not evolutionarily conserved but Grinnellian climatic niches were (Cooper *et al.*, 2010; Wiens *et al.*, 2010). Larson *et al.* (2010) predicted that highly vagile species with greater capacities to overcome geographic barriers and hence, more similar realized and fundamental Grinnellian niches, should show PNC in both Grinnellian and Eltonian niches. Accordingly, we expected that trophic niches would be phylogenetically conserved in mammals, in synchrony with the evolutionary pattern documented for their Grinnellian niches (Olalla-Tárraga *et al.*, 2011). In mammals, diet and habitat specialist species tend to have more evolutionarily conserved thermal niches than generalists (Cooper *et al.*, 2011), a finding that further supports our a priori prediction of consistency between Grinnellian and Eltonian niche conservatism. We also predicted that

evolutionary lability in trophic niches may be detectable at lower taxonomic levels of analysis (i.e. some mammal orders such as Carnivora may not display patterns consistent with PNC).

Materials and Methods

Dietary Databases

We estimated phylogenetic signal in dietary diversity and composition from three datasets that provide species-level data. First, we analysed MammalDIET (Kissling *et al.*, 2014), a large semi-quantitative database including observed dietary data for 2033 species representing 27 of the 29 mammalian orders recognized by Wilson & Reeder (2005), all except Sirenia and Cetacea (Fig. 1). Data extrapolated from genus or family information for an additional 3331 species were not included to avoid biasing the phylogenetic signal. Diet was described for each species using ranked importance for each of 12 food categories: Mammal, Bird, Herptile (including amphibians and reptiles), Fish, Invertebrate, Fruit, Nectar, Leaf: woody (Woody), Leaf: herbaceous (Grass), Seed, Root and Other. The importance of each item was ranked according to four levels: 0 (absent), 1 (primary food item), 2 (secondary food item) and 3 (occasional food item). Since, to our knowledge, estimating phylogenetic signal in an ordinal trait is not currently possible, we converted importance into a binary trait: absent (original score of 0) or present (grouping original scores of 1, 2, or 3), and into a continuous trait (numerical rank importance ranging from 1 to 4 with absence redefined to 4 to generate a range from commonly eaten to absent).

The second database, EltonTraits (Wilman *et al.*, 2014), describes semi-quantitative dietary information for 4352 mammalian species representing 28 mammalian orders (all except Sirenia; Fig. 1). Although not analysed here, EltonTraits also provides dietary data for bird species and for 1048 mammals for which diet is extrapolated from genus or family information. For each species, diet was described using ranked percentages (in 10% increments) reflecting the estimated relative usage of 10 food categories: unclassified or general vertebrates (Vert), mammal and bird (Vend), Herptile, Fish, Invertebrate, Carrion, Seed, Fruit, Nectar, and unclassified or general plant material

(Plant). We analysed the ranked percentages as a continuous trait and also reclassified them into binary format: absent (percentage =0) or present (percentage > 0).

The third database, CUFdiet, was compiled from the scientific literature (a list of the consulted data sources is found in Appendix S1 in Supporting Information) for three families of large carnivores: Canidae, Ursidae and Felidae (73 species). While taxonomically limited, this dataset is the only one that provides detailed quantitative dietary data. Dietary composition was described according to 12 food categories: Mammal, Bird, Herptile, Fish, Invertebrate, Fruit, Pollen, nectar and/or flower (Nectar), Leaf/branch (Woody), Grass, Seed, Root and/or tuber (Root), and Carrion. Note that although dietary categories were different in the three datasets, most categories were directly comparable. Dietary composition in CUFdiet was described using presence/absence data obtained from diverse types of evidence (e.g., direct observations, fecal samples, stomach contents) which included qualitative descriptions and quantitative estimates from the different sources (Appendix S1). We defined a category as present in a species' diet if there was evidence from at least one study that the item was consumed even if infrequently. In addition, CUFdiet includes two quantitative estimates of dietary composition based on numerical frequency (proportion of the total items found per sample that belong to a given food category) and frequency of occurrence (proportion of samples that contained at least one item from a given food category). When multiple quantitative estimates were available for one species we recalculated proportions combining all samples across studies rather than using average values to account for large variation in sample sizes among studies.

Data Analyses

We searched for evidence of PNC estimating the phylogenetic signal in distinct descriptors of dietary niche. First, dietary diversity was computed as: (1) dietary breadth: total number of dietary categories consumed, based on presence/absence data (available for all three datasets); and (2) the standardized Levin's index of dietary diversity: calculated as $B_A = (B - 1)/(n - 1)$, where n is the

number of possible food categories and $B = 1/\sum \hat{p}_j^2$, where \hat{p}_j is the observed frequency of each food category. For CUFdiet \hat{p}_j was calculated using numerical frequency data, and for EltonTraits using ranked proportions. Second, we defined dietary niches in relation to the consumption of the different dietary categories using qualitative presence/absence descriptors (available for all datasets), and quantitative descriptors defined as: ranked numerical importance for MammalDIET, ranked percentages for EltonTraits, and numerical frequency and frequency of occurrence for CUFdiet.

To facilitate interpretation we compared the phylogenetic signal detected in dietary preferences with values from other species' traits that represented a range of characteristics expected to vary in their phylogenetic signal. We included traits likely to show similar values among related species (strong signal) reflecting morphology (average adult body size) and life-history (average gestation length); as well as more labile traits like social organization (average group size), space use (average home range size), and biogeographic distribution (native range size). Data on adult body mass were obtained from EltonTraits, whereas gestation length, group size and home range size data were obtained from PanTHERIA (Jones *et al.*, 2009) with additional values available for some carnivores included in CUFdiet. Native range size was estimated from IUCN distribution range maps, selecting only areas described as native or reintroduced in origin and currently occupied (presence classified as extant or probably extant). Trait data were log₁₀-transformed prior to analyses.

Because estimates of phylogenetic signal are dependent on the degree of phylogenetic relatedness among the species in the focal taxon for which data are available, a significant degree of phylogenetic clustering among the species represented in MammalDIET or EltonTraits could affect our results. To explore this potential source of bias, we quantified the net relatedness index (NRI) of species represented in these databases. NRI is a standardized measure of the mean pairwise phylogenetic distance of species, which quantifies the extent of phylogenetic clustering and overdispersion (Webb *et al.*, 2002). NRI is expressed in units of standard deviation and its

significance can be determined from the value itself, with values < -1.96 being significantly overdispersed and > 1.96 being clustered. We calculated NRI using the `mpd.query` procedure of the ‘PhyloMeasures’ package (Tsirogiannis & Sandel, 2015) in R 3.1.1 (R Core Team 2014). In addition, to allow for a strict comparison of PNC in both global datasets, we also analysed phylogenetic signal considering only species represented in both datasets.

To estimate phylogenetic signal in dietary diversity metrics we calculated K values (Blomberg *et al.*, 2003) using the mammalian supertree (Bininda-Emonds *et al.*, 2007) as updated by Fritz *et al.* (2009). This supertree describes phylogenetic relationships, inferred using molecular data, for 5020 mammalian species. We tested two hypotheses regarding observed K values: (1) lack of phylogenetic signal: observed K is not greater than would be expected if trait values for species were randomized among tips (with 1000 randomized samples); and (2) consistency with BM: we calculated whether K significantly departed from the phylogenetic signal estimated from 1000 simulated datasets in which BM was the evolutionary model. The simulations drew random trait values from a normal distribution (mean=0 and variance equal to that observed in the empirical dataset), starting with an ancestral root value equal to the empirical mean from the dataset. We also defined biologically meaningful bounds (e.g., for dietary breadth values bounds were [1, maximum number of categories] and for the standardized Levin’s index bounds were 0 and 1). We used the `phylosig` and `fastBM` procedures from the package ‘phytools’ (Revell, 2012) in R.

To estimate phylogenetic signal in presence/absence data we calculated D as defined by Fritz & Purvis (2010). D values around 1 imply a random distribution of the binary trait across the tips of the phylogeny whereas values around 0 imply BM; negative values indicate highly conserved traits. We used 5000 permutations to estimate the probability of the observed D under a null model of no phylogenetic structure (data were randomly shuffled along the phylogeny to estimate possible D values) and under simulated BM. We used the procedure `phylo.d` from the package ‘caper’ (Orme *et al.*, 2013) in R.

Incompletely resolved phylogenies (like the mammalian supertree we used which includes polytomies) can inflate estimates of phylogenetic conservatism. Davies *et al.* (2012) have proposed a rarefaction-based approach to calculate unbiased K values. Their approach consists in repeatedly constructing new phylogenies in which individual species from existing polytomies are selected at random to define new, completely resolved (but smaller) phylogenies for which phylogenetic signal is calculated. Unfortunately, because in our case data were not available for all species, defining new smaller phylogenies by breaking polytomies at random also affected sample sizes (as by chance a species selected from a polytomy could have no data). Therefore, we did not estimate all K values using this approach. Nevertheless, we explored the influence that unresolved polytomies had on the estimates of K for the general species traits analysed, including dietary breadth and Levin's index. We used 100 replicates to estimate the mean and range of unbiased K values for each trait.

To facilitate reproducibility and encourage open science the complete dataset analysed in this study is available on (<https://dx.doi.org/10.6084/m9.figshare.3250540.v1>). The complete R script used to generate reported results is also available as Appendix S2.

Results

The mammalian supertree included 5020 species. MammalDIET provided dietary information for 1921 of these species (112 species with dietary data were not represented in the phylogeny), EltonTraits provided dietary data for 4246 mammals (106 species were not in the phylogeny), and CUFdiet, for 73 species (all of which were present in the phylogeny). In total, 1730 species were represented in both MammalDIET and EltonTraits. All 73 species in CUFdiet were in EltonTraits, but seven of these carnivores were not included in MammalDIET. Mammalian diversity was generally well represented in both global datasets, but MammalDIET over-represented some groups, such as Primates, Carnivora and Artiodactyla (Fig. 1). Despite this over-representation,

phylogenetic structure in these datasets was not significantly clustered, but was instead overdispersed (NRI = -2.05 and NRI = -5.35 for MammalDIET and EltonTraits, respectively).

In general, we found evidence of phylogenetic signal in dietary diversity (both for dietary breadth and Levin's index) indicating that diets of related species tend to resemble each other more often than would be expected by chance (Fig. 2; Table S1 in Appendix S3). However, this signal did not provide strong evidence of PNC (Revell *et al.*, 2008). Dietary breadth from MammalDIET and dietary breadth and Levin's index from CUFdiet resulted in a K value significantly lower than expected under BM. On the contrary, the signal in dietary breadth and Levin's index calculated from EltonTraits was apparently consistent with BM. These results could be biased by unresolved polytomies, as unbiased estimates obtained from the rarefaction-based approach were much smaller than the estimates based on the complete dataset (Table S2 in Appendix S3). To explore whether these smaller unbiased values were consistent with BM, we simulated 1000 datasets for each of 50 randomly thinned trees and determined the probability that these K values were consistent with BM (P_{BM}). Although unbiased estimates of diet breadth were generally consistent with those expected under BM, in 17 out of the 50 thinned trees the K values were significantly smaller than expected ($P_{BM} < 0.05$). On the other hand, unbiased estimates of phylogenetic signal in Levin's index were all consistent with BM (for all 50 thinned trees, $P_{BM} > 0.05$). For the other traits and databases unbiased estimates were largely equivalent to those based on the complete datasets and phylogeny, and thus apparently not greatly affected by the presence of polytomies (Table S2 in Appendix S3). We note that although it is often assumed that $K = 1$ under BM (Cooper *et al.*, 2010), this is not necessarily true for traits with defined bounds, as we show in our results.

Considering other species' traits for comparison, we found higher K values than expected under BM for gestation length, non-significant departures from BM for adult body mass, and lower signals than expected under BM but still stronger than expected if values were randomly distributed

along the phylogeny for home range size, group size and native range size (Fig. 2; Table S1 in Appendix S3).

Phylogenetic signal in dietary breadth differed among mammalian orders (Table 1), with some groups having strong signals (e.g., Afrosoricida) while for others, dietary breadth was not clearly associated with evolutionary relatedness (e.g., Carnivora). However, results for many orders were not consistent between databases (Spearman correlation of estimated K values, $\rho=0.46$) affording contradictory inferences about niche conservatism. For example, dietary breadth in bats and rodents (Chiroptera and Rodentia), as measured using EltonTraits, showed a phylogenetic signal consistent with BM, whereas data from MammalDIET for both taxa revealed a signal lower than expected under BM (Table 1). These discrepancies are unlikely to be explained by differences in the clustering and number of species evaluated, since both datasets were significantly overdispersed in the mammalian phylogeny and analyses for the subset of species with data on both sources (N=1730) also showed discrepancies (Fig. 3; Table S3 in Appendix S3). For instance, phylogenetic signal in dietary breadth for 41 species of Lagomorpha was consistent with BM if measured with MammalDIET, but indicated faster evolution based on data from EltonTraits. The opposite pattern was observed in Rodentia (531 species) and Chiroptera (366 species) for which dietary breadth was consistent with BM using data from EltonTraits but not using data from MammalDIET (Fig. 3; Table S3 in Appendix S3). In both datasets the strength of the phylogenetic signal was not clearly associated with the mean dietary breadth or its variability among species (Spearman correlation ρ values $< |0.25|$, Table 2). Note that inferences regarding phylogenetic signal from groups with relatively small sample sizes (more prevalent in the MammalDIET database) should be made with caution.

Analysing the phylogenetic signal of dietary composition based on the presence/absence of particular food items, we also found differences across categories and databases (Fig. 4). Fritz and Purvis' D estimates for MammalDIET and EltonTraits were always significantly different from

those expected if values had been randomly distributed along the phylogeny, but differed inconsistently from values based on BM simulations (Table S4 in Appendix S3). In both datasets the number of species classified as consuming a dietary category comprised a small percentage of the total (median < 10%, ranging from 6 - 55% in MammalDIET and 4-65% in EltonTraits. Table S4 in Appendix S3). For all categories, presence data from EltonTraits fitted the results expected under BM, while estimates from MammalDIET differed in some cases (e.g., Fruit or Woody. Fig. 3). Presence data from CUFdiet suggested weaker phylogenetic signals which often did not significantly differ from that expected from randomization.

