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A TAXON -FREE, MULTI-PROXY MODEL FOR MAKING PALEOECOLOGICAL
INTERPRETATIONS OF NEOGENE NORTH AMERICAN MAMMALIAN FAUNAS

by

Devra G. Hock

A THESIS

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A TAXON -FREE, MULTI-PROXY MODEL FOR MAKING PALEOECOLOGICAL
INTERPRETATIONS OF NEOGENE NORTH AMERICAN MAMMALIAN FAUNAS

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University of Nebraska, 2018

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Proxies used for interpreting the paleoecology of extinct vertebrate communities are usually based on modern ecosystems, with many developed from Old World ecosystems. However, because no model is completely taxon-free and phylogenetic influences cannot be entirely discounted, these proxies may not be appropriate for paleoecological interpretations of North American ecosystems. Additionally, many proxies based on modern vertebrate communities exclude small-bodied mammals. Here I explore several new paleoecological models based on the frequency of mammalian traits within three ecological categories: locomotion, diet, and body mass. Since these models are intended for interpreting paleoenvironments occupied by Neogene North American mammals, the data used to develop the models are from historical North American faunas. Pre-existing datasets were augmented with locomotion, diet, and body mass information from a variety of sources. Mammalian geographic occurrences were assigned to digital maps of Bailey's Ecoregions of North America in ESRI ArcMap and ecoregions were combined into broader biomes in an iterative process using preliminary Principle Component Analysis (PCA). Taxa were sorted by biome and two datasets were created, one where the number of individual occurrences were used to weight traits, and one where only a single taxonomic occurrence was used for each biome. Taxonomic analyses were

conducted on unweighted taxa both with and without rodents and lagomorphs. PCA was conducted using frequencies of trait classifications per biome for all datasets. Stacked area charts were created to visualize changing trait frequencies among biomes.

PCA analyses using unweighted data without the smallest mammals (<500 g) provides the strongest separation of biomes. High frequencies of grazer, cursorial, and size class G traits (<10500 g) are correlated traits in the grassland biome. Size classes C (500-1000 g) and D (1000 – 1500 g) are the second group of correlated traits, plotting in the opposite direction in grassland. High frequencies of arboreal/scansorial, omnivore, and granivore traits make up key indicators for the forest biome. Weighted datasets without small-bodied mammals (<500 g) work well to distinguish among biomes. I conclude that unweighted analyses excluding small-bodied mammals should provide the best separation of biomes and be most appropriate for certain paleoecological applications in North America.

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1. INTRODUCTION

In its broadest sense, the goals of paleoecology are to understand how ancient organisms interacted, and the kinds of habitats and biomes that were present where these organisms lived. Various proxies have been used to reconstruct ancient environments, such as stable carbon isotopes, soil types, sedimentary facies, and the compositions of fossil floras and fossil faunas (e.g., Edwards et al. 2010; Feranec 2007; Secord et al. 2008; Ehleringer et al. 1991). Key functional traits in vertebrates that have been shown to be correlated with environmental variables are sometimes used. For example, the frequency of hypsodonty (tooth crown height) in mammal species is significantly correlated with precipitation, with a higher percentage of hypsodont species in dry areas (Polly et al. 2011; J. T. Eronen, Polly et al. 2010). Although this approach is useful, it often serves to infer only one aspect of the environment. Broader approaches have also been employed that involve various functional aspects of an entire faunal community, or the frequencies of these aspects within the community (e.g., Andrews and Hixon, 2014). An example of this approach is the frequency of grazing (grass-eating) and browsing (leaf-eating) species in a mammal fauna. Grazers would be expected to occur in higher frequencies than browsers in grasslands, and the inverse in forests, based on modern analogs (Cerling & Harris 1999). This “community ecology” approach relies on the assumption that functional traits, which are physical adaptations that serve a specific function in an organism's environment (Polly et al. 2011), can be used to glean information about ancient environments. Functional traits in mammals generally occur in three ecological categories: locomotion, diet, and body mass. By analyzing the distribution of traits within these categories, paleoecological models can be developed for

interpreting past environments (e.g., Andrews and Hixon, 2014). Because the range of trait distributions in modern mammals is directly related to their respective environments, interpretations of past ecosystems are possible (Pineda-Munoz & Alroy 2014; Andrews & Hixson 2014).

As one goes further back in time the assumption that a taxon retains the same ecological niche becomes increasingly tenuous (Secord et al. 2008). Thus, it is desirable to use “taxon-free” community approaches when possible. Analyzing the frequency of traits within a community can be done without taxonomic consideration based on the assumption that these traits are adapted to a specific ecological niche independent of phylogeny. However, an organism’s phylogenetic history imposes constraints on the adaptability of that organism (e.g., Barnosky et al. 2001; Brooks and McLennan 1993; Losos 1996; Jablonksi and Sepkoski 1996; Ricklefs 2007), and it is doubtful that any approach is truly taxon free (e.g., see Andrews and Hixon, 2014). Nevertheless, the ability to directly study traits and trait distributions, instead of species, minimizes inherent taxonomic bias when applying modern observations to fossil communities. In order to identify traits useful for making both ecological and paleoecological interpretations, it is important to understand the processes controlling the relationship between these traits and associated environmental conditions.

The objective of this thesis is to develop a comprehensive model for interpreting Neogene biomes in North America. I explore the efficacy of several multi-proxy paleoenvironmental models based on the frequency of trait distributions in locomotion, diet, and body mass in modern mammalian communities. While many previous proxies have been developed from African or European ecosystems, there is a high potential for

error when regionally-derived proxies are applied globally (e.g., P. J. Andrews, Lord, and Evans 1979; P. Andrews and Hixson 2014; Meloro 2011; Plummer, Bishop, and Hertel 2008; Rodríguez 2004; Rodríguez, Hortal, and Nieto 2006; Van Valkenburgh 1988). Additionally, no model is completely taxon-free, and phylogenetic influences cannot be entirely discounted. For these reasons the models I develop are based on modern and historical North American faunas, rather than Old World faunas. Also, many studies that use mammalian traits as proxies exclude small-bodied mammals or group them with larger mammals (e.g., Liu et al. 2012; J. Eronen, Puolamäki, and Liu 2010; J T Eronen et al. 2010; Rodríguez 2004; P. Andrews and Hixson 2014; Soligo and Andrews 2005; Legendre 1986). There is a significant collection bias against small-bodied mammals in African-based proxies, and the implications of this bias on paleoecological interpretations are not fully understood (Soligo & Andrews 2005; Damuth & Janis 2011; Andrews & Hixson 2014). Hence I explore the impact that small-bodied mammals have on distinguishing biomes in the model. I also examine the impact of weighting traits by the number of geographic occurrences of a taxon, versus using only a single occurrence in each biome. Furthermore, I explore the differences between taxon-free and phylogenetic analyses by combining the unweighted dataset into two groups, rodents and lagomorphs, and all remaining taxa. Lastly, I compare models built for this study with some published models. Results of this study indicate which community models are best suited for paleoecological interpretations in North America and build the foundation for future Neogene paleoecological studies.

2. BACKGROUND

Research conducted by Andrews et al. (1979) provided much of the groundwork for subsequent studies of community ecology that examine mammalian traits and their relationship to the environment. Andrews, et. al focused on describing biomes solely on trait assemblages and applying those modern ecological relationships to the fossil record. Biomes, as used here, are broad, regional areas that share similar environmental factors (Bailey 1983), whereas habitats describe local conditions where an organism or community lives (Odum 1959). Andrews, Lord, and Evans divided extant African mammal communities into five general biomes: lowland forest, montane forest, woodland-bushland, grassland, and floodplain. They classified extant mammals by diet (carnivore, insectivore, grazers, browsers, frugivores, omnivores), size (< 1 kg, 1-45 kg, >45 kg), locomotion (aerial, arboreal, scansorial, terrestrial, fossorial, aquatic), and taxonomic groups (rodents and insectivores, primates, artiodactyls and carnivores) (Andrews et al. 1979). By analyzing the range of functional traits in each group, they created trait indices, which they subsequently applied to fossil communities. Three modern biomes had unique indices: forest, woodland-bushland, and grassland. These indices allowed for the interpretation of two (out of five) fossil communities as forest and woodland biomes (Andrews et al. 1979). This study demonstrated that modern biomes could be classified using the distribution of traits within mammalian communities, and these relationships can be used for paleoecological interpretations.

More recent research has been focused on developing taxon-free approaches, which has met with mixed success. One such example is the study of ecomorphological (or ecometric) traits, which are functional traits directly related to the ecosystem, of

extant African mammals by Andrews and Hixson (2014). They used body mass, locomotion, and diet as ecological categories, because these represent distinct divisions within communities: an organism's size, the space it occupies, and its trophic level. Their research focused on determining how well biomes can be distinguished by ecomorphological traits. Body mass did not show clear trends among the biomes and was determined to be the least useful category (Andrews & Hixson 2014); it is also not entirely taxon-free (e.g., rodents and lagomorphs have clear limits to maximum size). Regressions for calculating body mass are based on higher taxonomic groupings, and different clades exhibit different ranges for body mass (e.g., Legendre 1986), creating inherent bias within body mass metrics. Locomotion and diet, on the other hand, each showed clear differentiation among biomes, supporting the hypothesis that morphological traits can be used to infer biomes (Andrews & Hixson 2014). Building on prior ecological foundations (e.g., J T Eronen et al. 2010; Polly et al. 2011; Soligo and Andrews 2005), this research was a prime example of the “taxon-free” concept in paleoecological studies.

Dietary classifications can be used to analyze geographic differences in diet diversity among mammals. For example, Badgley and Fox (2000) related the locations of species to environmental and physiographic factors. They placed species in spatial quadrants across North America and analyzed the diversity of species' body sizes and diet classifications to establish thresholds (Badgley & Fox 2000). Results showed that species with smaller body sizes had higher diversity at lower latitudes, whereas species with larger body sizes exhibited higher diversity at higher latitudes. Furthermore, species diversity in frugivores, omnivores, granivores, and aerial insectivores, as well as those with the smallest body sizes (< 1kg), was affected by gradients in both temperature and

moisture. Aerial insectivores, frugivores, and terrestrial invertivores are also more diverse at lower latitudes. The diversity of species with medium to large body sizes increased from east to west, along with diversity of granivores and herbivores (Badgley & Fox 2000). This study showed geographic trends in both diet and body size, and their relationship to abiotic factors.

Pineda-Munoz et al. (2016) studied the relationship between diet and body mass in modern mammals. They grouped extant mammals into eight dietary categories based on stomach content data: herbivore, carnivore, frugivore, granivore, insectivore, fungivore, gumivore, and generalized. Pineda-Munoz et al. observed a significant separation of diets in mammals smaller than 1 kg and mammals larger than 30 kg using Principle Component Analyses (PCA). Smaller mammals had the largest diet diversity, encompassing insectivores, granivores, and mixed feeders, whereas large mammals had a narrow range of diets, including only carnivores and grazers. The medium-sized mammals (1-30 kg) consisted primarily of frugivores (51.55), while 75% of frugivores were placed in the medium size range. Frugivores were found to be the most distinct dietary group, with a significant body mass difference between frugivores and granivores, insectivores, and generalists (Pineda-Munoz et al. 2016). Frugivores had the third largest sample size (insectivore and herbivore with more), but the size range for the medium size bin was quite broad (1 kg to 30 kg). When applied to fossil assemblages, Pineda-Munoz et al. indicated that keeping dietary categories separate is most appropriate. For paleoecological interpretations conducted with both dietary categories and body sizes as proxies, combining diet categories may mask environmental factors (Pineda-Munoz et al. 2016). However, differentiating dietary groups can be difficult for fossil taxa. Diet is

interpreted from dental morphology, microwear, or stable carbon isotopes, but these proxies do not always match dietary categories in modern taxa, and all are not useful for the full dietary range observed in modern mammals (e.g., J. Eronen, Puolamäki, and Liu 2010; Liu, Puolamaki, et al. 2012; Evans et al. 2007; Cerling et al. 2003; Secord, Wing, and Chew 2008; Feranec 2007). This study demonstrated the relationship between ecometric categories and highlighted potential problems in paleoecological applications.