We also found significant phylogenetic signal in semi-quantitative descriptions of dietary composition in MammalDIET and EltonTraits (Table 2). Values were generally low and inconsistent with BM for MammalDIET, but mostly consistent with BM for EltonTraits. The detailed quantitative estimates from CUFdiet showed more variable patterns with consumption of certain types of food, such as Bird, being more closely associated with phylogeny than others (e.g. Fish). Interestingly, within this database we found that different quantitative estimates can lead to different results (e.g., numerical frequency versus frequency of occurrence of Bird) and that quantitative estimates of commonly consumed categories, such as Mammals, can reveal patterns that are not detectable with simpler presence/absence data (Table 2).

Discussion

Our global comparative analyses showed that dietary specialization is phylogenetically structured in mammals, with phylogenetic signal values similar to those of other ecological traits such as home range or group size (Fig. 2). In terms of their dietary diversity, and irrespective of the metric of dietary specialization, related mammalian species tended to resemble each other more than expected by chance. However, the existence of phylogenetic signal, albeit necessary to demonstrate niche conservatism, is not sufficient evidence that a trait has been strongly conserved over time. Under

our test of niche-drift PNC, the evolution of trophic preferences in mammals needed to be Brownian to be indicative of niche conservatism (Cooper *et al.*, 2010; Kamilar & Cooper, 2013). The two global datasets on mammal diets that we analysed provided potentially contrasting evidence. While values of Levin's dietary diversity index and, possibly, dietary breadth calculated from EltonTraits appeared to be phylogenetically conserved in mammals, dietary breadth estimates from MammalDIET suggested that trophic niches diverged faster than expected under BM with no evidence for PNC. Similarly, analysing mammalian dietary composition based on the presence or absence of particular food items showed that trophic preferences are non-randomly distributed across the phylogenetic tree. All dietary categories exhibited phylogenetic signal, but not all were consistent with BM (and again there were differences between datasets). Nectar consumption, a food resource that appears to be almost exclusively exploited by a few families of tropical bats (e.g. Phyllostomidae and Pteropodidae), and predation on Mammal and Bird were both consistent with BM in both datasets suggesting PNC. However, consumption of Fruit was only consistent with BM for EltonTraits.

The discrepancies between global databases cannot be explained by the different numbers of species represented in each case. MammalDIET provides dietary information for less than half the species in EltonTraits, but differences still existed when analysing subsets of species with dietary breadth data from the two sources (Fig. 3). A possible explanation for these discrepancies could be the effect of polytomies. For example, after accounting for the potential bias due to polytomies, which should be noted also greatly reduced sample size, patterns in dietary breadth using EltonTraits were not as clearly consistent with PNC. Even so, results from Levin's index still supported PNC once we accounted for the effect of polytomies. This leads us to suggest that underlying data quality played an important role in our ability to detect PNC in dietary specialization. Dietary preferences may vary temporally and spatially for the same species and such variation may be differently reflected in MammalDiet and EltonTraits (Fig. S1 in Appendix S3). Our analyses suggest that qualitative dietary descriptions and analyses of dietary breadth based on

the total number of food items consumed are not detailed enough for exploring PNC in trophic niches.

Niche conservatism is an emergent unifying concept for ecological and evolutionary theory with profound implications for the understanding of the origins of biogeographic patterns (Wiens & Graham, 2005; Wiens *et al.*, 2010). The geographic distributions of species and the existence itself of large-scale diversity gradients ultimately reflect dispersal, speciation and extinction dynamics. These three processes depend on the spatial configuration of the habitat and the combination of abiotic and biotic factors that determine the ecological niches of species. A tenet of biogeography posits that the range limits of species are primarily set by abiotic factors, which are typically conserved through evolutionary time (Wiens & Graham, 2005). For instance, the emergence of the latitudinal gradient in species richness across mammals is overall consistent with a process of climatic niche conservatism concomitantly acting with periodic niche shifts over evolutionary history (Buckley *et al.*, 2010). On the contrary, the importance of biotic interactions in shaping large-scale biogeographic patterns remains largely unexplored.

Analyses of Eltonian niches have typically been restricted to ecological studies focusing on the role of resource utilization for species coexistence in local communities (Ackerly *et al.*, 2006). Wiens (2011) recently called for a more integrative usage of Grinnellian and Eltonian traits to gain a better understanding on the factors that set the range limits of species and clades at biogeographic scales. He argued that climatic niche evolution may be constrained by species interactions that lead to niche pre-emption over macroevolutionary time scales. An indirect effect of trophic specialization limiting the rates of climatic niche evolution has been documented recently for damselfishes (Litsios *et al.*, 2012). Highly specialized trophic groups showed slower evolutionary rates in their environmental niches than generalists, a pattern also detected in mammals (Cooper *et al.*, 2011). Although not explicitly designed to explore these links, our analyses are also indicative of a possible connection between Eltonian and Grinnellian niches in determining the observed

geographic distribution of species. In bats, the inability of most New World lineages to radiate to temperate regions seems to be determined by their metabolic demands and the energetic costs associated to their highly specialized diets (Buckley *et al.*, 2010). This biogeographic pattern is consistent with the high degree of evolutionary conservatism in trophic niches detected for Chiroptera and for nectar consumption. All in all, these findings reinforce the view that the detection of phylogenetic conservatism is scale-dependent and highlight the importance of considering the evolution of Eltonian niche dimensions when studying physiological adaptations to novel climate regimes.

Globally, the biogeography of mammalian distributions is consistent with a scenario of prevailing climatic niche conservatism in the tropics and most novel adaptations, involving the expansion of niche breadth to new habitats and climatic regimes occurring in temperate regions (Buckley *et al.*, 2010; Olalla-Tárraga *et al.*, 2011; Safi *et al.*, 2011). This non-stationary pattern is congruent between studies that characterised either realized (Olalla-Tárraga *et al.*, 2011) or fundamental thermal niches in mammals worldwide (Khalik *et al.*, 2015). Within carnivores, for instance, Buckley *et al.* (2010) detected that the Feliformia clade with a tropical origin exhibits stronger phylogenetic conservatism of thermal niches than the largely temperate Caniformia clade. Such disparate sister-clade responses may also be present in trophic Eltonian niche dimensions (i.e. the highly specialized carnivore diets of felids against the more opportunistic diets of canids) and could obscure the detection of phylogenetic signal at the level of taxonomic order.

In this study we also analysed a more-detailed database (CUFdiet) that includes quantitative estimates of food resources consumed by 73 species in the order Carnivora. We found that macroevolutionary patterns emerged when we considered quantitative estimations of the food items consumed. While a binary qualitative treatment of dietary preferences did not reveal any evidence of PNC, our analyses based on quantitative diet data did. For example, even though nearly all canids, bears and felids consume mammalian prey, the proportion of Mammal in their diet was

variable and more similar among related species. This was not the case for the consumption of other vertebrate classes. Further, dietary specializations in Nectar, Woody and Seed were strongly phylogenetically conserved in Carnivora, showing pronounced PNC. These strong evolutionary signatures cannot be detected in analyses based on qualitative dietary descriptors again highlighting the importance of going beyond categorization and verbal descriptions in reporting and analysing diet data (Pineda-Munoz & Alroy, 2014).

Mammals and birds have both received a great deal of attention in the macroecological and macroevolutionary literature (e.g. Diniz-Filho *et al.*, 2009; Fritz *et al.*, 2009; Jones *et al.*, 2009; Cardillo, 2011; Morales-Castilla *et al.*, 2012). Despite efforts to develop characterization schemes for their dietary preferences (Pineda-Munoz & Alroy, 2014), it is only very recently that comprehensive species-level datasets on mammalian diets have become available for conducting global-scale analyses (Kissling *et al.*, 2014; Wilman *et al.*, 2014). As noted by Kissling *et al.* (2014), previous macroecological and/or macroevolutionary analyses of mammalian diets predominantly categorized species into three simple trophic levels, namely carnivores, omnivores and herbivores (see e.g. Kelt & Van Vuren, 2001; Price *et al.*, 2012; Pineda-Munoz & Alroy, 2014; Tucker *et al.*, 2014). This tripartite categorization prioritises trophic niche position, which characterizes the feeding resources used, but does not consider trophic niche breadth, which describes the number of feeding resources (Brändle *et al.*, 2002). As far as we know, only Ossi & Kamilar (2006) and Kamilar & Cooper (2013) have examined the relationship between diet and phylogenetic relatedness in a mammalian taxonomic order. Ossi & Kamilar (2006) analysed a small dataset for *Eulemur* species which was later reanalysed by Kamilar & Cooper (2013). This second study evaluated 31 traits for 213 primate species and found that dietary and climatic niches were among the most labile traits. Kamilar & Cooper (2013) described dietary niches based on the percentage of fruit, leaves and animal matter in the diet and report values of K similar to those we found for dietary breadth in Primates. Despite being low, our significance tests using biologically

meaningful bounds suggest K values for diet breadth are consistent with BM (Kamilar & Cooper did not test for significant departure from BM).

The paucity of phylogenetic comparative analyses of dietary specialization in mammals limits the interpretation of our findings on the evolution of this Eltonian niche-related trait. Studies of avian fauna, based on single datasets, have also yield contradictory messages. Böhning-Gaese & Oberrath (1999) found that phylogeny accounted for 7.2% of the variation in diet for 151 bird species in central Europe, much higher than the proportion accounted for by behavioural traits but lower than that explained by morphological or life history traits. Brändle *et al.* (2002) estimated that half the cross-species variation in dietary breadth of birds in eastern Germany was explained at the family and genus level, which they interpreted as a clear indication of phylogenetic conservatism. However, these studies did not explicitly test for PNC. On the other hand, Pearman *et al.* (2014) found no evidence for PNC in climatic, habitat and trophic niches of 405 species of breeding birds in Europe. All their niche axes exhibited phylogenetic signals lower than expected under a BM model based on a theoretical $K=1$. However, as we show here, smaller K values may actually be consistent with BM. In our analyses K values were also generally < 1 , but our simulation results show some of these low values support PNC.

Our study is the first global analysis of a vertebrate class aimed at examining whether or not evolutionary conservatism exists in Eltonian niches. Our findings offer novel insights to interpret which niche parameters are highly divergent or evolutionary conserved through speciation in mammals and the roles that Grinnellian and Eltonian niche conservatism may have played on the diversification and ecological differentiation of this clade. Contrary to our initial predictions, Eltonian trophic niches do not seem to show the same high levels of evolutionary conservatism consistently displayed by Grinnellian niches (Wiens & Graham, 2005; Soberón, 2007). This provides evidence that PNC is not ubiquitous. The cold tolerances of most tropical mammals appears to be niche-limiting as they are physiologically constrained to survive in warmer areas, but

trophic specialization does not seem to be subject to the same levels of stabilizing selection.

Although few quantitative data exist, conducting comparative studies at greater phylogenetic scales including entire clades does not always lead to detection of stronger phylogenetic signals (Losos 2008). Among-clade convergence can decrease evidence of PNC, thus analyses should be conducted considering both broad and narrow phylogenetic scales. Lack of a relationship between niche similarity and phylogenetic relatedness among species may also be due to an early burst of evolutionary divergence. Weak levels of phylogenetic signal would be expected if mammal species radiated adaptively with a burst of speciation early in the clade's history followed by slowdown evolutionary rates (Kamilar & Muldoon, 2010). There are numerous examples of adaptive radiations in which trophic niches were not evolutionary conserved but Grinnellian climatic niches were (Cooper *et al.*, 2010; Wiens *et al.*, 2010). The ecomorphological diversification of early Cenozoic mammals is a paradigmatic example of adaptive radiation driven by ecological opportunity that led to the exploitation of diverse niches vacated after the extinction of non-avian dinosaurs (Luo, 2007). The evolution of key innovations in trophic strategies, in combination with other biological traits such as body size, is thought to be critical for the diversification of mammals (Price *et al.*, 2012).

To conclude, we calculated different metrics of dietary specialization in extant mammal species and found that the detection of phylogenetic patterns for this Eltonian trait depended on the definition of trophic niche and on underlying data quality. The degree of similarity in trophic niches varied among different taxonomic groups and, importantly, even within the same group was contingent on the metric of dietary preferences used. Phylogenetic imprints on trophic niches cannot be safely inferred using only qualitative data regarding food items consumed and require more precise, quantitative or semi-quantitative descriptions of diet. Characterizing trophic niches requires capturing, or at least acknowledging, spatio-temporal variation in dietary preferences, ideally obtaining data from multiple studies and ensuring field data are not biased by methodological limitations (Martínez-Gutiérrez *et al.*, 2015). Going beyond verbal or categorical descriptions is a

first step towards this goal which, as we show here, can also bring interesting insights. Nearly all large carnivores eat mammals, but the proportion of their diets comprised by mammals varies such that related species are more likely to have similar proportions. Further assessments of phylogenetic imprints on dietary specialization would benefit from using well-resolved phylogenies jointly with detailed dietary information and diversity indices that enable analyses of quantitative, or at least semi-quantitative, dietary data. These analyses should also explore alternative evolutionary models to evaluate the different processes that underlie niche conservatism.

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SUPPORTING INFORMATION

Additional Supporting Information may be found in the online version of this article:

Appendix S1 Data sources for the CUFdiet database.

Appendix S2 Complete R script used to generate reported results.

Appendix S3. Supplementary tables and figure.

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MAOT and MGS designed the study. MGS and ER compiled the CUFdiet database. MGS and RBM processed the data. MGS helped draft the manuscript and analysed the data with contributions from FV. All authors revised the manuscript and gave final approval for publication.

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Table 1. Phylogenetic signal (Blomberg's K) detected in the dietary breadth (total number of food categories consumed) of species from different mammalian orders. Dietary data obtained from MammalDIET and EltonTraits. We report P_R as the P -values against a randomization test ($N=1000$) to determine if estimates significantly departed from expectations if there was no phylogenetic signal; and P_{BM} as the probability of the observed value being greater or smaller than the expected under a Brownian model of evolution (1000 simulated datasets). We also report the mean dietary breadth for each order/group and associated standard deviation (SD). N_p is the number of species with available data for each trait. Small orders includes mammalian orders with ≤ 20 species with diet data: Cingulata, Dermoptera, Hyracoidea, Macroscelidea, Microbiotheria, Monotremata, Notoryctemorphia, Paucituberculata, Peramelemorphia, Perissodactyla, Pholidota, Pilosa, Proboscidea, Scandentia and Tubulidentata.

Order	MammalDiet ($N=1921$)						EltonTraits ($N=4246$)					
	N_p	K	P_R	P_{BM}	mean	SD	N_p	K	P_R	P_{BM}	mean	SD
Afrosoricida	14	1.22	0.009	0.728	1.71	1.267	41	2.81	0.001	0.026	1.29	0.642
Didelphimorphia	38	0.66	0.046	0.258	2.24	1.261	70	1.81	0.001	0.026	3.66	1.328
Erinaceomorpha	8	0.72	0.106	0.668	2.50	1.414	20	1.71	0.001	0.454	3.80	1.765
Lagomorpha	44	0.44	0.003	0.389	1.18	1.206	79	0.11	0.708	0.001	1.03	0.158
Dasyuromorphia	16	0.46	0.475	0.170	1.25	0.577	61	0.39	0.137	0.001	2.49	0.698
Diprotodontia	39	0.36	0.608	0.006	1.69	1.217	117	0.60	0.001	0.543	2.13	1.236
Chiroptera	424	0.32	0.001	0.027	1.51	0.984	877	1.01	0.001	0.998	1.27	0.650
Soricomorpha	85	0.30	0.206	0.008	1.29	0.737	298	1.93	0.001	0.369	2.49	0.744

Primates	218	0.25	0.001	0.059	3.02	1.672	310	0.53	0.001	0.370	3.10	1.257
Small_Orders	58	0.23	0.014	0.003	1.62	1.057	125	0.29	0.001	0.058	1.68	0.930
Artiodactyla	149	0.17	0.035	0.001	2.01	1.297	216	0.49	0.001	0.528	1.70	1.081
Rodentia	626	0.15	0.001	0.001	1.84	1.237	1678	1.13	0.001	0.804	2.72	1.103
Carnivora	202	0.13	0.208	0.001	3.08	1.788	272	0.20	0.001	0.001	2.90	1.318
Cetacea	—	—	—	—	—	—	82	0.88	0.001	0.760	1.84	0.429

Table 2. Phylogenetic signal detected in quantitative descriptors of mammalian dietary composition. Descriptors included: ranked presence/importance for the MammalDIET database, and numerical frequency (proportion of the items found in a sample belonging to that food category) and frequency of occurrence (proportion of the samples that contained at least one item from that food category) for the CUFdiet database. Phylogenetic signal is estimated using Blomberg's K. We report P_R as the P -values against a randomization test ($N = 1000$) to test if estimates significantly departed from the expected if there was no phylogenetic signal; and P_{BM} as the probability of the observed value being greater or smaller than expected under a Brownian model of evolution (1000 simulated datasets). N_{f0} is the number of species with presence or frequency = 0 for each dietary category.

Dietary category	MammalDiet				EltonTraits				CUFdiet							
	Numerical importance ($N=1921$)				Numerical freq. ($N=4246$)				Numerical freq. ($N=53$)				Freq. occurrence ($N=50$)			
	N_{f0}	K	P_R	P_{BM}	N_{f0}	K	P_R	P_{BM}	N_{f0}	K	P_R	P_{BM}	N_{f0}	K	P_R	P_{BM}

Vert	–	–	–	–	3898	0.24	0.001	0.022	–	–	–	–	–	–	–	–
Vend	–	–	–	–	3860	0.37	0.001	0.313	2	0.11	0.054	0.064	–	–	–	–
Mammal	1739	0.21	0.001	0.002	–	–	–	–	2	0.10	0.090	0.015	4	0.12	0.025	0.124
Bird	1797	0.10	0.003	0.001	–	–	–	–	7	0.17	0.023	0.041	7	0.17	0.012	0.041
Herptile	1766	0.13	0.001	0.001	3849	0.27	0.001	0.059	14	0.10	0.266	0.001	16	0.13	0.092	0.005
Fish	1840	0.16	0.001	0.001	4056	0.32	0.001	0.118	40	0.08	0.666	0.001	40	0.13	0.187	0.004
Invertebrate	866	0.21	0.001	>0.999	1476	0.57	0.001	>0.999	12	0.09	0.393	0.001	14	0.08	0.304	0.001
Fruit	1198	0.14	0.001	0.941	2585	0.43	0.001	>0.999	32	0.32	0.001	0.378	31	0.05	0.858	0.001
Nectar	1818	0.18	0.001	0.001	4040	0.31	0.001	0.095	51	1.66	0.005	0.765	50	–	–	–
Woody	1749	0.11	0.002	0.001	–	–	–	–	48	1.76	0.003	0.757	42	0.33	0.051	0.420
Grass	1637	0.14	0.001	0.001	–	–	–	–	36	0.06	0.731	0.001	34	0.07	0.641	0.001
Seed	1523	0.16	0.001	0.188	2932	0.49	0.001	>0.999	46	0.50	0.013	0.691	43	0.02	0.908	0.001
Root	1792	0.12	0.001	0.001	–	–	–	–	53	–	–	–	50	–	–	–
Plant	–	–	–	–	2098	0.71	0.001	>0.999	–	–	–	–	–	–	–	–
Carrion	–	–	–	–	3895	0.48	0.001	0.590	43	0.07	0.655	0.001	44	0.08	0.69	0.001
Other	1565	0.10	0.001	0.001	–	–	–	–	–	–	–	–	–	–	–	–

Figure Legends

Figure 1. Available dietary data for all mammalian taxonomic orders from the two global databases (MammalDIET, N=1921; EltonTraits, N=4246) compared with taxonomic diversity (N=5020) represented by the mammalian phylogeny of Fritz *et al.* (2009). The CUFdiet dataset includes data for 73 species, all of them in the Order Carnivora.

Figure 2. Estimates of phylogenetic signal (Blomberg's K) detected in diverse mammal species' traits including dietary breadth (the total number of food categories consumed) as described by each dataset (MammalDIET, EltonTraits and CUFdiet) and the standardized Levin's diet index based on numerical frequency data from the EltonTraits and CUFdiet databases. Asterisks indicate significant (< 0.05) values for P_R (estimates were significantly different from those expected if there was no phylogenetic signal) and for P_{BM} (estimates were significantly different from those expected under a Brownian model of evolution). A point indicates marginal significance ($P < 0.10$).

Figure 3. Phylogenetic signal (Blomberg's K) detected in dietary breadth (total number of food categories consumed) of species from distinct mammalian orders. Dietary data obtained from MammalDIET and EltonTraits, including only species with data in both datasets to compare estimates. Small orders include mammalian orders with ≤ 20 species: Cingulata, Dermoptera, Hyracoidea, Macroscelidea, Microbiotheria, Monotremata, Notoryctemorphia, Paucituberculata, Peramelemorphia, Perissodactyla, Pholidota, Pilosa, Proboscidea, Scandentia and Tubulidentata. P_R and P_{BM} represented as in figure 2.

Figure 4. Phylogenetic signal detected in qualitative descriptors (presence/absence) of mammalian dietary composition. Phylogenetic signal is estimated using Fritz & Purvis D ($D = 1$ when there is no phylogenetic structure). Asterisks indicate significant values for P_R (estimates were significantly different those expected if there was no phylogenetic signal) and for P_{BM} (estimates were significantly different from those expected under a Brownian model of evolution). A point indicates marginal significance.