Additional research on the connection between body size and diet has demonstrated their interconnectedness. Price and Hopkins (2015) investigated large-scale ecological patterns in mammals by combining diet and body size data with a phylogenetic analysis. Dietary groups were broad: herbivore, carnivore, and omnivore. Using generalized Ornstein–Uhlenbeck phylogenetic models, Price and Hopkins (2015) showed a macroevolutionary relationship between diet and body size in mammals. They observed that terrestrial omnivores were generally larger than carnivores, and terrestrial herbivores were larger than omnivores. Rodents deviated from the general trend and separate patterns were displayed. Within the carnivore dietary group, rodents displayed a higher body mass, while omnivores displayed a lower body mass. Carnivorous rodents were not the majority in the data, as 21 of the 409 rodent species were classified as carnivores, and 11 of those rodent species were semi-aquatic with a diet of fish, crabs, and aquatic snails. Price and Hopkins (2015) concluded that the carnivorous preferences of these larger rodents potentially reflected that available prey increases with body mass. Research highlighting the relationship between phylogenetic evolution and ecometric traits suggests that ecometric traits are interconnected within and outside phylogenetic

clades. Price and Hopkins' research also suggests there is an inherent taxonomic presence in all ecometric studies.

In addition to both body size and diet analyzed together and separately, the relationship of locomotion and the environment has primarily been studied in isolation. Locomotion is often used to determine the openness of an environment (Polly 2010). In carnivores, highly digitigrade mammals are associated with open environments, such as prairies, steppes, or deserts, while plantigrade mammals are associated with closed environments including woodlands or forests (Polly 2010). Taxon-free approaches rely on the convergence of traits across phylogenetic classifications. Locomotion is a prime example of that convergence. Locomotion is primarily based on morphology of a species, and convergent morphology occurs when different species live in similar habitats (e.g., Jenkins and Camazine 1977; Alexander et al. 1979; Brown and Yalden 1973; Christiansen 1999; J. M. Smith and Savage 1956). Samuels et al. (2013) examined the range of locomotion within Carnivora, including both extant and extinct taxa of North American families that are not closely related: Amphicyonidae, Barbourfelidae, Canidae, Felidae, Miacidae, Mustelidae, Nimravidae, and Ursidae. They used 20 osteological measurements to determine locomotor habit and included extinct carnivores with no modern morphological analog. Locomotion was split into six groups: terrestrial, cursorial, scansorial, arboreal, semi-fossorial, and semi-aquatic. Both morphological indices and locomotor groups were found to be convergent for extant and extinct taxa. Cursorial and terrestrial hyaenids, canids, and felids all had relatively elongate and gracile limbs and grouped together; semi-fossorial mephitids and badgers also grouped together. The morphological indices were found to best discriminate cursorial and

arboreal species. In addition, species with similar locomotor groups converged towards similar morphology, regardless of the level of phylogenetic relationship (Samuels et al. 2013).

Meloro (2011) reconstructed locomotor behavior of Italian Plio-Pleistocene carnivore families by using long-bone metrics of extant and fossil species. He used 22 extant species of Canidae, Felidae, Hyaenidae, and Ursidae, accounting for phylogenetic relatedness since closely related species tend to have similar behavioral and morphological traits (Meloro 2011). He restricted modern carnivores to large taxa (>7kg) with a well-researched fossil record on the Italian peninsula and used related modern taxa to assign locomotor behavior to fossil taxa. Meloro (2011) found in a PCA of extant and extinct taxa that locomotor behavior and long bone measurements indicated general patterns of association between extinct carnivores and their habitat. Meloro (2011) found that carnivores were not habitat specialists, unlike ungulates and rodents. Instead, carnivores have large home ranges, and their habitat selection is dependent on the density of prey and other predators. Carnivores may be well adapted to specific habitats but will select sub-optimal habitats when pressured from external factors (Meloro 2011). The results of Samuels et al. (2013) and Meloro (2011) show that ecometric traits can be convergent, supporting the viability of taxon-free approaches.

While the relationship among ecometric traits is essential, understanding the relationship between mammalian body mass and the environment is equally necessary. Rosenzweig (1968) examined the influence that environmental factors have on body mass in modern mammalian carnivores. Temperature and latitude were suggested to represent measures of the same environmental pressure on body size (Rosenzweig 1968).

He found that body size for the female marten and male coyote, as well as both sexes of the red fox, gray fox, badger, and ermine, could be predicted by both temperature and latitude. Evapotranspiration also predicted body size in water-stressed and/or heat-stressed environments (Rosenzweig 1968). Furthermore, Rosenzweig (1968) observed a connection between diet and body size, concluding that a carnivore's body size is dependent on both prey size and the frequency with which it can obtain prey. Thus, large Carnivora taxa (e.g., bears) take in a high amount of vegetation when hunting smaller-sized prey that are not readily available, choosing an omnivorous diet rather than a carnivorous one. The results of Rosenzweig (1968) show the interconnectedness of body size and the environment, and the relationship between environmental factors and body size.

3. METHODS

3.1 North American Modern Mammal Database

To compile a database of modern mammal trait frequencies in North America, I downloaded a list of North American mammals from NatureServe Explorer (NatureServe 2016) and species field guides from the Smithsonian North American Mammals database (Smithsonian National Museum of Natural History). I removed the families Chiroptera, Sirenia, Cetacea, Odobenidae, and Otariidae to ensure the database included species that are native to North America and either non-marine aquatic, non-marine semi-aquatic, or terrestrial. This initial list totaled 537 species.

For each species in the modern North American list, I compiled data on body size, diet, and locomotion from a variety of sources. My primary source was NatureServe's online searchable database (NatureServe 2016). I supplemented body mass measurements from PanTHERIA (Jones et al. 2009), Quaarvark (University of Michigan Museum of Zoology 2013), and Wilman et al. 2014, and calculated averages for each species. I assigned taxa to body mass ranges ("Body Class"), giving a letter to each range: A (0-50 g), B (50-500 g), C (500-1,000 g), D (1,000-1,500 g), E (1,500-3,500 g), F (3,500-10,500 g) and G (>10,500 g) (Table A1c). To determine the body mass classes, I created a frequency histogram (Fig. 1) using the 'PivotTable' and 'Histogram' analyses functions in Excel 2016 (Microsoft Office 2016). While a clear bias towards smaller body masses is evident, distribution of body mass above 500 g remains even. I initially assigned diet and locomotion from NatureServe's previous designations and their description of each species' recorded diet (Table A1a, A1b). I then refined the diet categories with stomach content percentages from Wilman et al. (2014). Locomotion data were validated and

refined with Walker's Mammals of the World 6th ed. (Nowak 1999a; Nowak 1999b). Dietary categories are: carnivore, omnivore, frugivore, granivore, folivore, browser, grazer, mixed feeder, and herbivore (Table A1a). Here, carnivore is defined as consuming vertebrate and/or invertebrate animals, and omnivore is defined as consuming a mix of invertebrates, vertebrates, and plant material. Frugivore is defined as consuming fruit material, and folivore is defined as consuming plant material, such as grass, ground vegetation, weed, moss, lichen, twigs, bark, and leaves (see Table A1b for frequencies). Folivore is used only for non-ungulate mammals. Grazer (grass and sedges), browser (leaves and branches), and mixed feeder (grass and tree material) are assigned to ungulate mammals. Herbivore is defined as diets with an equal mix of either folivore, granivore, and frugivore. Locomotion frequencies are ambulatory, aquatic/semi-aquatic, arboreal/scansorial, cursorial, fossorial, non-cursorial, semi-fossorial (Table A1b). Terrestrial locomotion traits are ambulatory (defined as exhibiting plantigrade morphology), cursorial (defined as having digitigrade or unguligrade morphology), and non-cursorial (neither plantigrade, digitigrade, or unguligrade morphology). Aquatic/semi-aquatic groups both aquatic and semi-aquatic locomotion habits in one category due to low numbers of each when separated. Arboreal/scansorial is defined as the ability to readily climb trees (e.g. squirrels). Semi-fossorial is defined as spending active time on the ground surface and in burrows, and inactive time in burrows. Fossorial is defined as spending both active and inactive time in burrows. In cases where locomotion data were missing from available sources (Quaardvark, PanTHERIA, Wilman et al. 2014, NatureServe, and Walker's Mammals of the World), those species

were assigned as "Unknown". Species with unknown locomotion classification totaled 52, all consisting of rodents and shrews from understudied regions of Mexico.

3.2 Historical Database

Historical occurrence data were downloaded from the American Museum of Natural History's (AMNH) Online Mammalogy Database (American Museum of Natural History 2018). Searches used the original list of 537 species from the modern North American database, searching each family, genus, or species for localities in the United States, Mexico, and Canada. I trimmed the database to include only records collected before 1900 to reduce the potential for human disturbance. Historical occurrence data, as opposed to recent occurrences, were used to create a biome database that represented ecosystems that were less disturbed by humans. I also removed records with no associated date, records without county-level locality data, and records of island occurrences.

Next, taxonomic names were updated in the historical database to reflect changes in taxonomy. Taxonomic duplicates or discrepancies were observed mainly in rodents and shrews, as taxonomical reorganization has resulted in species being moved among genera, or changed from sub-species to species. I downloaded a significant proportion of the occurrence data using family or genus search queries, thus there is potential for taxonomic discrepancies. If there was overlap between old and new species names, I used the most current taxonomic nomenclature following Nowak (1999a;1999b), (Table A2). Frequency data for locomotion, diet, and body mass were brought in from the modern North American database. Historical species totaled 135 after correcting for taxonomy. The final historical database with associated biomes consisted of 8240 occurrences.

Both a weighted and unweighted dataset were created from the historical data. Faunas with only a few dominant taxa that are abundant throughout a biome are not accurately represented by unweighted data that do not account for number of occurrences. For example, bison occur with a very low frequency in the taxonomic list, but historically had high abundances where they occurred. There are very few grazers in the historical dataset, and including their abundances in the analyses could yield patterns that otherwise were masked. Additionally, the unweighted dataset was split into two groups for taxonomic analyses: rodents and lagomorphs, and all other taxa.

After finalization of the historical database, I plotted each occurrence record using Google Earth Pro (Google Earth Pro, 2018) by adding a placemark in the center of the observed county for each record. I saved these placemarks as a .KMZ file and imported into ESRI ArcMap 10.4.1 (ArcGIS 10.6).

3.3 Biome Assignment

I downloaded Bailey's Ecoregions of North America map (Fig. A1) from the United States Department of Agriculture Forest Service Rocky Mountain Research Station's website (Rocky Mountain Research Station 1996) and used it in conjunction with the AMNH historical data. In ArcMap, I combined the Ecoregions of North America map and AMNH historical occurrence data (ArcToolbox; Overlay; Analysis Tools; Spatial Join) (Rocky Mountain Research Station 1996). This allowed each occurrence to be assigned geographical ecoregion data. I kept the names of Bailey's Division ecoregions (Table A3) the same except for the 'Marine' Division ecoregion, renaming them as 'Coastal' as to avoid confusion about the terrestrial nature of the biomes. Bailey's ecoregions were re-assigned to broader biomes (Table A4) after preliminary Principle

Component Analyses (PCA). Temperate and precipitation ranges and averages of Divisions, along with Divisions consistently plotting together (i.e., Tropical/Subtropical Steppe and Prairie; Temperate Desert and Temperate Steppe) were used to group the divisions into the broad biomes. I used Bailey's Ecocodes to test variability in each biome. Ecocodes are numerical representations of Bailey's Divisions (Bailey 1995), and each biome contains multiple ecocodes that serve as sub-sampling points. To avoid including under-sampled local faunas, only sub-samples with sizes greater than 35% of the total taxa in the biome were used. Sub-samples of 35% or greater were found to best represent the community structure and recorded habitat (Andrews & Hixson 2014). Most sub-sample points have a higher percentage of taxa, ranging from 40% to 95%; however, there are a few points with 30%. Extreme habitats (Rainforest, Savanna, Subarctic, and Tundra) and all mountainous regions, which were clearly outside the range of understood North American Neogene habitats, were excluded to better tailor the model for Neogene applications. The final historical data distribution is displayed in Figure A2.

3.4 Statistical Analysis

I used RStudio (RStudio, Version 1.0.143; R Version 3.4.3) for statistical analyses. I used packages "Plotly" (Plotly, Version 4.7.1) and "Ggplot2" (Ggplot2, Version 2.2.1) to create plots and graphics, and "RSelenium" (RSelenium, Version 1.7.1) to export graphics into '.svg' files. I created figures in Adobe Illustrator CC (Adobe Creative Cloud, Illustrator Version 22.1). All analyses were conducted with the historical taxa list and associated trait frequencies. All RStudio script is included in Appendix-A.