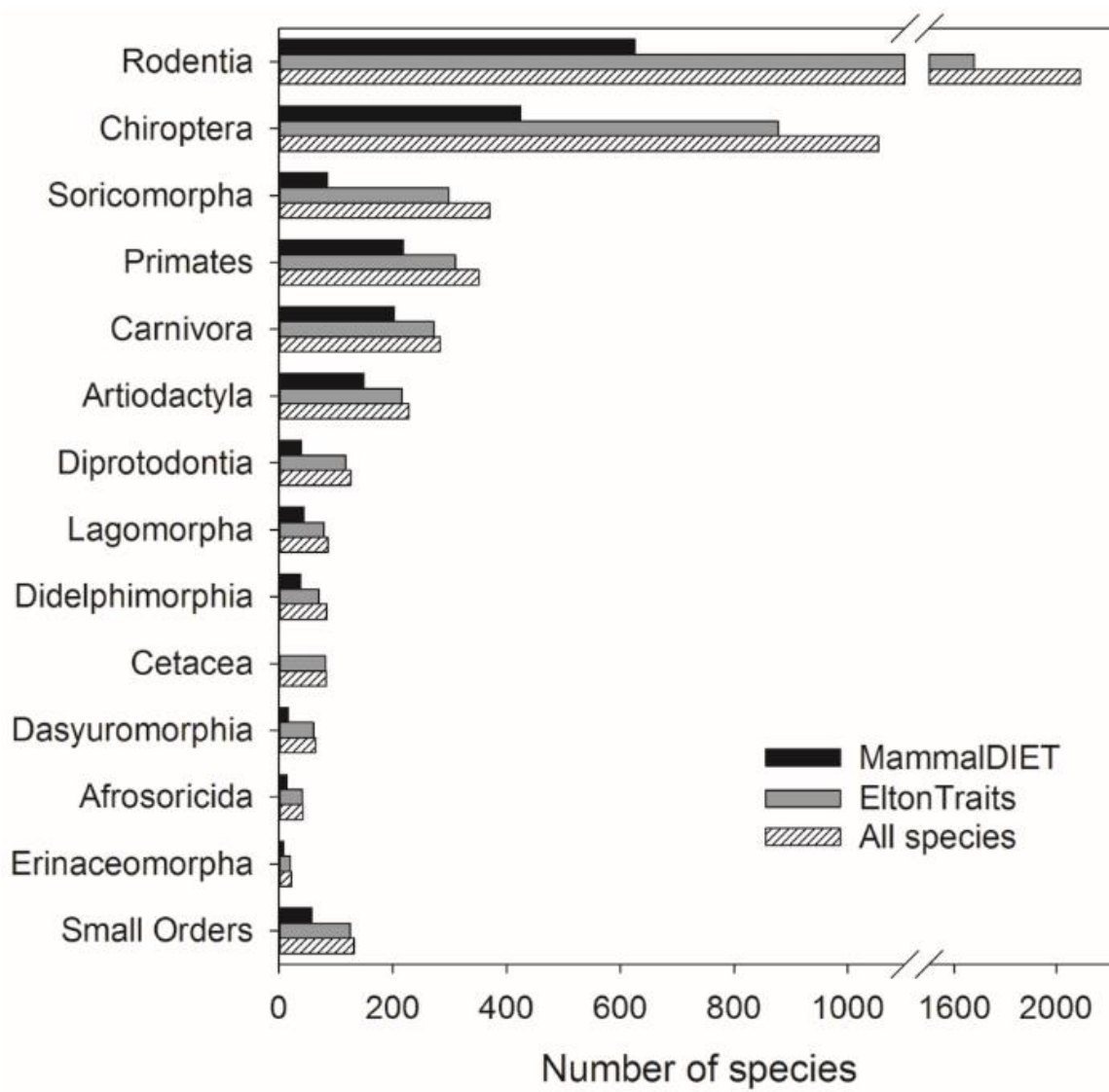


Figure 1

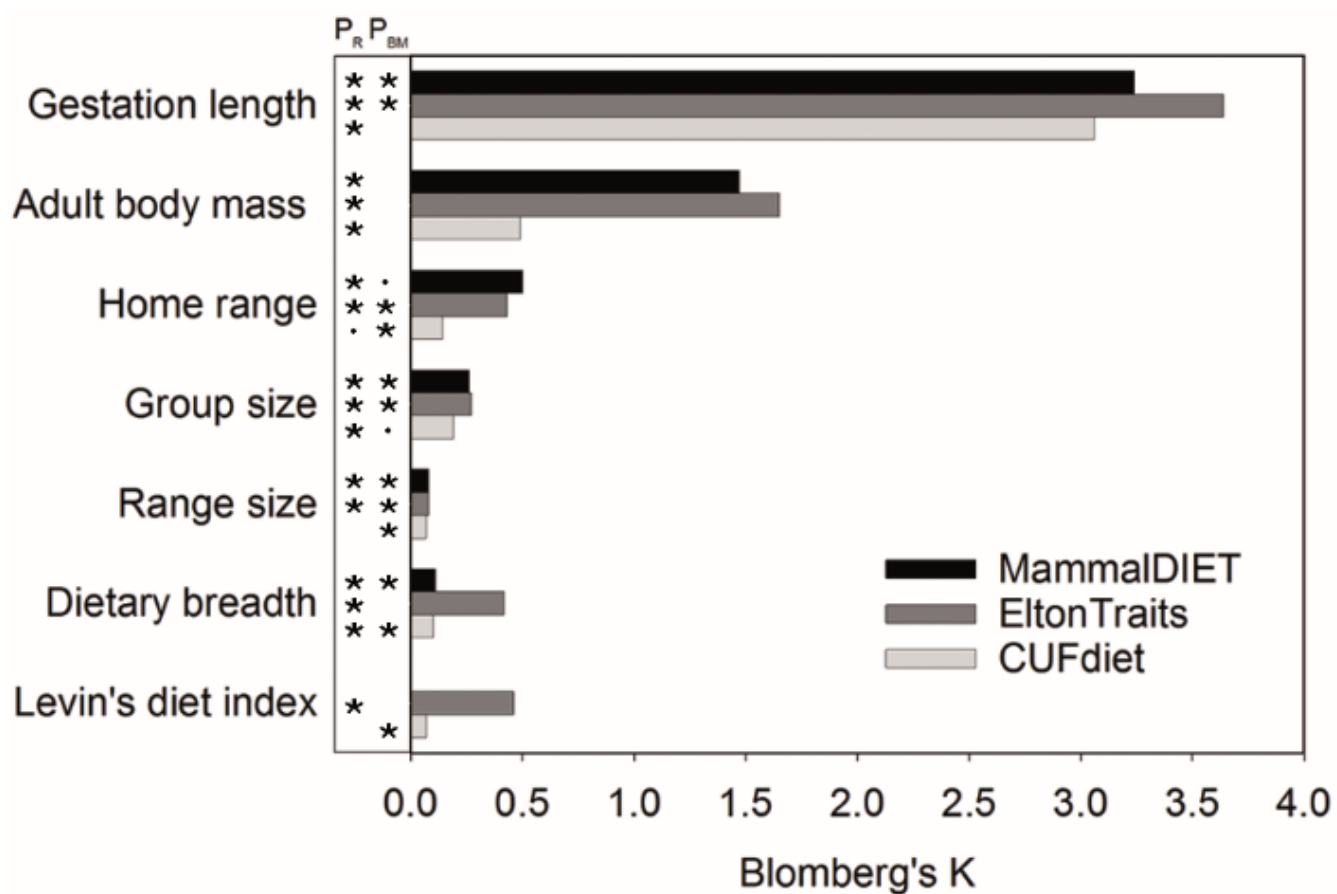


Figure 2

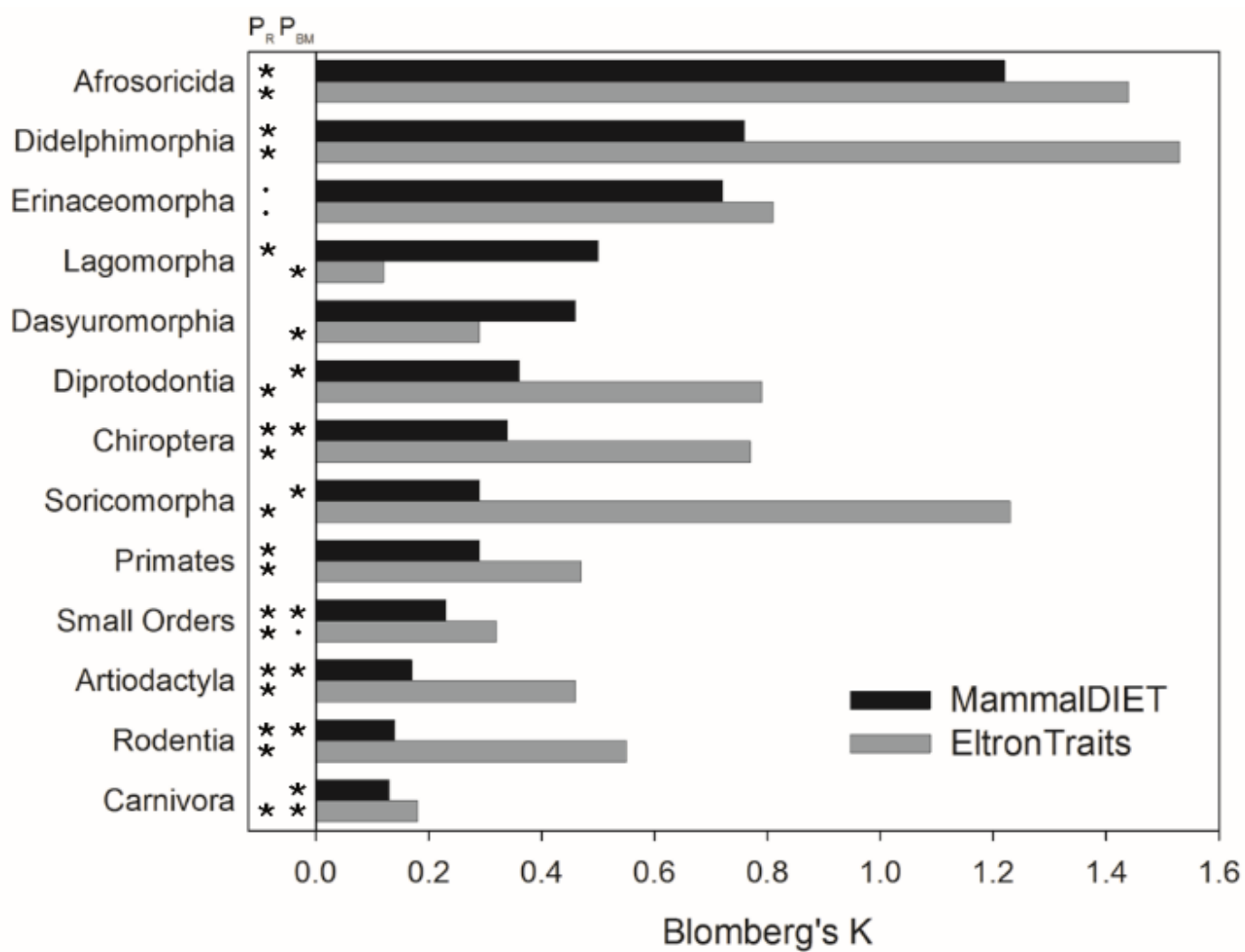


Figure 3

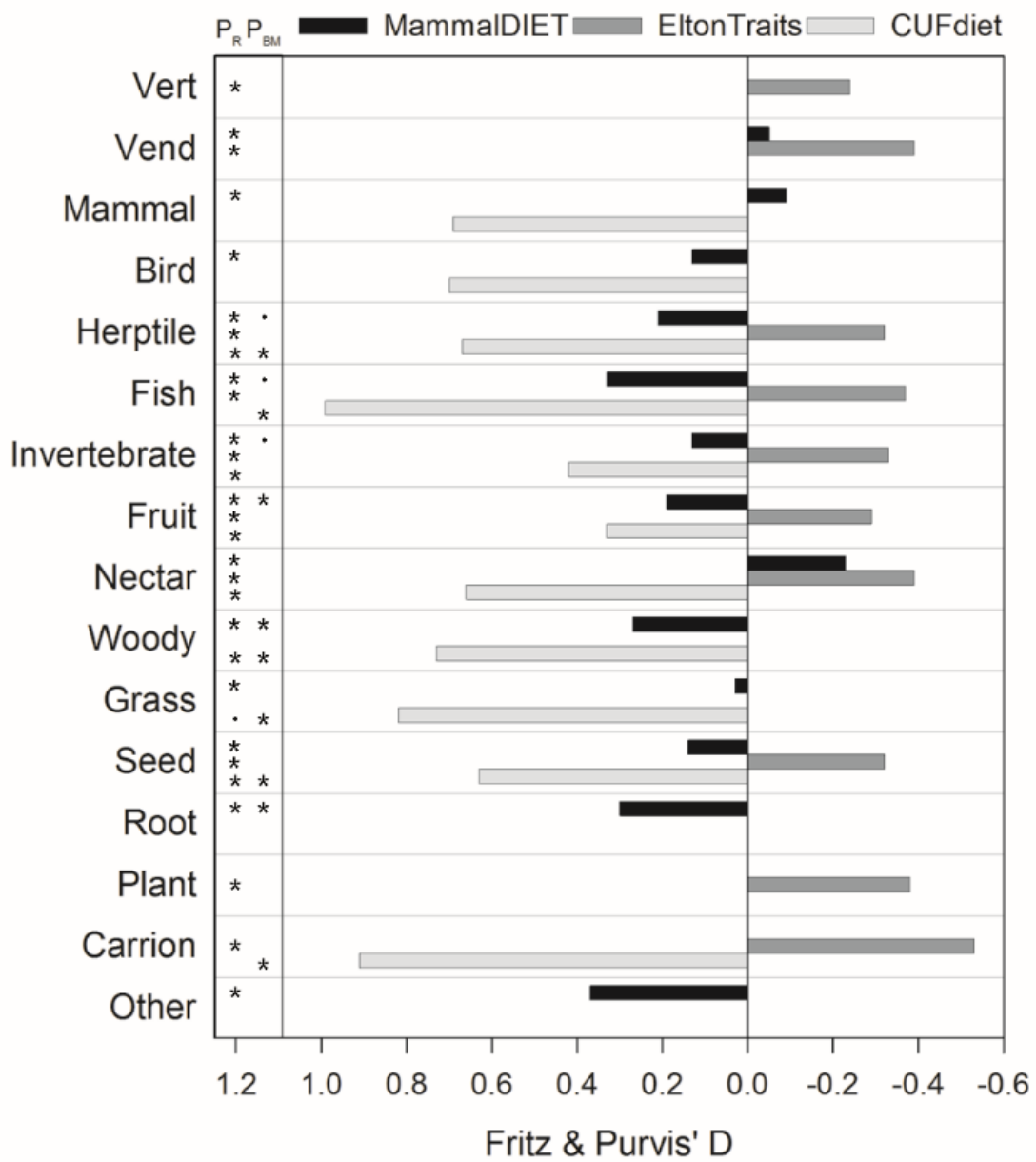


Figure 4

SUPPORTING INFORMATION

Appendix S1. Data sources for the CUFdiet database.

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Appendix S2. Complete R script used to generate reported results.

```
#####  
#####  
##Supporting Appendix S2 for the following publication:  
##Title: Contrasting evidence of phylogenetic trophic niche conservatism in mammals worldwide  
##Authors: Miguel Á. Olalla-Tárraga, Manuela González-Suárez, Rubén Bernardo-Madrid, Eloy Revilla, Fabricio Villalobos  
##Journal: Journal of Biogeography  
##  
##This is the complete R script used to generate reported results byt his publication  
##  
##CONTACT PERSON: Manuela Gonzalez Suarez, manuela.gonzalez.suarez@gmail.com  
##All data are freely available for download at [FIGSHARE DOI]  
#####  
#####  
  
#####  
#####  
##Read data and define data subsets####  
#####  
#####  
  
##phylogeny  
library(caper)  
library(phytools)  
tree=read.nexus("Fritz_tree.nex")  
  
###diet and life-history data  
data<- read.table("Olalla-Tarraga_et_al_Mammalian_Diet_Data.csv",sep="," , header=T )  
names(data)  
data$orders_analysis<-as.character(data$Order)  
data$orders_analysis[data$SMALL_ORDERS==1] <- "Small_orders"  
orders<-unique(data$orders_analysis)  
  
MammalDIET_sub<-subset(data,MammalDIET==1)  
EltonTraits_sub<-subset(data,EltonTraits==1)  
CUFdiet_sub<-subset(data, CUFdiet==1)  
  
#####  
#####  
#####PHYLOGENETIC SIGNAL IN GENERAL QUANTITATIVE DIET DESCRIPTORS AND OTHER  
TRAITS#####  
#####  
#####  
##REPRODUCES RESULTS DISPLAY IN FIGURE 2 AND TABLE S1 (NOTE THAT BECAUSE P-VALUES ARE  
BASED ON SIMULATIONS AND RANDOMIZATIONS VALUES WILL CHANGE EACH TIME)  
  
##Function K_P0_P1_function gives:  
## empirical K value  
## P0 is the P-value for the null hypothesis that there is no phylogenetic signal in the data based on a randomization  
test  
## P1 is the P-value for the null hypothesis that K is consistent with a Brownian model of evolution based on  
simulations  
  
##Simulation approach is based on code provided by Liam Revell http://blog.phytools.org/2011/12/testing-for-phylogenetic-signal-k.html  
##Using fastBM we can simulate the values of a trait along our phylogenetic tree if evolution followed a Brownian  
model with the value of the root taxa (parameter a) set to be the mean value of the trait in the observed data, the  
variance (sig2) set as the variance in the data.  
##to estimate these parameters from the data the tree needs to have no polytomies, so we apply a random break of the  
polytomies using the function multi2di from package ape to break polytomies
```

```

##For each trait we set bounds to the minimum and maximum possible values:
##[1,12] for the diet breadth of MammalDIET and CUFdiet and [1,10] for EltonTraits, these bounds are defined by the
food categories possible
##[0,Inf] for log10 of gestation length, assuming due to metabolic constrains gestation lengths <1 day would not
evolve.
##[0,Inf] for log10 of adult body mass, assuming due to metabolic constrains mammals weighting <1 gr would not
evolve.
##[-Inf,Inf] for log10 of home range size, assuming home range size can take any value.
##[0,Inf] for log10 of group size, group size <1 are not possible
##[0,Inf] for log10 of distribution range size, assuming species with global distribution areas <1 km2 would not
evolve.
##P1 is calculated following Liam Revell's suggestion "that we do this by counting the number of times that the
absolute value of the logarithm of our observed value for K is no smaller than the absolute values of our simulated
values for K. This just makes K=1.5 & K=0.6667 equivalent departures from BM."

K_P0_P1_function<-function(data_subset, trait, N_sim, bounds_sim, log=FALSE){
  if (log==FALSE){
    print("non-transformed variable")
    row.names(data_subset)=data_subset$binomial_tree
    test1=as.vector(as.matrix(subset(data_subset, select=trait)))
    names(test1)=row.names(data_subset)
    kappa<-phylosig(tree, test1, method="K",test=T)
    sss<-which(names(data_subset)==trait)
    selection<-subset(data_subset, data_subset[,sss]>0)
    tree1 <- multi2di(tree, random = TRUE)
    C1 <- comparative.data(phy = tree1, data = selection, names.col = binomial_tree, warn.dropped = FALSE,
na.omit=F)
    ss<-which(names(C1$data)==trait)
    nullK<-apply(fastBM(C1$phy, n=N_sim, sig2=mean(pic(C1$data[,ss],C1$phy)^2), a=mean(C1$data[,ss]),
bounds=bounds_sim),2, phylosig,tree=C1$phy)
    p1_value<-mean(abs(log(c(kappa$K,nullK)))>=abs(log(kappa$K)))
    return(list(trait, length(na.omit(C1$data[,ss])),round(kappa$K, digits=2),round(kappa$P, digits=3),round(p1_value,
digits=3)))
  }
  else {
    print("log-transformed variable")
    row.names(data_subset)=data_subset$binomial_tree
    test1=as.vector(as.matrix(subset(data_subset, select=trait)))
    test1=log10(test1)
    names(test1)=row.names(data_subset)
    kappa<-phylosig(tree, test1, method="K",test=T)
    sss<-which(names(data)==trait)
    selection<-subset(data_subset, data_subset[,sss]>0)
    tree1 <- multi2di(tree, random = TRUE)
    C1 <- comparative.data(phy = tree1, data = selection, names.col = binomial_tree, warn.dropped = FALSE,
na.omit=F)
    ss<-which(names(C1$data)==trait)
    nullK<-apply(fastBM(C1$phy, n=N_sim, sig2=mean(pic(log10(C1$data[,ss]),C1$phy)^2),
a=mean(log10(C1$data[,ss])), bounds=bounds_sim),2, phylosig,tree=C1$phy)
    p1_value<-mean(abs(log(c(kappa$K,nullK)))>=abs(log(kappa$K)))
    return(list(trait, length(na.omit(C1$data[,ss])),round(kappa$K, digits=2),round(kappa$P, digits=3),round(p1_value,
digits=3)))
  }
}

MD_diet<-K_P0_P1_function(MammalDIET_sub,"MD_Diet_breadth", 1000, c(1,12))
MD_ges<-K_P0_P1_function(MammalDIET_sub,"Gestation_length_days", 1000, c(-Inf,Inf), log=TRUE)
MD_mass<-K_P0_P1_function(MammalDIET_sub,"Adult_body_mass_g", 1000, c(-Inf,Inf), log=TRUE)
MD_home<-K_P0_P1_function(MammalDIET_sub,"Home_range_size_km2", 1000, c(-Inf,Inf), log=TRUE)
MD_group<-K_P0_P1_function(MammalDIET_sub,"Group_size_ind", 1000, c(-Inf,Inf), log=TRUE)
MD_dist<-K_P0_P1_function(MammalDIET_sub,"Distribution_range_area_km2", 1000, c(-Inf,Inf), log=TRUE)

```

```

MD_results<-rbind(MD_ges, MD_mass, MD_home, MD_group, MD_dist,MD_diet,c("NA", "NA", "NA", "NA",
"NA"))

ET_diet<-K_P0_P1_function(EltonTraits_sub,"ET_Diet_breadth", 1000, c(1,10))
ET_Levins<-K_P0_P1_function(EltonTraits_sub,"ET_Levins_stand", 1000, c(0,1))
ET_ges<-K_P0_P1_function(EltonTraits_sub,"Gestation_length_days", 1000, c(0,Inf), log=TRUE)
ET_mass<-K_P0_P1_function(EltonTraits_sub,"Adult_body_mass_g", 1000, c(0,Inf), log=TRUE)
ET_home<-K_P0_P1_function(EltonTraits_sub,"Home_range_size_km2", 1000, c(-Inf,Inf), log=TRUE)
ET_group<-K_P0_P1_function(EltonTraits_sub,"Group_size_ind", 1000, c(0,Inf), log=TRUE)
ET_dist<-K_P0_P1_function(EltonTraits_sub,"Distribution_range_area_km2", 1000, c(0,Inf), log=TRUE)

ET_results<-rbind(ET_ges, ET_mass, ET_home, ET_group, ET_dist,ET_diet, ET_Levins)

CUF_diet<-K_P0_P1_function(CUFdiet_sub,"CUF_Diet_breadth", 1000, c(1,12))
CUF_Levins<-K_P0_P1_function(CUFdiet_sub,"CUF_Levins_stand", 1000, c(0,1))
CUF_ges<-K_P0_P1_function(CUFdiet_sub,"Gestation_length_days", 1000, c(0,Inf), log=TRUE)
CUF_mass<-K_P0_P1_function(CUFdiet_sub,"Adult_body_mass_g", 1000, c(0,Inf), log=TRUE)
CUF_home<-K_P0_P1_function(CUFdiet_sub,"Home_range_size_km2", 1000, c(-Inf,Inf), log=TRUE)
CUF_group<-K_P0_P1_function(CUFdiet_sub,"Group_size_ind", 1000, c(0,Inf), log=TRUE)
CUF_dist<-K_P0_P1_function(CUFdiet_sub,"Distribution_range_area_km2", 1000, c(0,Inf), log=TRUE)

CUF_results<-rbind(CUF_ges, CUF_mass, CUF_home, CUF_group, CUF_dist,CUF_diet, CUF_Levins)

##generating results for table S1
Table_S1_results<-cbind(c("Gestation_length_days", "Adult_body_mass_g", "Home_range_size_km2",
"Group_size_ind", "Distribution_range_area_km2", "Diet_breadth", "Levin's index"),MD_results[,-1],ET_results[,-
1],CUF_results[,-1])
colnames(Table_S1_results)<-c("Variable", "MD_sample_size", "MD_K", "MD_P0", "MD_P1", "ET_sample_size",
"ET_K", "ET_P0", "ET_P1", "CUF_sample_size", "CUF_K", "CUF_P0", "CUF_P1")

#####
#####
#####PHYLOGENETIC SIGNAL IN DIET BREADTH FOR DISTINCT MAMMALIAN
ORDERS#####
#####
#####
##REPRODUCES RESULTS FOR TABLE 1
##Please note that there is no data on MammalDIET for Cetacea
results_orders<-list()

for (i in 1:length(orders)){
  j<-noquote(toString(orders[i]))
  if (j!="Cetacea"){
    sub<-subset(MammalDIET_sub, orders_analysis==j)
    compData_MD <- comparative.data(phy = tree, data = sub, names.col = binomial_tree, warn.dropped = FALSE,
na.omit=F)
    test1=as.vector(as.matrix(subset(compData_MD$data, select=MD_Diet_breadth)))
    names(test1)=compData_MD$phy$tip.label
    kappa_MD<-phylosig(tree, test1, method="K",test=T)
    compData_MD1 <- comparative.data(phy = tree1, data = sub, names.col = binomial_tree, warn.dropped = F,
na.omit=F)
    nullK_MD<-apply(fastBM(compData_MD1$phy, n=N_simulations,
sig2=mean(pic(compData_MD1$data$MD_Diet_breadth,compData_MD1$phy)^2),
a=mean(compData_MD1$data$MD_Diet_breadth), bounds=c(1,12)),2, phylosig,tree=compData_MD1$phy)

    sub1<-subset(EltonTraits_sub, orders_analysis==j)
    compData_ET<- comparative.data(phy = tree, data = sub1, names.col = binomial_tree, warn.dropped = FALSE,
na.omit=F)
    test2=as.vector(as.matrix(subset(compData_ET$data, select=ET_Diet_breadth)))
    names(test2)=compData_ET$phy$tip.label
    kappa_ET<-phylosig(tree, test2, method="K",test=T)

```

```

compData_ET1 <- comparative.data(phy = tree1, data = sub1, names.col = binomial_tree, warn.dropped = F,
na.omit=F)
nullK_ET<-apply(fastBM(compData_ET1$phy, n=N_simulations,
sig2=mean(pic(compData_ET1$data$ET_Diet_breadth,compData_ET1$phy)^2),
a=mean(compData_ET1$data$ET_Diet_breadth), bounds=c(1,10)),2, phylosig,tree=compData_ET1$phy)

results_orders[[j]]<-c(j,
  nrow(compData_MD$data),
  round(kappa_MD$K, digits=2),
  round(kappa_MD$P, digits=3),
  round(mean(abs(log(c(kappa_MD$K,nullK_MD))))>=abs(log(kappa_MD$K))), digits=3),
  round(mean(compData_MD$data$MD_Diet_breadth, na.rm=T), digits=2),
  round(sd(compData_MD$data$MD_Diet_breadth, na.rm=T), digits=3),
  nrow(compData_ET$data),
  round(kappa_ET$K, digits=2),
  round(kappa_ET$P, digits=3),
  round(mean(abs(log(c(kappa_ET$K,nullK_ET))))>=abs(log(kappa_ET$K))), digits=3),
  round(mean(compData_ET$data$ET_Diet_breadth, na.rm=T), digits=2),
  round(sd(compData_ET$data$ET_Diet_breadth, na.rm=T), digits=3))
}
else{
  sub1<-subset(EltonTraits_sub, Order==j)
  compData_ET<- comparative.data(phy = tree, data = sub1, names.col = binomial_tree, warn.dropped = FALSE,
na.omit=F)
  test2=as.vector(as.matrix(subset(compData_ET$data, select=ET_Diet_breadth)))
  names(test2)=compData_ET$phy$tip.label
  kappa_ET<-phylosig(tree, test2, method="K",test=T)
  compData_ET1 <- comparative.data(phy = tree1, data = sub1, names.col = binomial_tree, warn.dropped = F,
na.omit=F)
  nullK_ET<-apply(fastBM(compData_ET1$phy, n=N_simulations,
sig2=mean(pic(compData_ET1$data$ET_Diet_breadth,compData_ET1$phy)^2),
a=mean(compData_ET1$data$ET_Diet_breadth), bounds=c(1,10)),2, phylosig,tree=compData_ET1$phy)

  results_orders[[j]]<-c(j,"NA", "NA", "NA", "NA", "NA", "NA",
    nrow(compData_ET$data),
    round(kappa_ET$K, digits=2),
    round(kappa_ET$P, digits=3),
    round(mean(abs(log(c(kappa_ET$K,nullK_ET))))>=abs(log(kappa_ET$K))), digits=3),
    round(mean(compData_ET$data$ET_Diet_breadth, na.rm=T), digits=2),
    round(sd(compData_ET$data$ET_Diet_breadth, na.rm=T), digits=3))
}
}

##REPRODUCES RESULTS FOR FIGURE 3 TABLE S3
##Signal for species with data on both MammalDIET and EltonTraits####

shared_sub<-subset(data, MammalDIET==1 & EltonTraits==1)
orders_shared<-orders[-9] ##remove Cetacea from the list as no Cetacea species are described in MammalDIET

results_orders_shared<-list()

for (i in 1:length(orders_shared)){

  j<-noquote(toString(orders_shared[i]))

  sub<-subset(shared_sub, orders_analysis==j)
  compData_MD <- comparative.data(phy = tree, data = sub, names.col = binomial_tree, warn.dropped = FALSE,
na.omit=F)
  test1=as.vector(as.matrix(subset(compData_MD$data, select=MD_Diet_breadth)))
  names(test1)=compData_MD$phy$tip.label
  kappa_MD<-phylosig(tree, test1, method="K",test=T)

```

```

compData_MD1 <- comparative.data(phy = tree1, data = sub, names.col = binomial_tree, warn.dropped = F,
na.omit=F)
nullK_MD<-apply(fastBM(compData_MD1$phy, n=N_simulations,
sig2=mean(pic(compData_MD1$data$MD_Diet_breadth,compData_MD1$phy)^2),
a=mean(compData_MD1$data$MD_Diet_breadth), bounds=c(1,12)),2, phylosig,tree=compData_MD1$phy)

sub1<-subset(shared_sub, orders_analysis==j)
compData_ET<- comparative.data(phy = tree, data = sub1, names.col = binomial_tree, warn.dropped = FALSE,
na.omit=F)
test2=as.vector(as.matrix(subset(compData_ET$data, select=ET_Diet_breadth)))
names(test2)=compData_ET$phy$tip.label
kappa_ET<-phylosig(tree, test2, method="K",test=T)

compData_ET1 <- comparative.data(phy = tree1, data = sub1, names.col = binomial_tree, warn.dropped = F,
na.omit=F)
nullK_ET<-apply(fastBM(compData_ET1$phy, n=N_simulations,
sig2=mean(pic(compData_ET1$data$ET_Diet_breadth,compData_ET1$phy)^2),
a=mean(compData_ET1$data$ET_Diet_breadth), bounds=c(1,10)),2, phylosig,tree=compData_ET1$phy)

results_orders_shared[[j]]<-c(j,
      nrow(compData_MD$data),
      round(kappa_MD$K, digits=2),
      round(kappa_MD$P, digits=3),
      round(mean(abs(log(c(kappa_MD$K,nullK_MD))))>=abs(log(kappa_MD$K))), digits=3),
      round(kappa_ET$K, digits=2),
      round(kappa_ET$P, digits=3),
      round(mean(abs(log(c(kappa_ET$K,nullK_ET))))>=abs(log(kappa_ET$K))), digits=3))
}

#####
#####
#####PHYLOGENETIC SIGNAL IN BINARY PRESENCE DATA FOR DIFFERENT DIET
CATEGORIES#####
#####
#####
##REPRODUCES RESULTS FOR FIGURE 4 AND TABLE S4. P-VALUES ARE BASED ON PERMUTATION
TEST AND COULD CHANGE EACH TIME

N_permutations<-5000 ##defining the number of permutations to estimate P-values for D
compData_MD <- comparative.data(phy = tree, data = MammalDIET_sub, names.col = binomial_tree, warn.dropped =
TRUE, na.omit=F)
dim(compData_MD$data)
compData_ET <- comparative.data(phy = tree, data = EltonTraits_sub, names.col = binomial_tree, warn.dropped =
TRUE, na.omit=F)
dim(compData_ET$data)
compData_CUF <- comparative.data(phy = tree, data = CUFdiet_sub, names.col = binomial_tree, warn.dropped =
TRUE, na.omit=F)
dim(compData_CUF$data)

##unclassified vertebrates is only a category in EltonTraits
ET_PhyloDvert_unc <- phylo.d(compData_ET, binvar=ET_vert_unclassified, permut = N_permutations)
vert_unc<-list("NA", "NA", "NA", "NA",
      sum(EltonTraits_sub$ET_vert_unclassified), round(ET_PhyloDvert_unc$DEstimate,digits=2),
      round(ET_PhyloDvert_unc$Pval1, digits=3), round(ET_PhyloDvert_unc$Pval0, digits=3),
      "NA", "NA", "NA", "NA")

##Endotherm vertebrates (mammals and birds). In CUFdiet all species have presence for this category and those D
cannot be estimated
MD_PhyloDvend <- phylo.d(compData_MD, binvar=MD_vend, permut = N_permutations)
ET_PhyloDvend <- phylo.d(compData_ET, binvar=ET_vend, permut = N_permutations)
vend<-list(sum(MammalDIET_sub$MD_vend), round(MD_PhyloDvend$DEstimate,digits=2),
      round(MD_PhyloDvend$Pval1, digits=3), round(MD_PhyloDvend$Pval0, digits=3),