I imported two sets of data into RStudio: historical unweighted data (one taxon per biome) and historical weighted occurrence data (includes number of recorded

occurrences per biome). For each set of data, a new data frame was created, and new columns were then added for each of the individual biomes, with presence and absence data for each biome by row. Then, taxa were separated by trait, and the number of presences per biome were totaled. Tables were made for the proportion of trait classifications in each biome. Cumulative stacked proportions (totaling 100%) were also created for stacked area charts for each trait per biome, with the biomes arranged on the x-axis from closed (right) to open (left) (Appendix-A M1). Stacked area charts were used to analyze the composition of each trait frequency across biomes.

I conducted PCAs using trait frequencies expressed as percentages of the total traits per category (i.e., diet, locomotion, body mass) for each biome. For example, diet for the unweighted dataset in the grassland biome consists of 22.9% omnivores, 2.1% grazers, etc. For the analyses, I brought in Bailey's ecocodes (Rocky Mountain Research Station 1996) to ensure a sub-sampling within biomes (Appendix-A M2). Sub-sampling created 13 total data points in all PCA diagrams. Forest, grassland, and semi-desert all had three sub-sampling points, while woodland and desert each had two. I plotted confidence intervals onto the PCA plots for each biome with three subsampling points (Appendix-A M3). These were calculated assuming a normal, multi-variate distribution and with a 95% confidence level. Due to low sub-sample size, woodland and desert do not have 95% confidence ellipses plotted. In total, I used six datasets: unweighted (Table 1), unweighted without size classes A (0-50 g) and B (50-500 g) (Table 2), unweighted rodents and lagomorphs (Table 3), unweighted without rodents and lagomorphs (Table 4), weighted (Table 5), weighted without size classes A and B (Table 6). Each dataset was analyzed with all traits combined, and also separately with locomotion, diet, and

size. From the historical species list, 33 species weigh less than 50 g (24% of the total species list), and 46 species weigh between 50 and 500 g (34%). Removing both size classes A and B removed 51% of the unweighted dataset and 64.5% of the weighted occurrence dataset. Rodents and lagomorphs make up 44.7% of the unweighted data. I repeated the analyses four times per dataset, one with all the traits combined, and one for locomotion, diet, and size separately. For the taxonomically grouped data, analyses were only conducted on the traits combined. Removing size classes A and B created a weighted dataset of 2348 occurrences and an unweighted dataset of 187. Analyses were additionally conducted with and without rodents and lagomorphs for the unweighted data. Rodents and lagomorphs created an unweighted dataset of 243 taxonomic occurrences and the remaining taxa created a dataset of 138.

4. RESULTS

4.1 Principle Component Analysis

PCA diagrams consist of PC1 on the x-axis, and PC2 on the y-axis. Sub-sampling points and confidence ellipses for each biome (with n=3) are plotted using the scores of each point for the two principle components. Thirteen points were plotted in total, representing the five biomes. An explanatory PCA (Fig. 2) illustrates arrows and the relationships of variables. Variables consist of trait frequencies and are plotted as arrows from their respective loadings on PC1 and PC2. The longer the arrow, the higher association that frequency has with both principle components. In Figure 2, trait frequency 3 has a high association with PC1 and trait frequency 5 has a high association with PC2. Conversely, the shorter the arrow, the lower association, as seen in trait frequency 4 in the explanatory figure (Fig. 2). An arrow with a high association inside a biome's ellipse displays a trait frequency that best describes that biome (trait frequency 5; Fig. 2). The positions of arrows also indicate relationships between trait frequencies. Arrows that plot close together have a positive correlation with each other (trait frequency 1 & 2; Fig. 2), while arrows that plot in opposite directions have a negative or inverse correlation (trait frequency 1 & 3; Fig. 2). Trait frequencies with loadings 20% or higher are displayed on the figures, outside the plotting area (Fig. 2).

For the sake of brevity, PCA plots that show the greatest separation among biomes are shown in the main text, while those with poor separation are included in the appendix (Appendix-C).

4.1.1.1 Unweighted Diet, Locomotion, Medium & Large Body Size (≥ 500 g) PCA

PC1 explains 31.5% of variance; PC2 explains 24% (Fig. 3). Grassland, forest, and semi-desert have significant separation. Omnivore, granivore, arboreal/scansorial, and size class F plot in the forest ellipse. Omnivore, granivore, and arboreal/scansorial have high positive loadings on PC1 and high negative loadings on PC2, with size class F also having a high negative loading on PC2 (Table 7). Grazer, cursorial, aquatic/semi-aquatic, and size class G plot in the grassland ellipse, with grazer, cursorial and size class G plotting close to each other (Fig. 3), suggesting a positive relationship. Grazer, cursorial, and size class G have high negative loadings on PC1. Size classes C and D also plot in the grassland ellipse in the opposite direction (Fig. 3), indicating an inverse correlation. Size class C has a high positive loading on PC1 (Table 7). Non-cursorial plots on the border of the semi-desert ellipse, with a high positive loading on PC2 (Table 7).

4.1.1.2 Unweighted Locomotion PCA, Medium & Large Body Size (≥ 500 g)

PC1 explains 30.8% of variance; PC2 explains 25.2% (Fig. 4). Grassland, forest, and semi-desert have significant separation. Forest and grassland ellipses have larger separation than grassland and semi-desert ellipses. Arboreal/scansorial plots in the forest ellipse, and non-cursorial plots in the semi-desert ellipse in opposite directions (Fig. 4), suggesting an inverse relationship among the trait frequencies and their associated biomes. Arboreal/scansorial has a high positive loading on PC2. Non-cursorial has high negative loadings on both PC1 and PC2, with a higher loading on PC2 (Table 8). Cursorial plots in the grassland ellipse, with a high positive loading on PC1 and a high negative loading on PC2 (Table 8).

4.1.1.3 Unweighted Diet PCA, Medium & Large Body Size (≥ 500 g)

PC1 explains 31% of variance; PC2 explains 20% (Fig. 5). Semi-desert and grassland ellipses have clear separation, as do semi-desert and forest. Grassland and forest ellipses cross and have a small amount of overlap. Omnivore and granivore plot near each other in the forest ellipse (Fig. 5), suggesting a positive relationship. Browser plots in the opposite direction (Fig. 5), suggesting an inverse correlation. Omnivore and granivore both have high negative loadings and browser has a high positive loading on PC1 (Table 9). Omnivore and browser both have a high positive loading on PC2. Mixed feeder plots in the grassland ellipse with a high positive loading on PC1 and PC2, and folivore plots in the semi-desert ellipse with a high negative loading on PC2 (Table 9).

4.1.1.4 Unweighted Medium & Large Body Size PCA (≥ 500 g)

PC1 explains 37.3% of variance; PC2 explains 29.7% (Fig. A3). Grassland has the largest ellipse and overlaps all biomes. Forest and semi-desert ellipses have clear separation. Size class E plots in the semi-desert ellipse with high positive loadings on both PC1 and PC2 (Table 10). Size class F plots in the forest ellipse in the opposite direction with high negative loadings on PC1 and PC2 (Fig. A3; Table 10), suggesting an inverse relationship between trait frequencies and their biomes. Size class D and G plot in the grassland ellipse in opposite directions (Fig. A3), indicating a negative correlation between the two size classes within the grassland biome. Size class D has high negative loadings on PC1 and size class G has a high positive loading on PC1 and a high negative loading on PC2 (Table 10).

4.1.2.1 Weighted Diet, Locomotion, Medium & Large Body Size (≥ 500 g) PCA

PC1 explains 28.4% of variance; PC2 explains 20.7% (Fig. 6). Semi-desert's and grassland's ellipses have separation. Forest's ellipse crosses both individually, creating small pockets of overlap. Ambulatory and mixed feeder plot in the grassland ellipse. Ambulatory and mixed feeder has a high negative loading on PC1. Aquatic/semi-aquatic plots in the grassland ellipse in the opposite direction with low positive loadings on PC1 and PC2 (Fig. 6; Table 11), suggesting an inverse relationship. Arboreal/scansorial, granivore, semi-fossorial, omnivore, and size class F plot in the forest ellipse. Arboreal/scansorial, granivore, omnivore, and size class F have high positive loadings on PC1 (Table 11). Arboreal/scansorial, granivore, and size class F have high negative loadings on PC2 (Table 11). No trait classifications plot in the semi-desert ellipse, though carnivore, non-cursorial and folivore trend towards semi-desert (Fig. 6).

4.1.2.2 Weighted Locomotion PCA, Medium & Large Body Size (≥ 500 g)

PC1 explains 30.2% of variance; PC2 explains 28.5% (Fig. 7). Grassland's and semi-desert's ellipses show clear separation. Forest's ellipse crosses into grassland perpendicularly, creating an area of overlap. Arboreal/scansorial and semi-fossorial plot together in the forest ellipse (Fig. 7), suggesting a positive relationship. Arboreal/scansorial and semi-fossorial have high positive loadings on both PC1 and PC2 (Table 12). Cursorial and ambulatory plot in grassland, with aquatic/semi-aquatic plotting in an opposite direction (Fig. 7), suggesting an inverse relationship among the three trait frequencies. Cursorial and ambulatory have high positive loadings on PC1 and high negative loadings on PC2 (Table 12). Fossorial plots in semi-desert with a high negative loading on PC1 (Table 12).

4.1.2.3 *Weighted Diet PCA, Medium & Large Body Size (≥ 500 g)*

PC1 explains 33.8% of variance; PC2 explains 21.3% (Fig. A4). Grassland's and semi-desert's ellipses are separated, with the forest biome intersecting both perpendicularly. Granivore plots in the forest ellipse with a high negative loading on PC1 and a high positive loading on PC2 (Table 13). Browser also plots in the forest ellipse, though in area overlapping with grassland and with low loadings (Fig. A4; Table 13). Folivore plots in semi-desert, with a high negative loading on PC2 (Table 13). No traits plot inside grassland (Fig. A4).

4.1.2.4 *Weighted Body Size PCA, Medium & Large Body Size (≥ 500 g)*

PC1 explains 40.8% of variance; PC2 explains 31.7% (Fig. A5). Semi-desert has the largest ellipse, overlapping forest's ellipse. Grassland has the smallest ellipse, crossing through forest's and semi-desert's ellipses perpendicularly. Size class F plots in the forest ellipse (Fig. A5), with size classes D and E plotting in the opposite direction (overlapped by semi-desert's ellipse), suggesting a negative correlation. Size class F has a high negative loading on PC2, size class D has a high positive loading on PC1 and a high negative loading on PC2, and size class E has a high positive loading on PC1 (Table 14). Size class G plots in the semi-desert ellipse, with a high positive loading on PC2 (Table 14).

4.1.3.1 *Total Unweighted PCA*

PC1 explains 29.3% of variance; PC2 explains 17% (Fig. A6). Grassland displays the largest ellipse, overlapping the other biomes. Semi-desert and forest have substantive separation between their confidence ellipses. Aquatic/semi-aquatic, mixed feeder and size class F plot in the forest ellipse. Mixed feeder and size class F have high positive

loadings on PC1 and size class F has a high positive loading on PC2 (Table 15). Fossorial, grazer, and browser plot in the semi-desert ellipse. Browser and grazer plot close together, with high positive loadings on PC1. Fossorial plots in the opposite direction (Fig. A6) with a high negative loading on PC1, indicating a negative correlation (Table 15). In the grassland ellipse, granivore, omnivore, folivore, semi-fossorial, and size classes A and C group together (Fig. A6). From this first group, granivore and semi-fossorial display high negative loadings on PC1, with granivore displaying a high positive loading on PC2 (Table 15). Ambulatory, cursorial, and size class G plot together in a separate direction (Fig. A6), suggesting an inverse relationship among the trait frequencies. Cursorial and size class G have high positive loadings on PC1 (Table 15). Herbivore, non-cursorial, and size class B also group separately in the grassland ellipse, with all trait frequencies having high negative loadings on PC2 (Table 15).