```

```

sum(EltonTraits_sub$ET_vend), round(ET_PhyloDvend$DEstimate,digits=2), round(ET_PhyloDvend$Pval1,
digits=3), round(ET_PhyloDvend$Pval0, digits=3),
"NA", "NA", "NA", "NA")

##Mammal category is only described in MammalDiet and CUFdiet
MD_PhyloDmammal <- phylo.d(compData_MD, binvar=MD_mammal, permut = N_permutations)
CUF_PhyloDmammal <- phylo.d(compData_CUF, binvar=CUF_mammal, permut = N_permutations)
mammal<-list(sum(MammalDIET_sub$MD_mammal), round(MD_PhyloDmammal$DEstimate,digits=2),
round(MD_PhyloDmammal$Pval1, digits=3), round(MD_PhyloDmammal$Pval0, digits=3),
"NA", "NA", "NA", "NA",
sum(CUFdiet_sub$CUF_mammal), round(CUF_PhyloDmammal$DEstimate,digits=2),
round(CUF_PhyloDmammal$Pval1, digits=3), round(CUF_PhyloDmammal$Pval0, digits=3))

##Bird category is only described in MammalDiet and CUFdiet
MD_PhyloDbird <- phylo.d(compData_MD, binvar=MD_bird, permut = N_permutations)
CUF_PhyloDbird <- phylo.d(compData_CUF, binvar=CUF_bird, permut = N_permutations)
bird<-list(sum(MammalDIET_sub$MD_bird), round(MD_PhyloDbird$DEstimate,digits=2),
round(MD_PhyloDbird$Pval1, digits=3), round(MD_PhyloDbird$Pval0, digits=3),
"NA", "NA", "NA", "NA",
sum(CUFdiet_sub$CUF_bird), round(CUF_PhyloDbird$DEstimate,digits=2), round(CUF_PhyloDbird$Pval1,
digits=3), round(CUF_PhyloDbird$Pval0, digits=3))

MD_PhyloDherptile <- phylo.d(compData_MD, binvar=MD_herptile, permut = N_permutations)
ET_PhyloDherptile <- phylo.d(compData_ET, binvar=ET_herptile, permut = N_permutations)
CUF_PhyloDherptile <- phylo.d(compData_CUF, binvar=CUF_herptile, permut = N_permutations)
herptile<-list(sum(MammalDIET_sub$MD_herptile), round(MD_PhyloDherptile$DEstimate,digits=2),
round(MD_PhyloDherptile$Pval1, digits=3), round(MD_PhyloDherptile$Pval0, digits=3),
sum(EltonTraits_sub$ET_herptile), round(ET_PhyloDherptile$DEstimate,digits=2),
round(ET_PhyloDherptile$Pval1, digits=3), round(ET_PhyloDherptile$Pval0, digits=3),
sum(CUFdiet_sub$CUF_herptile), round(CUF_PhyloDherptile$DEstimate,digits=2),
round(CUF_PhyloDherptile$Pval1, digits=3), round(CUF_PhyloDherptile$Pval0, digits=3))

MD_PhyloDfish <- phylo.d(compData_MD, binvar=MD_fish, permut = N_permutations)
ET_PhyloDfish <- phylo.d(compData_ET, binvar=ET_fish, permut = N_permutations)
CUF_PhyloDfish <- phylo.d(compData_CUF, binvar=CUF_fish, permut = N_permutations)
fish<-list(sum(MammalDIET_sub$MD_fish), round(MD_PhyloDfish$DEstimate,digits=2),
round(MD_PhyloDfish$Pval1, digits=3), round(MD_PhyloDfish$Pval0, digits=3),
sum(EltonTraits_sub$ET_fish), round(ET_PhyloDfish$DEstimate,digits=2), round(ET_PhyloDfish$Pval1,
digits=3), round(ET_PhyloDfish$Pval0, digits=3),
sum(CUFdiet_sub$CUF_fish), round(CUF_PhyloDfish$DEstimate,digits=2), round(CUF_PhyloDfish$Pval1,
digits=3), round(CUF_PhyloDfish$Pval0, digits=3))

MD_PhyloDinvertebrate <- phylo.d(compData_MD, binvar=MD_invertebrate, permut = N_permutations)
ET_PhyloDinvertebrate <- phylo.d(compData_ET, binvar=ET_invertebrate, permut = N_permutations)
CUF_PhyloDinvertebrate <- phylo.d(compData_CUF, binvar=CUF_invertebrate, permut = N_permutations)
invertebrate<-list(sum(MammalDIET_sub$MD_invertebrate), round(MD_PhyloDinvertebrate$DEstimate,digits=2),
round(MD_PhyloDinvertebrate$Pval1, digits=3), round(MD_PhyloDinvertebrate$Pval0, digits=3),
sum(EltonTraits_sub$ET_invertebrate), round(ET_PhyloDinvertebrate$DEstimate,digits=2),
round(ET_PhyloDinvertebrate$Pval1, digits=3), round(ET_PhyloDinvertebrate$Pval0, digits=3),
sum(CUFdiet_sub$CUF_invertebrate), round(CUF_PhyloDinvertebrate$DEstimate,digits=2),
round(CUF_PhyloDinvertebrate$Pval1, digits=3), round(CUF_PhyloDinvertebrate$Pval0, digits=3))

MD_PhyloDfruit <- phylo.d(compData_MD, binvar=MD_fruit, permut = N_permutations)
ET_PhyloDfruit <- phylo.d(compData_ET, binvar=ET_fruit, permut = N_permutations)
CUF_PhyloDfruit <- phylo.d(compData_CUF, binvar=CUF_fruit, permut = N_permutations)
fruit<-list(sum(MammalDIET_sub$MD_fruit), round(MD_PhyloDfruit$DEstimate,digits=2),
round(MD_PhyloDfruit$Pval1, digits=3), round(MD_PhyloDfruit$Pval0, digits=3),
sum(EltonTraits_sub$ET_fruit), round(ET_PhyloDfruit$DEstimate,digits=2), round(ET_PhyloDfruit$Pval1,
digits=3), round(ET_PhyloDfruit$Pval0, digits=3),
sum(CUFdiet_sub$CUF_fruit), round(CUF_PhyloDfruit$DEstimate,digits=2), round(CUF_PhyloDfruit$Pval1,
digits=3), round(CUF_PhyloDfruit$Pval0, digits=3))

```



```

MD_PhyloDnectar <- phylo.d(compData_MD, binvar=MD_nectar, permut = N_permutations)
ET_PhyloDnectar <- phylo.d(compData_ET, binvar=ET_nectar, permut = N_permutations)
CUF_PhyloDnectar <- phylo.d(compData_CUF, binvar=CUF_nectar, permut = N_permutations)
nectar<-list(sum(MammalDIET_sub$MD_nectar), round(MD_PhyloDnectar$DEstimate,digits=2),
round(MD_PhyloDnectar$Pval1, digits=3), round(MD_PhyloDnectar$Pval0, digits=3),
sum(EltonTraits_sub$ET_nectar), round(ET_PhyloDnectar$DEstimate,digits=2),
round(ET_PhyloDnectar$Pval1, digits=3), round(ET_PhyloDnectar$Pval0, digits=3),
sum(CUFdiet_sub$CUF_nectar), round(CUF_PhyloDnectar$DEstimate,digits=2),
round(CUF_PhyloDnectar$Pval1, digits=3), round(CUF_PhyloDnectar$Pval0, digits=3))

##Woody category is only described in MammalDiet and CUFdiet
MD_PhyloDwoody <- phylo.d(compData_MD, binvar=MD_woody, permut = N_permutations)
CUF_PhyloDwoody <- phylo.d(compData_CUF, binvar=CUF_woody, permut = N_permutations)
woody<-list(sum(MammalDIET_sub$MD_woody), round(MD_PhyloDwoody$DEstimate,digits=2),
round(MD_PhyloDwoody$Pval1, digits=3), round(MD_PhyloDwoody$Pval0, digits=3),
"NA", "NA", "NA", "NA",
sum(CUFdiet_sub$CUF_woody), round(CUF_PhyloDwoody$DEstimate,digits=2),
round(CUF_PhyloDwoody$Pval1, digits=3), round(CUF_PhyloDwoody$Pval0, digits=3))

##Grass category is only described in MammalDiet and CUFdiet
MD_PhyloDgrass <- phylo.d(compData_MD, binvar=MD_grass, permut = N_permutations)
CUF_PhyloDgrass <- phylo.d(compData_CUF, binvar=CUF_grass, permut = N_permutations)
grass<-list(sum(MammalDIET_sub$MD_grass), round(MD_PhyloDgrass$DEstimate,digits=2),
round(MD_PhyloDgrass$Pval1, digits=3), round(MD_PhyloDgrass$Pval0, digits=3),
"NA", "NA", "NA", "NA",
sum(CUFdiet_sub$CUF_grass), round(CUF_PhyloDgrass$DEstimate,digits=2),
round(CUF_PhyloDgrass$Pval1, digits=3), round(CUF_PhyloDgrass$Pval0, digits=3))

MD_PhyloDseed <- phylo.d(compData_MD, binvar=MD_seed, permut = N_permutations)
ET_PhyloDseed <- phylo.d(compData_ET, binvar=ET_seed, permut = N_permutations)
CUF_PhyloDseed <- phylo.d(compData_CUF, binvar=CUF_seed, permut = N_permutations)
seed<-list(sum(MammalDIET_sub$MD_seed), round(MD_PhyloDseed$DEstimate,digits=2),
round(MD_PhyloDseed$Pval1, digits=3), round(MD_PhyloDseed$Pval0, digits=3),
sum(EltonTraits_sub$ET_seed), round(ET_PhyloDseed$DEstimate,digits=2), round(ET_PhyloDseed$Pval1,
digits=3), round(ET_PhyloDseed$Pval0, digits=3),
sum(CUFdiet_sub$CUF_seed), round(CUF_PhyloDseed$DEstimate,digits=2), round(CUF_PhyloDseed$Pval1,
digits=3), round(CUF_PhyloDseed$Pval0, digits=3))

##root category is only described in MammalDiet and CUFdiet, but in CUFdiet no species are listed as consuming roots
MD_PhyloDroot <- phylo.d(compData_MD, binvar=MD_root, permut = N_permutations)
root<-list(sum(MammalDIET_sub$MD_root), round(MD_PhyloDroot$DEstimate,digits=2),
round(MD_PhyloDroot$Pval1, digits=3), round(MD_PhyloDroot$Pval0, digits=3),
"NA", "NA", "NA", "NA",
"NA", "NA", "NA", "NA")

##plant unclassified category is only described in EltonTraits
ET_PhyloDplant_unc <- phylo.d(compData_ET, binvar=ET_plant_unclassified, permut = N_permutations)
plant_unc<-list("NA", "NA", "NA", "NA",
sum(EltonTraits_sub$ET_plant_unclassified), round(ET_PhyloDplant_unc$DEstimate,digits=2),
round(ET_PhyloDplant_unc$Pval1, digits=3), round(ET_PhyloDplant_unc$Pval0, digits=3),
"NA", "NA", "NA", "NA")

##carrion category is only described in EltonTraits and CUFdiet
ET_PhyloDcarrion <- phylo.d(compData_ET, binvar=ET_carrion, permut = N_permutations)
CUF_PhyloDcarrion <- phylo.d(compData_CUF, binvar=CUF_carrion, permut = N_permutations)
carrion<-list("NA", "NA", "NA", "NA",
sum(EltonTraits_sub$ET_carrion), round(ET_PhyloDcarrion$DEstimate,digits=2),
round(ET_PhyloDcarrion$Pval1, digits=3), round(ET_PhyloDcarrion$Pval0, digits=3),
sum(CUFdiet_sub$CUF_carrion), round(CUF_PhyloDcarrion$DEstimate,digits=2),
round(CUF_PhyloDcarrion$Pval1, digits=3), round(CUF_PhyloDcarrion$Pval0, digits=3))

##Other category is only described in MammalDiet

```

```

MD_PhyloDother <- phylo.d(compData_MD, binvar=MD_other, permut = N_permutations)
other<-list(sum(MammalDIET_sub$MD_other), round(MD_PhyloDother$DEstimate,digits=2),
round(MD_PhyloDother$Pval1, digits=3), round(MD_PhyloDother$Pval0, digits=3),
      "NA", "NA", "NA", "NA",
      "NA", "NA", "NA", "NA")

##generating results for table S3
table_PhyloD<- rbind(vert_unc,vend, mammal, bird, herptile, fish, invertebrate, fruit, nectar, woody, grass, seed, root,
plant_unc, carrion, other)
row.names(table_PhyloD)<-c("vert_unclassified", "vend", "mammal", "bird", "herptile", "fish", "invertebrate",
"fruit", "nectar", "woody", "grass", "seed", "root", "plant_unclassified", "carrion", "other")
colnames(table_PhyloD)<-
c("Np_MammalDiet", "D_MammalDiet", "P1_MammalDiet", "P0_MammalDiet", "Np_EltonTraits", "D_EltonTraits", "P1_EltonTraits", "P0_EltonTraits", "Np_CUFdiet", "D_CUFdiet", "P1_CUFdiet", "P0_CUFdiet")

#####
#####
#####PHYLOGENETIC SIGNAL IN QUANTITATIVE DATA FOR DIFFERENT DIET
CATEGORIES#####
#####
#####
##REPRODUCES RESULTS FOR TABLE 2
##uses function K_P0_P1_function defined in lines 43-75

MD_Mammal_quant_K<-K_P0_P1_function(MammalDIET_sub,"MD_Mammal_quant", 2, c(1,4))
MD_Bird_quant_K<-K_P0_P1_function(MammalDIET_sub,"MD_Bird_quant", 2, c(1,4))
MD_Herptile_quant_K<-K_P0_P1_function(MammalDIET_sub,"MD_Herptile_quant", 2, c(1,4))
MD_Fish_quant_K<-K_P0_P1_function(MammalDIET_sub,"MD_Fish_quant", 2, c(1,4))
MD_Invertebrate_quant_K<-K_P0_P1_function(MammalDIET_sub,"MD_Invertebrate_quant", 2, c(1,4))
MD_Fruit_quant_K<-K_P0_P1_function(MammalDIET_sub,"MD_Fruit_quant", 2, c(1,4))
MD_Nectar_quant_K<-K_P0_P1_function(MammalDIET_sub,"MD_Nectar_quant", 2, c(1,4))
MD_Woody_quant_K<-K_P0_P1_function(MammalDIET_sub,"MD_Woody_quant", 2, c(1,4))
MD_Grass_quant_K<-K_P0_P1_function(MammalDIET_sub,"MD_Grass_quant", 2, c(1,4))
MD_Seed_quant_K<-K_P0_P1_function(MammalDIET_sub,"MD_Seed_quant", 2, c(1,4))
MD_Root_quant_K<-K_P0_P1_function(MammalDIET_sub,"MD_Root_quant", 2, c(1,4))
MD_Other_quant_K<-K_P0_P1_function(MammalDIET_sub,"MD_Other_quant", 2, c(1,4))

ET_Vert_uncl_quant_K<-K_P0_P1_function(EltonTraits_sub,"ET_Vert_uncl_quant", 2, c(0,100))
ET_Vend_quant_K<-K_P0_P1_function(EltonTraits_sub,"ET_Vend_quant", 2, c(0,100))
ET_Herptile_quant_K<-K_P0_P1_function(EltonTraits_sub,"ET_Herptile_quant", 2, c(0,100))
ET_Fish_quant_K<-K_P0_P1_function(EltonTraits_sub,"ET_Fish_quant", 2, c(0,100))
ET_Invertebrate_quant_K<-K_P0_P1_function(EltonTraits_sub,"ET_Invertebrate_quant", 2, c(0,100))
ET_Fruit_quant_K<-K_P0_P1_function(EltonTraits_sub,"ET_Fruit_quant", 2, c(0,100))
ET_Nectar_quant_K<-K_P0_P1_function(EltonTraits_sub,"ET_Nectar_quant", 2, c(0,100))
ET_Seed_quant_K<-K_P0_P1_function(EltonTraits_sub,"ET_Seed_quant", 2, c(0,100))
ET_Plant_unc_quant_K<-K_P0_P1_function(EltonTraits_sub,"ET_Plant_unc_quant", 2, c(0,100))
ET_Carrion_quant_K<-K_P0_P1_function(EltonTraits_sub,"ET_Carrion_quant", 2, c(0,100))

CUF_Vend_num_freq_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Vend_num_freq", 2, c(0,1))
CUF_Mammal_num_freq_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Mammal_num_freq", 2, c(0,1))
CUF_Bird_num_freq_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Bird_num_freq", 2, c(0,1))
CUF_Herptile_num_freq_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Herptile_num_freq", 2, c(0,1))
CUF_Fish_num_freq_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Fish_num_freq", 2, c(0,1))
CUF_Invertebrate_num_freq_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Invertebrate_num_freq", 2, c(0,1))
CUF_Fruit_num_freq_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Fruit_num_freq", 2, c(0,1))
CUF_Nectar_num_freq_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Nectar_num_freq", 2, c(0,1))
CUF_Woody_num_freq_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Woody_num_freq", 2, c(0,1))
CUF_Grass_num_freq_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Grass_num_freq", 2, c(0,1))
CUF_Seed_num_freq_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Seed_num_freq", 2, c(0,1))
CUF_Carrion_num_freq_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Carrion_num_freq", 2, c(0,1))

```



```

CUF_Mammal_freq_occu_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Mammal_freq_occu", 2, c(0,1))
CUF_Bird_freq_occu_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Bird_freq_occu", 2, c(0,1))
CUF_Herptile_freq_occu_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Herptile_freq_occu", 2, c(0,1))
CUF_Fish_freq_occu_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Fish_freq_occu", 2, c(0,1))
CUF_Invertebrate_freq_occu_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Invertebrate_freq_occu", 2, c(0,1))
CUF_Fruit_freq_occu_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Fruit_freq_occu", 2, c(0,1))
CUF_Woody_freq_occu_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Woody_freq_occu", 2, c(0,1))
CUF_Grass_freq_occu_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Grass_freq_occu", 2, c(0,1))
CUF_Seed_freq_occu_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Seed_freq_occu", 2, c(0,1))
CUF_Carrion_freq_occu_K<-K_P0_P1_function(CUFdiet_sub,"CUF_Carrion_freq_occu", 2, c(0,1))

##generating table results
Table_2_results<-rbind(list("Vert_unc1","NA","NA", "NA", "NA",ET_Vert_unc1_quant_K,"NA","NA", "NA",
"NA","NA","NA", "NA", "NA"),
list("Vend", "NA","NA", "NA", "NA", ET_Vend_quant_K,CUF_Vend_quant_K, "NA","NA", "NA",
"NA"),
list("Mammal", MD_Mammal_quant_K, "NA","NA", "NA", "NA",CUF_Mammal_num_freq_K,
CUF_Mammal_freq_occu_K),
list("Bird", MD_Bird_quant_K,"NA","NA", "NA", "NA",CUF_Bird_num_freq_K,
CUF_Bird_freq_occu_K ),
list("Herptile", MD_Herptile_quant_K, ET_Herptile_quant_K, CUF_Herptile_num_freq_K,
CUF_Herptile_freq_occu_K),
list("Fish", MD_Fish_quant_K, ET_Fish_quant_K, CUF_Fish_num_freq_K, CUF_Fish_freq_occu_K),
list("Invertebrate", MD_Invertebrate_quant_K, ET_Invertebrate_quant_K,
CUF_Invertebrate_num_freq_K, CUF_Invertebrate_freq_occu_K),
list("Fruit", MD_Fruit_quant_K, ET_Fruit_quant_K, CUF_Fruit_num_freq_K,
CUF_Fruit_freq_occu_K),
list("Nectar", MD_Nectar_quant_K, ET_Nectar_quant_K, CUF_Nectar_num_freq_K,"NA","NA", "NA",
"NA"),
list("Woody", MD_Woody_quant_K,"NA","NA", "NA", "NA",CUF_Woody_num_freq_K,
CUF_Woody_freq_occu_K ),
list("Grass", MD_Grass_quant_K,"NA","NA", "NA", "NA", CUF_Grass_num_freq_K,
CUF_Grass_freq_occu_K),
list("Seed", MD_Seed_quant_K, ET_Seed_quant_K, CUF_Seed_num_freq_K,
CUF_Seed_freq_occu_K),
list("Root", MD_Root_quant_K,"NA","NA", "NA", "NA", "NA","NA", "NA", "NA" ),
list("Plant", "NA","NA", "NA", "NA", ET_Plant_unc_quant_K, "NA","NA", "NA", "NA", "NA","NA",
"NA", "NA"),
list("Carrion", "NA","NA", "NA", "NA", ET_Carrion_quant_K,CUF_Carrion_num_freq_K,
CUF_Carrion_freq_occu_K),
list("Other", MD_Other_quant_K, "NA","NA", "NA", "NA", "NA","NA", "NA", "NA", "NA","NA",
"NA", "NA" ))

colnames(Table_2_results)<-c("Food category","MD_sample_size", "MD_K", "MD_P0", "MD_P1","ET_sample_size",
"ET_K", "ET_P0", "ET_P1","CUF_num_sample_size", "CUF_num_K", "CUF_num_P0",
"CUF_num_P1","CUF_freq_sample_size", "CUF_freq_K", "CUF_freq_P0", "CUF_freq_P1")

#####
#####
##TESTING THE EFFECT OF POLYTOMIES IN THE RESULTS###
#####
#####
## REPRODUCES RESULTS FOR TABLE S2

## Code based on code written by Nathan Kraft- nkraft@biodiversity.ubc.ca
## available at http://www.esapubs.org/archive/ecol/E093/023/thin\_terminal\_polytomies.R
## presented in publication "T. Jonathan Davies, Nathan J. B. Kraft, Nicolas Salamin, and Elizabeth M. Wolkovich
2012. Incompletely resolved phylogenetic trees inflate estimates of phylogenetic conservatism. Ecology 93:242-247.
http://dx.doi.org/10.1890/11-1360.1"

## R-function to identify terminal polytomies, then randomly thin those

```

```

## polytomies until only 'keep' number of taxa remain in each polytomy.
## Designed to work on an object of class "phylo" as defined in the R-
## package, ape (Paradis et al. 2004 ).

thin_terminal_polytomies=function(phy, keep=2){
  require(ape)
  phy$edge->edges
  length(phy$tip.label)->ntips
  edges[which(edges[,2]<=ntips),]->terminal_edges
  if(sum(table(terminal_edges[,1])>2)==0){
    print("no polytomies- returning original tree")
    return(phy)
  }
  names(which(table(terminal_edges[,1])>2))->poly_list
  droplist<-NULL
  for(i in 1:length(poly_list)){
    terminal_edges[which(terminal_edges[,1]==poly_list[i]),2]->tips
    droplist<-c(droplist, sample(tips, size=(length(tips)-keep)))
  }
  drop.tip(phy, droplist)->phy_thin
  return(phy_thin)
}

library(caper)
tree=read.nexus("Fritz_tree.nex")

##function to estima effect of polytomies and if interested also P1 values associated with simulating Brownian motion
in the thinned trees.
##Please note that estimating P1 for all thinned trees can be a computationally long proccess, also default simulation
values especially bounds may need to be changed for certain traits
##Output may be summary data from the multiple trees or the results from each tree

politomies_effects<-function(data_subset, trait, N_datasets,log=FALSE, FullRes=FALSE, P1_estimate=FALSE,
N_sim=1000, bounds_sim=c(-Inf, Inf)){
  row.names(data_subset)=data_subset$binomial_tree
  test1=as.vector(as.matrix(subset(data_subset, select=trait)))
  if (log==TRUE){
    print("log-transformed variable")
    test1<-log10(test1)
  }
  names(test1)=row.names(data_subset)
  results<-matrix(nrow=N_datasets, ncol=3)
  resultsP1<-matrix(nrow=N_datasets, ncol=4)
  for (i in 1:N_datasets){
    treK_t<-thin_terminal_polytomies(tree)
    sss<-which(names(data_subset)==trait)
    selection<-subset(data_subset, data_subset[,sss]>-1)
    C1 <- comparative.data(phy = treK_t, data = selection, names.col = binomial_tree, na.omit=F)
    kappa<-phylosig(C1$phy, test1, method="K",test=T)
    results[[i,1]]<-c(nrow(C1$data))
    results[[i,2]]<-c(kappa$K)
    results[[i,3]]<-c(kappa$P)
    if (P1_estimate==TRUE){
      print("Estimating P1 - simulating Brownian evolution")
      tree1 <- multi2di(C1$phy, random = TRUE)
      ss<-which(names(C1$data)==trait)
      if (log==TRUE){
        print("log-transformed variable")
        nullK<-apply(fastBM(C1$phy, n=N_sim, sig2=mean(pic(log10(C1$data[,ss]),C1$phy)^2),
a=mean(log10(C1$data[,ss])), bounds=bounds_sim),2, phylosig,tree=C1$phy)
      }
    }
  }
}

```

```

    nullK<-apply(fastBM(tree1, n=N_sim, sig2=mean(pic(C1$data[,ss],tree1)^2), a=mean(C1$data[,ss]),
bounds=bounds_sim),2, phylosig,tree=tree1)
  }
  resultsP1[[i,1]]<-c(nrow(C1$data))
  resultsP1[[i,2]]<-c(kappa$K)
  resultsP1[[i,3]]<-c(kappa$P)
  resultsP1[[i,4]]<-c(round(mean(abs(log(c(kappa$K,nullK))))>=abs(log(kappa$K))),digits=5))

}
if (P1_estimate==TRUE){
  if (FullRes==TRUE){ return(resultsP1)}
  return(c(round(min(resultsP1[,1]), digits=0),round(max(resultsP1[,1]), digits=0),round(mean(resultsP1[,2]),
digits=3),round(min(results[,2]), digits=3),round(max(results[,2]),
digits=3),round((sum(resultsP1[,3]<0.05)/nrow(resultsP1)), digits=3),round((sum(resultsP1[,4]<0.05)/nrow(resultsP1)),
digits=3)))
}
else {
  if (FullRes==TRUE){ return(results)}
  return(c(round(min(results[,1]), digits=0),round(max(results[,1]), digits=0),round(mean(results[,2]),
digits=3),round(min(results[,2]), digits=3),round(max(results[,2]),
digits=3),round((sum(results[,3]<0.05)/nrow(results)), digits=3)))
}
}

MD_res_pol_Diet<-politomies_effects(MammalDIET_sub, "MD_Diet_breadth" , 100, P1_estimate = FALSE,
N_sim=1000, bounds_sim=c(1,12))
MD_res_pol_ges<-politomies_effects(MammalDIET_sub, "Gestation_length_days" ,log=TRUE, 100, P1_estimate =
FALSE, N_sim=1000, bounds_sim=c(0,Inf))
MD_res_pol_mass<-politomies_effects(MammalDIET_sub, "Adult_body_mass_g" ,100, log=TRUE, P1_estimate =
FALSE, N_sim=1000, bounds_sim=c(0,Inf))
MD_res_pol_home<-politomies_effects(MammalDIET_sub, "Home_range_size_km2" ,100, log=TRUE, P1_estimate
= FALSE, N_sim=1000, bounds_sim=c(-Inf,Inf))
MD_res_pol_group<-politomies_effects(MammalDIET_sub, "Group_size_ind" ,100, log=TRUE, P1_estimate =
FALSE, N_sim=1000, bounds_sim=c(0,Inf))
MD_res_pol_dist<-politomies_effects(MammalDIET_sub, "Distribution_range_area_km2" ,100, log=TRUE,
P1_estimate = FALSE, N_sim=1000, bounds_sim=c(0,Inf))

MD_pol<-rbind(MD_res_pol_ges, MD_res_pol_mass, MD_res_pol_home,MD_res_pol_group, MD_res_pol_dist,
MD_res_pol_Diet, c("NA", "NA", "NA","NA","NA", "NA"))

ET_res_pol_Diet<-politomies_effects(EltonTraits_sub, "ET_Diet_breadth" , 100, P1_estimate = FALSE, N_sim=1000,
bounds_sim=c(1,10))
ET_res_pol_Levins<-politomies_effects(EltonTraits_sub, "ET_Levins_stand" , 10, P1_estimate = TRUE, N_sim=1000,
bounds_sim=c(0,100))
ET_res_pol_ges<-politomies_effects(EltonTraits_sub, "Gestation_length_days" ,100, log=TRUE, P1_estimate =
FALSE, N_sim=1000, bounds_sim=c(0,Inf))
ET_res_pol_mass<-politomies_effects(EltonTraits_sub, "Adult_body_mass_g" ,100, log=TRUE, P1_estimate =
FALSE, N_sim=1000, bounds_sim=c(0,Inf))
ET_res_pol_home<-politomies_effects(EltonTraits_sub, "Home_range_size_km2" ,100, log=TRUE, P1_estimate =
FALSE, N_sim=1000, bounds_sim=c(-Inf,Inf))
ET_res_pol_group<-politomies_effects(EltonTraits_sub, "Group_size_ind" ,100, log=TRUE, P1_estimate = FALSE,
N_sim=1000, bounds_sim=c(0,Inf))
ET_res_pol_dist<-politomies_effects(EltonTraits_sub, "Distribution_range_area_km2" ,100, log=TRUE, P1_estimate
= FALSE, N_sim=1000, bounds_sim=c(0,Inf))

ET_pol<-rbind(ET_res_pol_ges, ET_res_pol_mass, ET_res_pol_home,ET_res_pol_group, ET_res_pol_dist,
ET_res_pol_Diet, ET_res_pol_Levins)

CUF_res_pol_Diet<-politomies_effects(CUFdiet_sub, "CUF_Diet_breadth" , 100, P1_estimate = FALSE,
N_sim=1000, bounds_sim=c(1,12))
CUF_res_pol_Levins<-politomies_effects(CUFdiet_sub, "CUF_Levins_stand" , 100, P1_estimate = FALSE,
N_sim=1000, bounds_sim=c(0,1))