4.1.3.2 Total Unweighted Locomotion PCA

PC1 explains 34.2% of variance; PC2 explains 23.9% (Fig. A7). Grassland has the largest ellipse and overlaps with other biomes. Forest and semi-desert cross confidence ellipses, resulting in a small amount of separation. However, no trait classifications plot inside either biome. Semi-fossorial and cursorial plot opposite of each other close to forest's ellipse (Fig. A7), suggesting a negative correlation, but do not plot inside. Semi-fossorial has high negative loadings on PC1 and PC2, while cursorial has high positive loadings on PC1 and PC2 (Table 16). Arboreal/scansorial and non-cursorial plot in the grassland ellipse, with no overlap and in opposite directions (Fig. A7), indicating an inverse relationship. Arboreal/scansorial has a high positive loading on PC1 and a high negative loading on PC2, while non-cursorial has a high negative loading on

PC1 and a high positive loading on PC2 (Table 16). Fossorial, ambulatory, and aquatic/semi-aquatic additionally plot in opposite directions (Fig. A7), with aquatic/semi-aquatic plotting close to the semi-desert ellipse. Fossorial has a high negative loading and aquatic/semi-aquatic has a high positive loading on PC1. Ambulatory has a high positive loading on PC2 with a high negative loading from aquatic/semi-aquatic (Table 16).

4.1.3.3 Total Unweighted Dataset Diet PCA

PC1 explains 36% of variance; PC2 explains 22.9% (Fig. A8). Forest has the largest ellipse, overlapping with grassland. Semi-desert and grassland have substantive separation, though no trait classifications plot inside their ellipses. Granivore and omnivore plot in the same direction (Fig. A8), with omnivore plotting inside the forest ellipse. Granivore and omnivore have high negative loadings on PC1, and high positive loadings on PC2 (Table 17). Mixed feeder and browser also plot near each other in the forest ellipse, suggesting a positive relationship between the two pairs of trait frequencies. Mixed feeder and browser have high positive loadings on PC1, with mixed feeder also having a high positive loading on PC2 (Table 17). Folivore and carnivore and grazer plot in opposite directions (Fig. A8), indicating an inverse correlation. Folivore has a high negative loading on PC1, while carnivore has a high positive loading (Table 17). Herbivore plots outside the semi-desert ellipse (Fig. A8), with high negative loadings on PC2 (Table 17).

4.1.3.4 Total Unweighted Size PCA

PC1 explains 31.1% of variance; PC2 explains 25.4% (Fig. A9). Grassland has the largest ellipse and overlaps with other biomes. Forest and semi-desert are distinctly separate. Size class B plots inside the semi-desert ellipse with high negative loadings on

PC1 and PC2 (Table 18). Size classes A, C, and D plot in grassland. Size classes A and C have high negative loadings on PC1, and size classes C and D have high positive loadings on PC2 (Table 18). Size classes E and G also plot in the grassland ellipse. Size class G has a high positive loading on PC1 and size class E a high positive loading on PC2 (Table 18). Size class A plots opposite of G, and size class D opposite of E (Fig. A9), suggesting negative correlations.

4.1.4.1 Total Weighted PCA

PC1 explains 24.8%; PC2 explains 16.3% (Fig. A10). Grassland has the largest ellipse, overlapping with forest and semi-desert ellipses. Semi-desert has the second largest ellipse and overlaps the forest ellipse. Herbivore, fossorial, folivore, and carnivore plot in the semi-desert ellipse. Folivore has a high positive loading on PC1, while herbivore, and fossorial have high positive loadings on PC2 (Table 19).

Arboreal/scansorial plots in the forest ellipse, along with size classes D and F in the opposite direction (Fig. A10), suggesting a negative correlation. Size class D has a high negative loading on PC2 (Table 19). Browser plots just outside of the forest ellipse, landing in the middle of the groups and has substantially low loadings on PC1 and PC2 (Table 19). Cursorial, mixed feeder, ambulatory, grazer, and size classes G and C all plot in the grassland and semi-desert ellipses. Cursorial, mixed feeder, ambulatory, grazer, and size class G have high negative loadings on PC1 (Table 19). Non-cursorial, semi-fossorial, granivore, omnivore, and size classes A and E plot in the grassland and semi-desert ellipses in the opposite direction (Fig. A10), indicating an inverse relationship between the two groups. Non-cursorial, semi-fossorial, and size class A have high positive loadings on PC1. Size class A, semi-fossorial, and granivore have high negative

loadings on PC2 (Table 19). Aquatic/semi-aquatic plots in the grassland and semi-desert ellipses, landing between those groups (Fig. A10).

4.1.4.2 Total Weighted Locomotion PCA

PC1 explains 32.8%; PC2 explains 21.1% (Fig. A11). Grassland, forest, and semi-desert have close to equal sized ellipses, and all overlap in some areas. Forest's ellipse overlaps with semi-desert's ellipse and a small amount of grassland's. Fossorial and aquatic/semi-aquatic plot in the semi-desert ellipse in regions with no overlap and plot in opposite directions (Fig. A11), suggesting an inverse relationship. Fossorial has a high negative loading on PC1 (Table 20). Ambulatory and cursorial plot in the grassland ellipse, with ambulatory and cursorial having high positive loadings on PC1 and PC2 (Table 20). Semi-fossorial and non-cursorial plot in the grassland and semi-desert ellipses. Semi-fossorial and non-cursorial have high negative loadings on PC1 and high positive loadings on PC2 (Table 20). Arboreal/scansorial plots in the forest and semi-desert ellipses, in the opposite direction of semi-fossorial and non-cursorial (Fig. A11), suggesting a negative correlation. Arboreal/scansorial has a high positive loading on PC1 and a high negative loading on PC2 (Table 20).

4.1.4.3 Total Weighted Diet PCA

PC1 explains 24.4% of variance; PC2 explains 22% (Fig. A12). Grassland has the largest ellipse, encompassing all biomes. Semi-desert's ellipse overlaps with forest's. Mixed feeder and grazer plot close together, with grazer landing in the semi-desert and grassland ellipses and mixed feeder just in the grassland ellipse (Fig. A12). Mixed feeder and grazer have high positive loadings on PC1 and PC2 (Table 21). Herbivore also plots in the semi-desert and grassland ellipses, with herbivore having a high positive loading

on PC2 (Table 21). Folivore and granivore plot close to each other in the grassland ellipse and in the opposite direction of carnivore, omnivore, and browser (Fig. A12), suggesting a negative relationship between the sets of trait frequencies and a positive relationship within the two sets. Folivore and granivore have high negative loadings on PC1 (Table 21). Carnivore, omnivore and browser have high positive loadings on PC1 and high negative loadings on PC2 (Table 21).

4.1.4.4 Total Weighted Size PCA

PC1 explains 34.1% of variance; PC2 explains 22.5% (Fig. A13). Forest and semi-grassland form circular confidence intervals, while grassland forms an elliptical interval. There is a high level of overlap among all the biome ellipses. Size class A and B plot in the forest ellipse (without overlap) and in different directions (Fig. A13), suggesting an inverse relationship. Size class A has a high positive loading and size class B has a high negative on PC1, while both size classes have high negative loadings on PC2 (Table 22). Size classes D and E plot close to each other (Fig. A13), indicating a positive correlation. Size class D plots inside all three biomes, with a high positive loading on PC1, and size class E plots in the semi-desert and forest ellipses with high positive loadings on PC1 and PC2 (Table 22). Size classes C and G also plot close and inside all three biomes (Fig. A13), suggesting a positive relationship. Size class C has a high positive loading on PC2 (Table 22). Size class F plots in the semi-desert and forest ellipses, with low loadings on PC1 and PC2 (Table 22).

4.1.5.1 Rodents and Lagomorphs Unweighted PCA

PC1 explains 27.4% of variance; PC2 explains 22.3% (Fig. A14). Grassland, forest, and semi-desert all have similar sizes of ellipses and overlap each other. Folivore,

aquatic/semi-aquatic, and size class F and G plot within the forest ellipse. Semi-fossorial and omnivore plot in the grassland ellipse in opposite directions (Fig. A14), suggesting a negative relationship. Semi-fossorial has a high positive loading on PC2 (Table 23). Non-cursorial and size class D plot in the semi-desert ellipse. Non-cursorial has a high positive loading on PC1 and high negative loading on PC2 (Table 23). Carnivore plots in the grassland and semi-desert ellipses and plots opposite of non-cursorial (Fig. A14), indicating an inverse correlation.

4.1.5.2 No Rodents and Lagomorphs Unweighted PCA

PC1 explains 33.8% of variance; PC2 explains 25.5% (Fig. A15). Grassland has a large circular ellipse. Semi-desert's ellipse overlaps with grassland's, and forest's ellipse plots entirely within grassland's. All traits plot within the grassland ellipse (Fig. A15). Grazer, mixed feeder, cursorial and size class G plot together, suggesting a positive correlation. Grazer, mixed feeder, cursorial, and size class G all have high negative loadings on PC1, and all but mixed feeder have high negative loadings on PC2 (Table 24). Arboreal/scansorial, omnivore, and size classes D and F plot in a different direction (Fig. A15), indicating an inverse relationship with the previous group of trait frequencies. Arboreal/scansorial, omnivore, and size classes D and F have high negative loadings on PC2 (Table 24). Ambulatory and size class C plot between those groups, with size class C having high negative loadings on PC1 and PC2 (Table 24). Carnivore, fossorial, semi-fossorial, browser, and size classes A and B plot near each other (Fig. A15), suggesting a positive correlation. Carnivore, fossorial, and size classes A and B have high positive loadings on PC1, with carnivore having a high positive loading on PC2 (Table 24). Carnivore also trends towards the semi-desert ellipse, but does not plot inside. Browser,

non-cursorial, and semi-fossorial plot past forest's ellipse, but do not plot inside its region (Fig. A15).

4.2 Trait Composition – Stacked Area Charts

Stacked area charts consist of biomes on the x-axis, ordered from closed to open (left to right) and percentage on the y-axis, marked every 20%. Composition of trait frequencies for locomotion, diet, and body mass are displayed for each biome. Changes or trends in trait composition can be observed within biomes vertically or across biomes horizontally.

4.2.1a Total Unweighted Locomotion

Ambulatory and aquatic/semi-aquatic trait percentages make up a minimal amount of the total community in all biomes, not appearing at all in woodland (Fig. 8; Table 5-A). Out of the two, aquatic/semi-aquatic occurs with higher frequency in forest (3.9%) and ambulatory with frequency higher in grassland (2.08%). They are equal in desert (1.6%), and ambulatory doesn't appear in semi-desert. There is an increase of semi-fossorial and fossorial traits from forest (18.6%; 20.5%) to desert (29.5%; 26.2%), with a sharper increase in woodland (31.9%; 29.7%). Arboreal/scansorial is highest in forest (28.4%) and drops slightly from forest to desert (19.6%). Cursorial is smallest in woodland (6.3%) and increases in the more open biomes. Non-cursorial is smallest in forest (9.8%) and desert (8.2%), increasing in semi-desert (16.8%).

4.2.1b Total Unweighted Diet

Browser makes up very little of the composition in forest (1.9%) and grassland (1.04%) (Fig. 8; Table 5-B). Grazer only appears in grassland (2.08%) and semi-desert (2.6%), making up a low percentage. Granivore stays constant across the biomes. Mixed

feeder and herbivore do as well; however, herbivore increases (10.6%) and mixed feeder drops out in woodland. Carnivore has a significant amount in forest (31.3%), dropping steadily across the biomes to desert (13.1%). Folivore has a high amount in semi-desert (36.3%) but stays constant in the other biomes. Omnivore stays constant as well, decreasing in semi-desert (10.3%).

4.2.1c Total Unweighted Size

Size classes A (0-50 g) and B (50-500 g) make up half of the total composition in every biome, reaching about 60% in woodland. Size classes C (500-1000 g), D (1000 – 1500 g), E (1500 – 3500 g), and F (3500 – 10500 g) are relatively equal (Fig. 8; Table 5-C). Size class E is slightly higher (12.9%), and size class C (10.3%) is slightly lower in semi-desert. Size class C also has a slight increase from forest (7.8%) to desert (16.3%). Size class F slightly drops from forest (13.7%) to desert (8.2%), dropping more in semi-desert (2.6%). Size class G (>10500 g) lowers in woodland (4.2%) while increasing in grassland (19.7%) and semi-desert (20.7%).

4.2.2a Medium & Large Mammals (≥ 500 g), Unweighted Locomotion

Aquatic/semi-aquatic and ambulatory, while still low, have a higher presence in the composition of biomes, dropping out in woodland and semi-desert (for ambulatory). Ambulatory appears more in grassland (3.8%), while aquatic/semi-aquatic appears more in forest (5.7%) (Fig. 9; Table 6-A). They occur equally in desert (3.4%). Semi-fossorial is low in all biomes but does have a slight decrease from forest (5.7%) to desert (3.4%). Arboreal/scansorial and cursorial make up more than half of forest (32.6%; 34.6%), then decrease in woodland (21.4%). There is no clear pattern across biomes for either of arboreal/scansorial or cursorial. Cursorial increases more in grassland (34.6%) and

remains constant. Arboreal/scansorial decreases in semi-desert (5%) but increases again in desert (24.1%). Fossorial increases from forest (9.6%) to desert (20.6%), with a substantial increase in woodland (28.5%). Non-cursorial also increases from forest (9.6%) to desert (17.2%). Semi-fossorial remains low from forest (5.7%) to desert (3.4%).

4.2.2b Medium & Large Mammals (≥ 500 g), Unweighted Diet

Browser appears in only forest (3.8%) and grassland (1.9%) and makes up a small amount of the composition (Fig. 9; Table 6-B). Grazer appears in grassland (3.8%) and semi-desert (5%) but does not make up a significant proportion of the composition. Mixed feeder drops out of woodland, with a slight decrease from forest (11.5%) to desert (3.4%). Granivore decreases slightly from forest (15.3%) to desert (13.7%), dropping significantly in semi-desert (2.5%). Carnivore remains roughly the same, decreasing slightly in woodland (14.2%) and desert (17.2%), and increasing again in grassland (23.08%) and semi-desert (27.5%). Folivore makes up a significant proportion of every biome, and peaks above half in semi-desert (55%). Omnivore increases slightly from forest (19.2%) to desert (27.5%), with a more substantial increase in woodland (28.5%) and a substantial decrease in semi-desert (2.5%).

4.2.2c Medium & Large Mammals (≥ 500 g), Unweighted Size

With size classes A and B (<500 g) removed, it is easier to see the proportions of the remaining size classes (Fig. 9; Table 6-C). Size classes C (500 – 1000 g) and G (>10500 g) make up around half of the composition in all biomes. Size class C increases in woodland (42.8%) and desert (34.4%), but decreases in forest (15.3%) and semi-desert (20%). Size class G increases in forest (34.6%), grassland (36.5%), and semi-desert

(40%). Size class D (1000 – 1500 g) remains the same across the biomes. Size class E (1500 – 3500 g) increases in woodland (21.4%) and semi-desert (25%). Size class F (3500 – 10500 g) decreases from forest (26.9%) to desert (17.2%), notably decreasing in semi-desert (5%).

4.2.3a Total Weighted Locomotion

Ambulatory and aquatic/semi-aquatic make up very little of any biome (Fig. 10; Table 7-A). Ambulatory only appears in grassland (1.2%), and aquatic/semi-aquatic has small amounts in all but woodland. Arboreal/scansorial declines from forest (46.8%) to desert (23.1%), with a more substantial decrease in woodland (18.5%) and a slight increase in semi-desert (29.7%). Cursorial has large numbers in grassland (30.1%) and semi-desert (20.1%), with minimal occurrences in forest (3.9%), woodland (0.78%), and desert (2.2%). Fossorial stays constant across biomes, with an increase in woodland (29.3%). Non-cursorial decreases slightly from forest (9.6%) to desert (4.1%), with an increase in woodland (16.8%). Semi-Fossorial increases from forest (24.1%) to desert (47.1%), with a slight decrease in semi-desert (21.8%).

4.2.3b Total Weighted Diet

Browser barely occurs in forest (0.32%) and grassland (0.41%) (Fig. 10; Table 7-B). Carnivore has a decline from forest (23.2%) to desert (2.2%), with a slight increase in semi-desert (14.6%). Folivore stays constant across biomes, slightly increasing in grassland (19.03%) and decreasing in forest (17.9%) and woodland (19.03%). Grazer appears in grassland (4.9%) and semi-desert (6.8%), but not in large amounts. Herbivore increases in woodland (22.5%) and semi-desert (25.05%), increasing from forest (4.2%) to desert (16.1%). Mixed feeder is present in small proportions in all but grassland

(18.4%) and doesn't appear in woodland or desert. Omnivore is highest in forest (33.5%) and desert (29.98%) and decreases from woodland (18.5%) to semi-desert (15.1%).

4.2.3c Total Weighted Size

Size classes A (0 – 50 g) and B (50 – 500 g) make up more than half up the composition in any biome, with size class B higher than size class A (Fig. 10; Table 7-C). Size class A does increase from forest (17.2%) to desert (39.5%), with a slight dip in semi-desert (13.8%). Size class B increases from forest (47.7%) to woodland (67.1%), drops in grassland (26.5%), then increases again in semi-desert (43.7%) and desert (40.5%). Size class C (500 – 1000 g) stays constant across biomes, decreasing very slightly in woodland (9.3%) and desert (8.4%). Size classes D (1000 – 1500 g), E (1500 – 3500 g), and F (3500 – 10500 g) stay constant, as well, but make up a much smaller part of the composition. Size class G (>10500 g) is small except in grassland (31.7%) and semi-desert (19.6%).

4.2.4a Medium & Large Mammals (≥ 500 g), Weighted Locomotion

Ambulatory appears in grassland (0.13%) in minimal proportions (Fig. 11; Table 8-A). Aquatic/semi-aquatic increases from forest (0.92%) to desert (11.4%), dropping out of woodland and decreasing in semi-desert (0.51%). Arboreal/scansorial decreases from forest (58.5%) to desert (33.3%), significantly decreasing in semi-desert (2.3%) and increasing slightly in desert. Cursorial stays consistent from forest (11.3%) to desert (11.4%), with large increases in grassland (56.6%) and semi-desert (47.5%). Fossorial increases across biomes, decreasing slightly in grassland (9.6%). Non-cursorial increases from forest (15.3%) to desert (20.7%), with a dip in grassland (9.7%). Semi-fossorial decreases from forest (8.2%) to woodland (3.8%), barely occurring in grassland to desert.

For general trends, arboreal/scansorial acts in reverse of fossorial and non-cursorial moving from forest to desert.

4.2.4b Medium & Large Mammals (≥ 500 g), Weighted Diet

Browser occurs in minimal proportions in forest (0.92%) and grassland (0.77%) (Fig. 11; Table 8-B). Carnivore stays consistent from forest (13.8%) to desert (8.2%), with substantial decreases in woodland (2.9%) and increases in semi-desert (22.2%). Folivore increases from forest (30%) to desert (50.8%), decreasing in grassland (20.5%). Granivore decreases from forest (41.8%) to desert (22.9%), with a substantial decrease in semi-desert (2.05%). Grazer increases from grassland (9.2%) to semi-desert (16.1%), not occurring in the other biomes. Mixed feeder occurs in forest (5.1%) in small numbers, then increases in grassland (34.6%), dropping again in semi-desert (9.2%) and desert (1.09%), and not occurring in woodland. Omnivore increases from forest (8.2%) to desert (16.9%), dropping out of semi-desert. Mixed feeder and grazer act in opposition of each other, as does granivore and folivore.

4.2.4c Medium & Large Mammals (≥ 500 g), Weighted Size

Size class C (500 – 1000 g) has a high abundance in forest (15.3%), peaks in woodland (42.8%), then drops in grassland (26.9%) before increasing from semi-desert (20%) to desert (34.4%) (Fig. 11; Table 8-C). Size class D (1000 – 1500 g) stays consistent in forest (11.5%), semi-desert (10%), and desert (13.7%), dropping in woodland (7.1%) and grassland (9.6%). Size class E (1500 – 3500 g) stays constant from forest (11.5%) to desert (10.3%). Size class F (3500 – 10500 g) stays constant in forest (26.9%) and desert (17.2%), dropping in woodland (14.2%), grassland (13.4%), and semi-desert (5%). Size class G (>10500 g) decreases slightly from forest (34.6%) to

desert (24.1%), increasing substantially in grassland (36.5%) before decreasing slightly from semi-desert (40%) to desert. Size class C and G have an opposing relationship, whereas the other size classes remain constant among the biomes.

5. DISCUSSION

5.1 PCA Analyses

Unweighted datasets generally exhibit the highest degree of separation among biomes. The dataset with traits from all three categories (diet, locomotion, and body mass) for medium and large mammals ($\geq 500\text{g}$), showed especially clear separation among grassland, forest, and semi-desert (Fig. 3). Notably, in this dataset a clear gradient from forest to grassland to semi-desert is captured. This pattern is similar to patterns expected across a precipitation gradient. Differences in precipitation across the biomes are observed when recorded climate data for the biome ecocodes are compiled and annual averages are calculated (Table A5; Bailey 1995). In Figure 3, vertical separation is observed between semi-desert, grassland, and forest, representing differences present on PC2. This vertical succession matches with annual average precipitation differences for the three biomes (Table A5). Semi-desert has an annual precipitation average of 412.75 mm, grassland 706.12 mm, and forest 1100.6 mm. Semi-desert plots completely in the positive side of PC2, forest plots completely on the negative, and grassland plots in both positive and negative (Fig. 3). The positive end of the second principle component's axis appears to match with lower annual precipitation averages, and the negative end matches with higher precipitation averages. This gradient suggests that PC2 represents precipitation for this primary analysis.

In the unweighted PCA of all traits (Fig. 3), the grassland biome has the broadest range of traits. Grazer, cursorial, aquatic/semi-aquatic, and size class G ($>10,500\text{ g}$) plot in the western quadrant of the biome, while size classes C (500 – 1,000 g) and D (1,000 – 1,500 g) plot on the opposite end. Grazer, cursorial, and size class G are closely

correlated with each other. Additionally, they have high associations with the first principle component. This suggests that grazer, cursorial, and size class G are the key traits for defining grassland. Cursorial and size class G have similar occurrence frequencies in the overall trait composition, as well, composing about a third of grassland's trait composition. Grazer occurs in much lower frequencies, but still is an important trait within grassland (Fig. 9). The forest biome contains fewer traits that are all clustered in the west and northwest quadrant of the biome, plotting in the southeast quadrant of the entire PCA. Granivore, omnivore, and arboreal/scansorial plot together in the forest ellipse and appear to have a close correlation with each other. They also have high positive loadings on the first principle component, as opposed to the strongly negative loadings from grazer, cursorial, and size class G (Table 7), suggesting an inverse correlation between the two sets of trait frequencies. Granivore, omnivore, and arboreal/scansorial all also have high negative loadings on the second principle component, suggesting these three trait frequencies are more associated with higher levels of precipitation. Size class F, while not clustering with the other trait frequencies in the forest ellipse, also has a high negative loading on PC2, suggesting mammals with body masses of 3,500 g to 10,500 g prefer biomes with higher annual precipitation. It is unlikely, however, that precipitation has a direct effect on body mass. Rather, body mass is probably correlated with the "openness" of the biome, with lower rainfall in more open areas (grasslands) and higher rainfall in more closed areas (forests).

In the unweighted analysis of all traits (Fig. 3), arboreal/scansorial comprises about 30% of total trait composition for forest (Fig. 9). Omnivore and granivore individually occur with lower frequency but together comprise about 40% of total trait

composition (Fig. 9). However, these trait frequencies (cursorial, granivore, omnivore, arboreal/scansorial, size class G) are rather consistent among biomes (Fig. 9; Table 2), potentially due to sampling and collection bias. Both subsamples of woodland plot inside the forest ellipse, in the western quadrant, and plot closest to size class C (500–1,000 g). Although it might be expected that woodland would plot between forest and grassland, because it contains a mixture of both, in this analysis the forest component appears to be stronger. One subsample of desert plots inside forest, in the southwestern quadrant, near size class D (1,000–1,500 g). The second subsample of desert plots outside any biome's ellipse and does not align with any traits (Fig. 3).

Separation among the forest, grassland, and semi-desert biomes is visible when the locomotion is analyzed separately, with forest and semi-desert separated by grassland (Fig. 4). This is similar to the gradient visible with all trait frequencies analyzed together (Fig. 3); however, the biomes have flipped on the second principle component axis. In the locomotion analysis, semi-desert plots entirely on the negative side on PC2, forest plots entirely in the positive, and grassland remains between these two (Fig. 4). Again, a precipitation gradient is suggested, only with the gradient flipped. The negative side of the second principle component axis matches with lower annual precipitation averages, while the positive side matches with higher averages. In the locomotion analysis, non-cursorial has a positive correlation with the semi-desert biome (Fig. 4). Non-cursorial has an especially high negative loading on PC2 (Table 8), indicating its association with low levels of precipitation. Non-cursorial taxa (i.e., *Lepus townsendii*, *Lepus californicus*, *Sylvilagus nuttalli*) make up just under a quarter of locomotion composition in the semi-desert biome (Fig. 9), suggesting it is an important trait for distinguishing semi-desert.