```

```

CUF_res_pol_ges<-politomies_effects(CUFdiet_sub, "Gestation_length_days" ,100, log=TRUE, P1_estimate =
FALSE, N_sim=1000, bounds_sim=c(0,Inf))
CUF_res_pol_mass<-politomies_effects(CUFdiet_sub, "Adult_body_mass_g" ,100, log=TRUE, P1_estimate =
FALSE, N_sim=1000, bounds_sim=c(0,Inf))
CUF_res_pol_home<-politomies_effects(CUFdiet_sub, "Home_range_size_km2" ,100, log=TRUE, P1_estimate =
FALSE, N_sim=1000, bounds_sim=c(-Inf,Inf))
CUF_res_pol_group<-politomies_effects(CUFdiet_sub, "Group_size_ind" ,100, log=TRUE, P1_estimate = FALSE,
N_sim=1000, bounds_sim=c(0,Inf))
CUF_res_pol_dist<-politomies_effects(CUFdiet_sub, "Distribution_range_area_km2" ,100, log=TRUE, P1_estimate =
FALSE, N_sim=1000, bounds_sim=c(0,Inf))

CUF_pol<-rbind(CUF_res_pol_ges, CUF_res_pol_mass, CUF_res_pol_home, CUF_res_pol_group, CUF_res_pol_dist,
CUF_res_pol_Diet, CUF_res_pol_Levins)

##Generating Table S2
Table_S2_results<-cbind(MD_pol, ET_pol, CUF_pol)
colnames(Table_S2_results)<-c("MD_min_N", "MD_max_N", "MD_mean_K", "MD_min_K",
"MD_max_K", "MD_P0",
"ET_min_N", "ET_max_N", "ET_mean_K", "ET_min_K", "ET_max_K", "ET_P0",
"CUF_min_N", "CUF_max_N", "CUF_mean_K", "CUF_min_K", "CUF_max_K", "CUF_P0")

#####
#####
##ESTIMATING THE NET RELATEDNESS INDEX###
#####
#####

library(ape)
library(PhyloMeasures)
library(caper)

##generate a database all species in the phylogeny with 0 indicating no data in the diet database and 1 indicating data
available. Please note that because in the original dataset species that have no data for either global database were
excluded we generated a new dataset with 5020 species (those in the phylogeny), as a result some species have zero for
both MammalDIET and EltonTraits

diet_availability<-merge(as.data.frame(tree$tip.label),(data[,c("binomial_tree", "MammalDIET", "EltonTraits")])),
by.x="tree$tip.label", by.y="binomial_tree", all=T)
diet_availability[is.na(diet_availability)]<-0
colnames(diet_availability)<-c("binomial", "MammalDIET", "EltonTraits")

spp_matrix<-as.matrix(t(diet_availability[,2:3]))
colnames(spp_matrix) <- diet_availability$binomial

#### MPD #### (NRI) Phylogenetic structure
#get the standardized MPD values, NRI=-MPD
spp.mpd <- mpd.query(tree,spp_matrix,TRUE)
spp.mpd
#check the result by using permutations as implemented in Picante's functions
library(picante)
spp.ses.mpd<-ses.mpd(samp = spp_matrix,dis=cophenetic(tree),null.model = "taxa.labels")
spp.ses.mpd

```

Appendix S3 Supplementary tables and figure

Table S1. Phylogenetic signal (Blomberg's K) in species' traits. We report P_R as the P -values against a randomization test ($N=1000$) to determine if estimates significantly departed from those expected if traits vary randomly along the phylogeny; and P_{BM} as probability of the observed value being greater or smaller than the expected under a Brownian model of evolution (1000 simulated datasets). N_p is the number of species with available data for each trait.

Trait	MammalDiet(N=1921)				EltonTraits (N=4246)				CUFdiet (N=73)			
	N_p	K	P_R	P_{BM}	N_p	K	P_R	P_{BM}	N_p	K	P_R	P_{BM}
Gestation length*	793	3.24	0.001	0.007	1328	3.64	0.001	0.002	67	3.06	0.001	0.149
Adult body mass*	1569	1.47	0.001	0.356	3584	1.65	0.001	0.229	72	0.49	0.001	0.380
Home range*	473	0.50	0.001	0.082	698	0.43	0.001	0.023	51	0.14	0.097	0.001
Group size*	453	0.26	0.001	0.002	735	0.27	0.001	0.002	61	0.19	0.001	0.072
Range size*	1912	0.08	0.002	0.001	4193	0.08	0.001	0.001	71	0.07	0.564	0.001
Diet breadth	1921	0.11	0.001	0.001	4246	0.42	0.001	0.247	73	0.10	0.031	0.001
Levin's diet index	—	—	—	—	4246	0.46	0.001	0.352	53	0.07	0.601	0.001

* Log₁₀-transformed

Table S2. Unbiased estimates of phylogenetic signal (Blomberg's K) from diverse species' traits obtained from the rarefaction-based solution proposed by Davies et al. (2012). We report the mean and range (min-max) K calculated from 100 replicates. N_p is the range for the number of species used in each replicate and $P_{0.05}$ is the proportion of the replicates in which K was significantly different from the expected in a randomization test ($N=1000$). Because data were not available for all species in the tree, randomly selecting one species from existing polytomies changed the available sample size. The maximum number of species in a completely resolved phylogeny based on the mammalian supertree is 2716 (the tree includes information for 5020 species but many are reconstructed in polytomies).

Trait	MammalDiet			EltonTraits			CUFdiet		
	N_p	K	$P_{0.05}$	N_p	K	$P_{0.05}$	N_p	K	$P_{0.05}$
Gestation length*	626-654	3.10 (2.92-3.24)	1.00	1001-1041	3.57 (3.39-3.75)	1.00	59-62	3.07 (2.84-3.29)	1.00
Adult body mass*	1171-1214	1.35 (1.27-1.43)	1.00	2319-2357	1.42 (1.31-1.57)	1.00	63-65	0.54 (0.47-0.69)	1.00
Home range*	379-405	0.48 (0.45-0.52)	1.00	546-580	0.41 (0.38-0.43)	1.00	44-48	0.16 (0.14-0.19)	0.31
Group size*	364-387	0.26 (0.24-0.28)	1.00	564-589	0.26 (0.24-0.27)	1.00	53-55	0.20 (0.17-0.24)	1.00
Range size*	1402-1446	0.09 (0.08-0.10)	1.00	2602-2632	0.08 (0.078-0.08)	1.00	62-64	0.08 (0.07-0.09)	0.00
Diet breadth	1397-1447	0.11 (0.10-0.11)	1.00	2640-2664	0.31 (0.30-0.32)	1.00	64-66	0.11 (0.10-0.12)	0.79
Levin's diet index	—	—		2642-2665	0.34 (0.32-0.37)	1.00	44-47	0.07 (0.05-0.10)	0.00

* Log₁₀-transformed

Table S3. Phylogenetic signal (Blomberg's K) detected in the dietary breadth (total number of food categories consumed) of species from different mammalian orders. Dietary data obtained from MammalDIET and EltonTraits but considering only species with data in both datasets to compare estimates. We report P_R as the P -values against a randomization test ($N=1000$) to test if estimates significantly departed from the expected if there was no phylogenetic signal; and P_{BM} as the probability of the observed value being greater or smaller than the expected under a Brownian model of evolution (1000 simulated datasets). N_p is the number of species with available data for each trait. Small orders includes mammalian orders with ≤ 20 species with dietary data: Cingulata, Dermoptera, Hyracoidea, Macroscelidea, Microbiotheria, Monotremata, Notoryctemorphia, Paucituberculata, Peramelemorphia, Perissodactyla, Pholidota, Pilosa, Proboscidea, Scandentia, and Tubulidentata.

Order	N_p	MammalDiet			EltonTraits		
		K	P_R	P_{BM}	K	P_R	P_{BM}
Afrosoricida	14	1.22	0.016	0.736	1.44	0.002	0.428
Didelphimorphia	37	0.76	0.017	0.449	1.53	0.001	0.115
Erinaceomorpha	8	0.72	0.098	0.673	0.81	0.072	0.789
Lagomorpha	41	0.50	0.001	0.474	0.12	0.778	0.001
Dasyuromorphia	16	0.46	0.475	0.166	0.29	0.883	0.003
Diprotodontia	39	0.36	0.598	0.008	0.79	0.001	0.614
Chiroptera	366	0.34	0.001	0.039	0.77	0.001	0.846
Soricomorpha	75	0.29	0.283	0.005	1.23	0.001	0.727
Primates	198	0.29	0.001	0.101	0.47	0.001	0.310
Small_Orders	56	0.23	0.011	0.008	0.32	0.003	0.076
Artiodactyla	148	0.17	0.025	0.001	0.46	0.001	0.455
Rodentia	531	0.14	0.001	0.006	0.55	0.001	0.212
Carnivora	201	0.13	0.175	0.001	0.18	0.002	0.001

Table S4. Phylogenetic signal detected in qualitative descriptors (presence/absence) of mammalian dietary composition. Phylogenetic signal is estimated using Fritz and Purvis' D ($D=1$ when there is no phylogenetic structure). We report two P -values (based on 5000 replicates): P_R estimated from randomization tests, and P_{BM} estimated from simulated BM. N_p is the number of species with presence =1 for each dietary category.

Diet category	MammalDiet ($N=1921$)				EltonTraits ($N=4246$)				CUFdiet ($N=73$)			
	N_p	D	P_R	P_{BM}	N_p	D	P_R	P_{BM}	N_p	D	P_R	P_{BM}
Vert	–	–	–	–	348	-0.24	<0.001	0.921	–	–	–	–
Vend	195	-0.05	<0.001	0.658	386	-0.39	<0.001	0.991	72*	–	–	–
Mammal	182	-0.09	<0.001	0.721	–	–	–	–	71	0.69	0.327	0.316
Bird	124	0.13	<0.001	0.266	–	–	–	–	69	0.70	0.219	0.176
Herptile	155	0.21	<0.001	0.099	397	-0.32	<0.001	0.977	55	0.67	0.035	0.030
Fish	81	0.33	<0.001	0.050	190	-0.37	<0.001	0.948	27	0.99	0.432	<0.001
Invertebrate	1055	0.13	<0.001	0.082	2770	-0.33	<0.001	>0.999	61	0.42	0.006	0.151
Fruit	723	0.19	<0.001	0.016	1661	-0.29	<0.001	0.998	43	0.33	<0.001	0.217
Nectar	103	-0.23	<0.001	0.879	206	-0.39	<0.001	0.953	4	0.66	0.186	0.202
Woody	172	0.27	<0.001	0.026	–	–	–	–	16	0.73	0.071	0.020
Grass	284	0.03	<0.001	0.431	–	–	–	–	39	0.82	0.062	0.007
Seed	398	0.14	<0.001	0.119	1314	-0.32	<0.001	0.998	20	0.63	0.016	0.037

Diet category	MammalDiet (N=1921)				EltonTraits (N=4246)				CUFdiet (N=73)			
	<i>N_p</i>	D	<i>P_R</i>	<i>P_{BM}</i>	<i>N_p</i>	D	<i>P_R</i>	<i>P_{BM}</i>	<i>N_p</i>	D	<i>P_R</i>	<i>P_{BM}</i>
Root	129	0.30	<0.001	0.038	–	–	–	–	1*	–	–	–
Plant	–	–	–	–	2148	-0.38	<0.001	>0.999	–	–	–	–
Carrion	–	–	–	–	351	-0.53	<0.001	>0.999	23	0.91	0.248	0.004
Other	356	0.37	<0.001	<0.001	–	–	–	–	–	–	–	–

*These groups were not analyzed because either all-but-one or none-but-one species were classified as consuming the diet category.

Figure S1. Phylogenetic relationships and dietary composition for 66 large mammalian carnivores (Families Canidae, Ursidae, and Felidae). Dietary composition is described by the presence (black symbol) of seven distinct food item categories: Vemd (Mammal and Bird), Herptile, Fish, Invertebrate, Fruit, Nectar, and Seeds from three different diet databases: MammalDIET (triangle), EltonTraits (asterisk) and CUFdiet (square).