Cursorial has a positive correlation with the grassland biome (Fig. 4) and a high negative loading on the second principle component (Table 8). Cursorial appears to also have an association with open environments. Cursorial plots in the grassland ellipse on the negative side of the second principle component (Fig. 4), suggesting its association with the drier areas of the grassland biome. Cursorial also occurs with a high proportion in grassland (Fig. 9). Arboreal/scansorial has a positive correlation with the forest biome and a high positive loading on PC2 (Table 8). Arboreal/scansorial appears to have a high association with closed environments. As mentioned above, arboreal/scansorial comprises about 30% of the trait composition for the forest biome (Fig. 9), coming in second for frequency. Due to its high correlation (Fig. 4), arboreal/scansorial is clearly an important trait for distinguishing the forest biome, as would be expected. The locomotion analysis appears to identify locomotion frequencies that accurately distinguish biomes, providing a higher resolution analysis compared to all the traits combined.

Separation among the forest, grassland, and semi-desert biomes is also achieved when diet is analyzed separately, with forest and semi-desert separated by grassland (Fig. 5), as in the previous analyses (Fig. 3 & 4). The diet analysis follows the same precipitation gradient as locomotion, with lower annual averages matching with the negative side of the second principle component axis and higher annual averages with the positive. Semi-desert plots mainly in the negative side of PC2, while forest plots mainly in the positive side (Fig. 5). Grazer still has a high positive loading on PC2 (Table 9), suggesting its association with closed environments. Mixed feeder plots within the grassland ellipse, with a high positive loading on PC2. Mixed feeder plots in grassland on the positive side of the second principle component axis (Fig. 5), indicating its

association with the wetter areas of the biome. Within forest, granivore and omnivore maintain their correlation with each other when diet is analyzed separately (Fig. 5). Omnivore has a high positive loading on PC2, suggesting an association with closed environments. Browser also has high positive loadings on PC2 (Table 9). Browser also plots in the more positive end of forest on the second principle component axis, while omnivore and granivore plot closer to the negative side of the axis. Browser appears to also be associated with closed environments in the forest biome.

Unlike the other traits, body mass does not clearly distinguish biomes when analyzed separately (Fig. A3). The forest and semi-desert biomes are overlapped by the grassland biome, contrary to the expected gradient (Fig. 3, 4, & 5). Size class E (1,500 – 3,500 g) has a positive correlation with the semi-desert biome (Fig. A3). Size class E composes a fourth of the trait composition in the semi-desert biome; however, size class G (>10,500 g) dominates the composition (Fig. 9). Size class E is important for distinguishing the semi-desert biome, regardless of its low occurrence. Size classes D (1,000 – 1,500 g) and G (>10,500 g) have an inverse relationship in the grassland biome, plotting on opposite ends of the ellipse and with opposite loadings (Fig. A5; Table 10). Body mass does not do an effective job separating the biomes when analyzed separately, yet certain body mass frequencies have positive correlations with diet and locomotion when all traits are analyzed.

Significant biases may exist in the datasets due to a low number of ungulates (see discussion below). As a possible compensation, datasets were weighted by the number of occurrences of individual taxa within a biome before PCA analysis. This method may help compensate for situations where a trait occurs in a few taxa, but these taxa are

abundantly represented and geographically widespread. An example is *Bison bison*, which was historically widespread and abundant. Grasslands favored by *B. bison* may have supported a low diversity of grazing ungulates but the abundance of *B. bison* compensated for this low diversity with a significant biomass of grazing individuals. However, although this method could hypothetically help compensate for low species diversity, the weighted PCAs done here do not appear to separate biomes as well as the more conventional unweighted analyses.

Weighted data with no small body sizes (<500 g) show separation between the semi-desert and grassland biomes (Fig. 6), following the gradient displayed in the unweighted data (Fig. 3). The forest biome crosses perpendicularly both the semi-desert and grassland biomes (Fig. 6); however, many of the trait frequencies plotted in forest are in the negative side of the ellipse, where there is no overlap. The precipitation gradient observed in Figure 3 roughly applies here, with lower annual precipitation averages matching with the positive side of the second principle component axis, and higher annual averages with the negative side. Trait frequencies are more tightly clustered, forming three distinct sets of correlations (Fig. 6): grazer, cursorial, mixed feeder, carnivore, ambulatory, and size class G; non-cursorial, folivore, fossorial, and size classes D and E; and omnivore, arboreal/scansorial, granivore, semi-fossorial, and size classes C and F. Granivore, omnivore, semi-fossorial, arboreal/scansorial, and size classes C and F plot close to each other in forest, having a positive strong correlation (Table 11). Granivore, arboreal/scansorial, semi-fossorial, and size class F also have high negative loadings on PC2, suggesting an association with more closed environments. Arboreal/scansorial occurs with over half of the occurrence in forest, followed by

granivore just under half (Fig. 11; Table 6A & 6B). Browser does plot in forest; however, browser shows low correlation with other trait frequencies (Table 11) and plots where there is overlap with grassland (Fig. 6). *Alces alces* is the only taxon classified as a browser, but it occurs equally in the grassland and forest biomes with seven occurrences. Non-cursorial, folivore, fossorial, and size classes D and E have a positive correlation with each other, all with high positive loadings on PC2, indicating an association with open environments. Mixed feeder, grazer, cursorial, carnivore, ambulatory and size class G have a positive correlation with each other in the grassland biome (Table 11). Ambulatory only occurs in one taxon (*Ursus americanus*), but has a large number of occurrences in grassland. Mixed feeder occurs in many of the ungulate taxa (*Antilocapra americana*, *Odocoileus hemionus*, *Odocoileus virginianus*, *Cervus canadensis*, *Rangifer tarandus*). *Antilocapra americana* and *Odocoileus hemionus* occur in very high numbers in grassland. Both ambulatory and mixed feeder represent another trait occurring in a low number of taxa that are abundantly represented.

Both the unweighted and weighted datasets with the full range of body sizes included show poor separation of biomes when the total data are analyzed together. The total unweighted dataset does show separation between the semi-desert and forest biomes. However, grassland overlaps both, and all trait frequencies plot in the grassland biome and show no distinction for other biomes (Fig. A6). The total weighted dataset shows no separation among the forest, grassland, and semi-desert biomes (Fig. A10). There are a few trait frequencies that plot in an area of the semi-desert biome not overlapped by the grassland or forest ellipses, but no clear correlation among trait frequencies is observed (Fig. A10). Associations with closed or open environments are

not evident in either analysis. Lack of significant separation of biomes indicate small-bodied mammals are masking correlations that are seen without these mammals.

Comparing the total unweighted dataset with the unweighted dataset with small-bodied mammals removed, relationships among trait frequencies are clear and correspond to biome separation with small-bodied mammals removed (Fig. 3). With the total dataset, correlations among trait frequencies are less clear and do not relate to biomes, as there is substantial overlap and no significant separation (Fig. A6). Additionally, mammals smaller than 500 g make up 51% of the total unweighted dataset, and in the weighted dataset, that proportion jumps to 64.5%. Visible in Figures 8 & 9, the relationships of the size frequencies in the unweighted dataset are better observed with the small-bodied mammals removed.

5.2 Sources of Potential Biases

In considering the high amount of overlap by grassland in almost all analyses of total data (e.g., Fig. A6, A7, A9, A10, A12), it is important to note that trait data were not collected directly from the taxa being sampled. Instead, I gathered trait data from the literature and from databases. For some specialist taxa (e.g., bison, wolves, moles) traits are not going to differ among biomes. However, generalist taxa may not match their recorded trait classification with behavior in certain biomes. For example, many squirrels are classified as arboreal/scansorial but also occur in grasslands. This clearly does not reflect mammals' ability to adapt to different environments and suggests these mammals may not be well-suited for environmental tracking. Furthermore, smaller mammals can be over-sampled, as they are easier to track and the same species can get sampled multiple times across a biome, creating an appearance that a species is more prevalent

than it truly is. This has the potential to skew results, especially with weighted occurrence data. Adding occurrence data into the analyses, while not affecting the number of taxa in a biome, does create biases towards more commonly sampled species.

The original data might have inherent biases that are affecting potential for biome separation in the various analyses. Grassland has the highest number of taxa with 75, capturing 55% of the total taxonomic diversity. Forest has the second highest number with 48 (35%), but desert is nearly the same with 47 (34%) taxa. This is an unexpected product of the original data, as forest is assumed to have higher species richness. The latitudinal diversity gradient of mammals is well documented (Rolland et al. 2014; Simpson 1964; Wilson 1974; Badgley & Fox 2000; Lyons & Willig 2002) as species richness increases from higher to lower latitudes. The tropics are associated with high productivity, which in turn increases diversity and richness of those regions. However, my data show that North American grasslands have the highest taxonomic richness. Grassland occurs between 40°N and 50°N, indeed all my data originate above 20°N, spanning subtropical to temperate climates. Results displayed here are consistent with the hypothesis of a second diversity and richness peak at 40°N (McCoy & Connor 1980). McCoy and Connor showed North American mammals had equal richness peaks at 20°N and 40°N. When quadrupeds were isolated, the richness at 40°N was higher than at 20°N (McCoy & Connor 1980). Increasing richness and diversity into lower latitudes is clearly not a universal rule as seen in this mid-latitude, historically-sampled North American mammal database. Further exploration of historical sampling to include higher and lower latitudes (i.e. into the tropics and boreal forests) is needed to fully compare diversity

gradients with previous studies and to understand the inherent processes shaping diversity in North America.

As noted above, potential sources of sampling bias in the dataset and possible historical biases need to be considered. Of particular concern is a general low diversity of ungulates across all the biomes (Tables 1B, 2B, 4B, 5B, & 6B). Mixed feeder consistently has the highest trait frequency for the ungulates. There are only two grazing ungulates in the grassland biome, *Bison bison* and *Ovis canadensis*, with five mixed feeders, *Antilocapra americana*, *Odocoileus hemionus*, *Odocoileus virginianus*, *Cervus canadensis*, *Rangifer tarandus*. Based on the distribution of food resources, a higher diversity of ungulate grazers would be expected in grasslands, similar to the pattern seen in African faunas (e.g., Cerling and Harris, 1999; Andrews and Hixon, 2014). It is possible that the low ungulate diversity is a result of collecting methods for the historical dataset. Collecting was done by multiple people over a wide range of time, likely incorporating many inconsistencies in collection methods and the geographic distribution of samples. It is also possible that some ungulates were locally extirpated by settlers before data were collected, such as elk, moose, and sheep on the Great Plains. Of additional concern is that the diversity of ungulates in North America was affected by the end Pleistocene megafaunal extinction that occurred about 12,000 years ago (e.g., Smith et al. 2004; Martin & Wright 1967; Janis et al. 2000). This extinction resulted in the loss of grazing horses, camels, and proboscideans. The weighted PCA analyses might be a way to partially compensate for these losses, but results from this study suggest that the unweighted analyses do a better job of distinguishing among biomes.

5.3 Comparison to African Faunas

Results from this study contrast with those of Andrews and Hixon (2014), who performed similar analyses using African faunas. Their study found that analyzing all traits (diet, locomotion, and body mass) together yielded poor separation of habitats (biomes as used here). My study suggests that the best separation is achieved using all traits and excluding small taxa (<500 g), although separation is also achieved using some of the other categories. Andrews and Hixon (2014) found that locomotion analyzed separately yielded the strongest results for the African faunas. Differences in results could occur because of inherent differences in faunal composition between North American and African faunas. However, there were also important differences in methodology between these studies. Their study did not use the frequency of traits, as was done here, but rather used PCAs to plot individual taxa. They then evaluated their data by examining which dataset (diet, locomotion, body mass, or all traits) resulted in the best clustering of taxa into known biomes. A rigorous examination of differences in results between these studies would require use of the same methodology but the dataset used in their study does not appear to be available to other researchers.

Although a direct comparison of PCA results from Andrews and Hixon (2014) is not possible, direct, qualitative comparisons of frequency distributions of traits in stacked area charts is possible. Andrews and Hixon (2014) created species richness charts for size, diet, and locomotion to show the range of composition from closed to open biomes. They used 92 modern mammalian species from 23 modern communities from Africa and Asia (forming nine biomes), whereas my historical dataset consisted of 135 species from 19 modern communities from North America (forming five biomes). The initial and

largest difference is their range of body mass. There appears to be a trend towards larger animals in the African data, whereas the North American data trend towards smaller sizes, possibly as the result of end-Pleistocene extinctions. A significant bias towards large mammals is present in the African and Asian data, and a significant bias towards small mammals occurs in the North American data (Fig. 8). Andrews and Hixson (2014) used very generalized dietary categories, while those used here were more specific representing greater trait diversity. As noted above, the most substantial difference is the number of grazers in Africa. African grazers occur in high abundance in woodland and grasslands, while grazer taxa occur in very small numbers in North America, although grazers occur in high total abundance. Locomotion is the most difficult to compare with Andrews and Hixson, because of substantial differences in the categories. They include aerial mammals (bats) in their data, and grouped terrestrial mammals into one category. I did not have aerial mammals in my dataset, and I split terrestrial into three categories. In the African data, there is a clear trend from open to closed with arboreal/scansorial and terrestrial occurring opposite each other (Andrews and Hixson 2014). The North American data show consistent proportions among biomes (Fig. 8), and the relationship between terrestrial and arboreal in Andrews and Hixson's data is not visible in the North American data.

Overall, clear trends in locomotion, diet, and size composition among biomes are seen in African and Asian data (Andrews and Hixson 2014), but are not seen in North American data. Both trait and taxonomic composition must be examined to understand the differences between African and North American data. Grouping African mammalian data in higher taxonomic groups appeared to provide better separation. However,

Andrews and Hixson needed an overlay of individual PCA results for taxonomical groups to show this separation in their overall dataset.

For comparison with Andrews and Hixson (2014), I conducted PCAs of taxonomic groupings of the North American historical dataset. The group with rodents and lagomorphs showed some overlap of biome ellipses (Fig. A14). Clear separation was not observed. Analyses of the non-rodent and lagomorph taxa (Fig. A15) showed no clear separation of trait frequencies into biomes. Whereas Andrews and Hixson (2014) observed better separation of biomes when using higher order taxonomic groups, this did not occur with the North American datasets. This appears to be the result of fundamental differences in faunas between the continents. A significant difference is the taxonomy of large-bodied ungulates between North America and Africa. African faunas consist of a high diversity of bovids, whereas North American faunas consist of a low diversity of bovids and cervids (Nowak 1999b; Gentry 1990). Bovids occur with much higher frequency in African faunas (Spencer 1995) and are often used for paleoecological proxies (e.g., Vrba 1980; Reed 1998; Shipman & Harris 1988), and that pattern is reversed in the North American historical data. Cervidae are frequently found in higher latitudes, as they are better adapted to temperate vegetation, and are often smaller in size (Janis 1989; Nowak 1999b). Out of the ungulates sampled in the North American historical data, only *Bison bison* and *Ovis canadensis* is placed in the Bovidae family. The other ungulate taxa (*Antilocapra americana*, *Odocoileus hemionus*, *Odocoileus virginianus*, *Cervus canadensis*, *Rangifer tarandus*) are in the Cervidae family. As mentioned above, a drop in ungulate diversity at the end of the Miocene is observed in North America (Janis et al. 2000) that is not observed in African fossil ungulate taxa.

The second notable difference in the datasets is the proportion of rodent species. The African dataset has considerably proportionally fewer rodents than the North America one, though without access to primary data it is unclear the level of inclusion of rodents. Rodents comprise 34% of the Africa fauna and 68% of the North America fauna (Smith et al. 2004). Rodents species make up 51% of the AMNH historical dataset and 67% of the modern North American mammal dataset. The differences in percentages between historical and modern is most likely from an under-sampling of taxa collected by AMNH before 1900. While this taxonomic discrepancy accounts for some size differences between Africa and North America, not all rodents are small bodied (e.g., *Marmota monax*, *Castor canadensis*). Africa has a greater number of larger-bodied species in Eulipotyphla (twice as large as insectivores in North America) resulting in a greater size range (Smith et al. 2004).

5.4 Paleoecological Implications

When choosing the best models to use for making paleoenvironmental interpretations one must consider the taxonomic composition of the fossil fauna. North America in the Neogene may have been more similar to modern African than to the modern North American faunas, due to a considerable decrease in North American ungulate diversity in the late Miocene and Pliocene (e.g., Janis et al. 2000) and the end-Pleistocene megafaunal extinction (e.g., Smith et al. 2004; Martin and Wright 1967). North American fossil faunas with high percentages of grazing taxa (i.e., ungulates) and a small percentage of rodents may be better suited to be used with African modern proxies. However, North American fossil faunas with a high frequency of rodents, lagomorphs, and non-ungulate taxa may be better suited for interpretation with North American

modern proxies. Finally, the differences within ungulate taxa (i.e., bovids vs cervids; perissodactyls vs artiodactyls) must also be considered for paleoecological interpretations. As mentioned previously, bovids make up a considerable portion of African mammalian faunas, and have historically been used for paleoecological proxies (e.g., Spencer 1995; Vrba 1980; Reed 1998; Shipman & Harris 1988). Furthermore, perissodactyls make up the majority of fossil faunas from their appearance at the beginning of the Eocene (Radinsky 1969) through the Oligocene, when artiodactyls begin to dominate the fauna (Cifelli 1981). Within artiodactyls, cervids and bovids diversify in the Pliocene and Pleistocene (Cifelli 1981), creating communities with higher similarity to modern faunas. As the North American historical data consist of cervids and bovids, although in low diversity and abundance, the PCA models constructed appear to be best suited for late Miocene (Hemphillian), Pliocene, and Pleistocene fossil faunas.

6. CONCLUSION

Of the various analyses explored in this study, the unweighted dataset excluding small-bodied mammals (<500 g) provided the best separation of biomes. Grassland, forest, and semi-desert showed clear separation in the PCA with all traits combined. Grassland has two sets of differentiating traits: Grazer, cursorial, and size class G (<10500 g) are one set of substantial indicators, whereas size classes C (500-1000 g) and D (1000-1500 g) comprise the second set, situated in the opposing direction in the grassland ellipse. Forest also has a strong group of traits. Arboreal/scansorial, omnivore, and granivore have a close relationship and occur with each other whether the traits are analyzed together or separately. Separate plots of the categories considered (diet, locomotion, and body mass) also show fairly good separation of biomes. However, individual points sometimes plot in places inconsistent with expectations from the original datasets. Occurrence weighted data do not distinguish well among the biomes, and biomes typically show partial or complete overlap. Within these PCA plots some of the same correlations of trait frequencies are seen in the unweighted plots, but they often have smaller loading scores and plot outside the biome ellipses.

Results from this study differ considerably from those of a similar large-scale African study (Andrews and Hixon, 2014). This study found that the dataset with all traits analyzed together yielded the best separation of biomes in North America, whereas the African based study found that that biomes could not be distinguished using the all traits dataset of African mammals. Only their locomotion dataset was able to distinguish biomes. These differences could be the result of the different taxonomic compositions between the continents, or the result of differences in methodology. When stacked

frequency charts are considered, African mammals show different trends than North American mammals in all three categories. Taxonomic differences in ungulates (Bovidae vs Cervidae) between the two continents must be considered when comparing diversity and frequency differences between African and North American faunas. Bovids have high diversity in African faunas, while bovids and cervids have much lower diversity in North American historical faunas. Rodents make up a larger part of North American data, but rodents as a group do not provide clear separation of biomes. When separate PCAs are performed using taxonomic groups, better biome resolution is achieved in the African datasets, whereas no advantage is gained in the North American one.

Despite potential sampling or historical biases for ungulates in the North American dataset, results indicate that an unweighted dataset is mostly likely to yield accurate results. It also appears that using subsets of the larger North American dataset by grouping the fauna taxonomically does not help to separate biomes, nor does grouping the fauna by traits. Evolutionary history does not positively impact the relationships of traits and their environments, as neither the rodents+lagomorph dataset nor the dataset without rodents and lagomorphs display clear separation of biomes. Finally, I conclude that small-body sizes mask the relationships between traits, and it is best to exclude small bodied mammals (<500 g) from the North American analysis.

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TABLES

Table 1: Percentage of trait frequencies from total unweighted dataset

Table 1A: Percentage of locomotion frequencies from total unweighted dataset.

Locomotion	Forest	Woodland	Grassland	Semi-Desert	Desert
Ambulatory	0.98	0	2.08	0	1.63
Aquatic/ Semi-Aquatic	3.92	0	1.04	2.59	1.63
Arboreal/ Scansorial	28.43	14.89	23.95	16.88	19.67
Cursorial	17.64	6.38	18.75	20.77	13.11
Fossorial	20.58	29.78	20.83	22.07	26.22
Non-Cursorial	9.80	17.02	14.58	16.88	8.19
Semi-Fossorial	18.62	31.91	18.75	20.77	29.50

Table 1B: Percentage of diet frequencies from total unweighted dataset.

Diet	Forest	Woodland	Grassland	Semi-Desert	Desert
Browser	1.96	0.00	1.04	0.00	0.00
Carnivore	31.37	19.15	21.88	22.08	13.11
Folivore	22.55	25.53	26.04	36.36	29.51
Granivore	17.65	19.15	15.63	14.29	21.31
Grazer	0.00	0.00	2.08	2.60	0.00
Herbivore	1.96	10.64	6.25	10.39	6.56
Mixed Feeder	5.88	0.00	4.17	3.90	1.64
Omnivore	18.63	23.40	22.92	10.39	27.87

Table 1C: Percentages of size frequencies from total unweighted dataset.

Size Class	Forest	Woodland	Grassland	Semi-Desert	Desert
A	17.65	27.66	15.63	19.48	19.67
B	31.37	42.55	30.21	28.57	32.79
C	7.84	12.77	14.58	10.39	16.39
D	5.88	2.13	5.21	5.19	6.56
E	5.88	6.38	7.29	12.99	4.92
F	13.73	4.26	7.29	2.60	8.20
G	17.65	4.26	19.79	20.78	11.48

Table 2: Percentage of trait frequencies from unweighted dataset with no size class A (0-50g) and B (50-100 g).

Table 2A: Percentage of locomotion frequencies from unweighted dataset with no size class A (0-50g) and B (50-100 g).

Locomotion	Forest	Woodland	Grassland	Semi-Desert	Desert
Ambulatory	1.92	0.00	3.85	0.00	3.45
Aquatic/ Semi-Aquatic	5.77	0.00	1.92	5.00	3.45
Arboreal/Scansorial	32.69	21.43	21.15	5.00	24.14
Cursorial	34.62	21.43	34.62	40.00	27.59
Fossorial	9.62	28.57	15.38	20.00	20.69
Non-Cursorial	9.62	21.43	21.15	27.50	17.24
Semi-Fossorial	5.77	7.14	1.92	2.50	3.45

Table 2B: Percentage of diet frequencies from unweighted dataset with no size class A (0-50g) and B (50-100 g).

Diet	Forest	Woodland	Grassland	Semi-Desert	Desert
Browser	3.85	0.00	1.92	0.00	0.00
Carnivore	19.23	14.29	23.08	27.50	17.24
Folivore	30.77	35.71	32.69	55.00	37.93
Granivore	15.38	14.29	11.54	2.50	13.79
Grazer	0.00	0.00	3.85	5.00	0.00
Mixed Feeder	11.54	0.00	7.69	7.50	3.45
Omnivore	19.23	28.57	19.23	2.50	27.59

Table 2C: Percentage of size frequencies from unweighted dataset with no size class A (0-50g) and B (50-100 g).

Size Classes	Forest	Woodland	Grassland	Semi-Desert	Desert
C	15.38	42.86	26.92	20.00	34.48
D	11.54	7.14	9.62	10.00	13.79
E	11.54	21.43	13.46	25.00	10.34
F	26.92	14.29	13.46	5.00	17.24
G	34.62	14.29	36.54	40.00	24.14

Table 3: Percentage of trait frequencies from unweighted dataset with rodents and lagomorphs.

Table 3A: Percentage of locomotion traits from unweighted dataset with rodents and lagomorphs.

Locomotion	Forest	Woodland	Grassland	Semi-Desert	Desert
Aquatic/ Semi-Aquatic	7.69	0.00	1.69	3.70	2.33
Arboreal/Scansorial	38.46	17.14	30.51	22.22	20.93
Fossorial	17.31	28.57	27.12	25.93	30.23
Non-Cursorial	15.38	11.43	15.25	20.37	6.98
Semi-Fossorial	21.15	42.86	25.42	27.78	39.53

Table 3B: Percentage of dietary traits from unweighted dataset with rodents and lagomorphs.

Diet	Forest	Woodland	Grassland	Semi-Desert	Desert
Carnivore	0.00	0.00	1.69	0.00	0.00
Folivore	44.23	34.29	42.37	51.85	41.86
Granivore	34.62	25.71	25.42	20.37	27.91
Herbivore	3.85	14.29	10.17	14.81	9.30
Omnivore	17.31	22.86	20.34	12.96	20.93

Table 3C: Percentage of size classes traits from unweighted dataset with rodents and lagomorphs.

Size Class	Forest	Woodland	Grassland	Semi-Desert	Desert
A	13.46	22.86	18.64	18.52	23.26
B	40.38	51.43	42.37	38.89	41.86
C	15.38	17.14	18.64	14.81	18.60
D	9.62	2.86	6.78	7.41	4.65
E	9.62	5.71	11.86	14.81	4.65
F	5.77	0.00	0.00	1.85	4.65
G	5.77	0.00	1.69	3.70	2.33

Table 4: Percentage of trait frequencies from unweighted dataset with no rodents and lagomorphs.

Table 4A: Percentage of locomotion traits from unweighted dataset with no rodents and lagomorphs.

Locomotion	Forest	Woodland	Grassland	Semi-Desert	Desert
Ambulatory	2.00	0.00	5.41	0.00	5.88
Arboreal/ Scansorial	18.00	9.09	13.51	4.35	17.65
Cursorial	36.00	27.27	48.65	69.57	47.06
Fossorial	24.00	36.36	10.81	13.04	17.65
Non-Cursorial	4.00	27.27	13.51	8.70	11.76
Semi-Fossorial	16.00	0.00	8.11	4.35	0.00

Table 4B: Percentage of dietary traits from unweighted dataset with no rodents and lagomorphs.

Diet	Forest	Woodland	Grassland	Semi-Desert	Desert
Browser	4.00	0.00	2.70	0.00	0.00
Carnivore	64.00	72.73	54.05	73.91	47.06
Grazer	0.00	0.00	5.41	8.70	0.00
Mixed Feeder	12.00	0.00	10.81	13.04	5.88
Omnivore	20.00	27.27	27.03	4.35	47.06

Table 4C: Percentage of size classes from unweighted dataset with no rodents and lagomorphs.

Size Classes	Forest	Woodland	Grassland	Semi-Desert	Desert
A	22.00	36.36	10.81	21.74	5.88
B	22.00	18.18	10.81	4.35	11.76
C	0.00	0.00	8.11	0.00	11.76
D	2.00	0.00	2.70	0.00	11.76
E	2.00	9.09	0.00	8.70	5.88
F	22.00	18.18	18.92	4.35	17.65
G	30.00	18.18	48.65	60.87	35.29

Table 5: Percentage of trait frequencies from total weighted dataset.

Table 5A: Percentage of locomotion frequencies from total weighted dataset.

Locomotion	Forest	Woodland	Grassland	Semi-Desert	Desert
Ambulatory	0.046	0	1.28	0	0.108
Aquatic/ Semi-Aquatic	0.46	0	0.93	0.21	2.27
Arboreal/Scansorial	46.86	18.57	21.19	29.718	23.16
Cursorial	3.96	0.77	30.12	20.17	2.27
Fossorial	14.83	29.36	14.06	15.18	20.88
Non-Cursorial	9.63	16.79	5.89	12.90	4.11
Semi-Fossorial	24.19	34.48	26.50	21.80	47.18

Table 5B: Percentage of diet frequencies from total weighted dataset.

Diet	Forest	Woodland	Grassland	Semi-Desert	Desert
Browser	0.32	0.00	0.41	0.00	0.00
Carnivore	23.23	10.12	8.41	14.64	2.27
Folivore	17.97	32.26	19.03	24.08	25.97
Granivore	18.80	16.02	23.93	10.30	25.43
Grazer	0.00	0.00	4.90	6.83	0.00
Herbivore	4.29	22.58	9.46	25.05	16.13
Mixed Feeder	1.80	0.00	18.45	3.90	0.22
Omnivore	33.59	18.58	15.41	15.18	29.98

Table 5C: Percentages of size frequencies for total weighted dataset.

Size class	Forest	Woodland	Grassland	Semi-Desert	Desert
A	17.28	21.36	20.32	13.88	39.50
B	47.70	67.19	26.50	43.71	40.58
C	14.65	9.34	13.08	11.39	8.44
D	5.07	0.44	2.04	6.29	3.25
E	5.39	0.67	3.79	4.88	1.84
F	6.87	0.67	2.57	0.22	2.49
G	3.04	0.33	31.70	19.63	3.90

Table 6: Percentage of trait frequencies from weighted dataset with no size class A (0-50g) and B (50-100g).

Table 6A: Percentage of locomotion frequencies from weighted dataset with no size class A (0-50g) and B (50-100g).

Locomotion	Forest	Woodland	Grassland	Semi-Desert	Desert
Ambulatory	0.13	0.00	2.41	0.00	0.55
Aquatic/ Semi-Aquatic	0.92	0.00	1.76	0.51	11.48
Arboreal/Scansorial	58.55	24.27	19.65	2.30	33.33
Cursorial	11.32	6.80	56.64	47.57	11.48
Fossorial	5.39	28.16	9.66	22.51	21.86
Non-Cursorial	15.39	36.89	9.77	26.85	20.77
Semi-Fossorial	8.29	3.88	0.11	0.26	0.55

Table 6B: Percentage of diet frequencies from weighted dataset with no size class A (0-50g) and B (50-100g).

Diet	Forest	Woodland	Grassland	Semi-Desert	Desert
Browser	0.92	0.00	0.77	0.00	0.00
Carnivore	13.82	2.91	11.20	22.25	8.20
Folivore	30.00	59.22	20.53	50.13	50.82
Granivore	41.84	22.33	15.48	2.05	22.95
Grazer	0.00	0.00	9.22	16.11	0.00
Mixed Feeder	5.13	0.00	34.69	9.21	1.09
Omnivore	8.29	11.65	8.12	0.26	16.94

Table 6C: Percentage of size frequencies from weighted dataset with no size class A (0-50g) and B (50-100g).

Size Class	Forest	Woodland	Grassland	Semi-Desert	Desert
C	41.84	81.55	24.59	26.85	42.62
D	14.47	3.88	3.84	14.83	15.85
E	15.39	5.83	7.14	11.51	9.29
F	19.61	5.83	4.83	0.51	12.57
G	8.68	2.91	59.60	46.29	19.67

Table 7: Loadings for first four principle components from unweighted with small body sizes removed (A & B) PCA with all trait frequencies combined (Fig. 3).

Trait Frequency	PC1	PC2	PC3	PC4
C	0.26	0.15	0.11	0.34
D	0.19	0.07	-0.38	-0.13
E	-0.12	0.28	0.34	-0.23
F	0.14	-0.36	0.04	-0.14
G	-0.37	-0.10	-0.14	-0.01
Ambulatory	-0.20	-0.20	0.08	0.19
Aquatic/ Semi-Aquatic	-0.05	-0.03	-0.22	-0.60
Arboreal/Scansorial	0.26	-0.29	0.04	-0.21
Cursorial	-0.31	-0.09	-0.24	0.22
Fossorial	0.26	0.29	-0.15	0.19
Non-Cursorial	-0.09	0.38	0.27	-0.04
Semi-Fossorial	-0.09	-0.17	0.47	-0.08
Browser	-0.23	-0.23	0.21	-0.06
Carnivore	-0.33	0.12	-0.09	0.11
Folivore	0.01	0.40	-0.06	-0.31
Granivore	0.25	-0.21	0.08	-0.13
Grazer	-0.31	0.01	0.19	0.05
Mixed-Feeder	-0.18	-0.21	-0.37	0.06
Omnivore	0.27	-0.22	0.20	0.17

Table 8: Loadings for first four principle components from unweighted with small body sizes removed (A & B) PCA with locomotion frequencies (Fig. 4).

Trait Frequency	PC1	PC2	PC3	PC4
Ambulatory	0.47	-0.11	-0.24	0.42
Aquatic/ Semi-Aquatic	0.09	0.18	0.60	-0.59
Arboreal/Scansorial	-0.02	0.73	-0.10	0.12
Cursorial	0.43	-0.40	0.40	0.17
Fossorial	-0.63	-0.06	0.03	0.24
Non-Cursorial	-0.26	-0.50	-0.35	-0.41
Semi-Fossorial	0.36	0.14	-0.54	-0.45

Table 9: Loadings for first four principle components from unweighted with small body sizes removed (A & B) PCA with diet frequencies (Fig. 5).

Trait Frequencies	PC1	PC2	PC3	PC4
Browser	0.23	-0.48	0.46	-0.45
Carnivore	0.55	0.02	-0.04	-0.17
Folivore	0.07	0.71	0.09	-0.12
Granivore	-0.48	-0.16	0.27	-0.39
Grazer	0.37	-0.18	0.44	0.64
Mixed Feeder	0.24	-0.37	-0.71	-0.10
Omnivore	-0.47	-0.27	-0.08	0.42

Table 10: Loadings for first four principle components from unweighted with small body sizes removed (A & B) PCA with size frequencies (Fig. A3).

Trait Frequencies	PC1	PC2	PC3	PC4
C	-0.51	0.47	-0.30	-0.37
D	-0.34	-0.14	0.88	0.00
E	0.37	0.56	0.11	0.64
F	-0.30	-0.59	-0.35	0.52
G	0.63	-0.31	-0.01	-0.42

Table 11: Loadings for first four principle components from weighted with small body sizes removed (A & B) PCA with all trait frequencies combined (Fig. 6).

Trait Frequencies	PC1	PC2	PC3	PC4
C	0.22	-0.08	-0.43	-0.27
D	0.10	0.26	0.28	0.22
E	0.05	0.23	0.51	-0.20
F	0.20	-0.26	0.14	0.40
G	-0.41	-0.04	-0.03	0.07
Ambulatory	-0.24	-0.18	0.06	-0.32
Aquatic/ Semi-Aquatic	0.02	0.02	0.07	0.36
Arboreal/Scansorial	0.25	-0.33	0.20	-0.08
Cursorial	-0.40	-0.07	-0.08	0.07
Fossorial	0.11	0.29	-0.42	-0.07
Non-Cursorial	0.11	0.40	0.17	-0.09
Semi-Fossorial	0.11	-0.23	0.13	0.16
Browser	-0.07	-0.08	0.35	-0.43
Carnivore	-0.25	0.12	0.21	0.16
Folivore	0.17	0.42	-0.11	0.02
Granivore	0.22	-0.35	0.01	-0.23
Grazer	-0.33	-0.01	-0.09	0.10
Mixed Feeder	-0.34	-0.09	-0.06	0.07
Omnivore	0.22	-0.16	-0.04	0.34

Table 12: Loadings for first four principle components from weighted with small body sizes removed (A & B) PCA with locomotion frequencies (Fig. 7).

Trait Frequencies	PC1	PC2	PC3	PC4
Ambulatory	0.41	-0.39	0.02	-0.45
Aquatic/Semi-Aquatic	-0.06	0.07	-0.89	0.06
Arboreal/Scansorial	0.31	0.55	0.06	-0.47
Cursorial	0.29	-0.59	-0.04	0.35
Fossorial	-0.51	-0.12	0.39	-0.02
Non-Cursorial	-0.55	0.05	-0.16	-0.04
Semi-Fossorial	0.30	0.42	0.15	0.67

Table 13: Loadings for first four principle components from weighted with small body sizes removed (A & B) PCA with diet frequencies (Fig. A4).

Trait Frequencies	PC1	PC2	PC3	PC4
Browser	0.03	-0.31	0.76	-0.21
Carnivore	0.48	0.14	0.19	-0.58
Folivore	-0.13	0.73	0.15	0.24
Granivore	-0.41	-0.52	0.05	0.24
Grazer	0.46	-0.16	-0.21	0.28
Mixed Feeder	0.46	-0.24	-0.34	0.05
Omnivore	-0.40	-0.03	-0.46	-0.65

Table 14: Loadings for first four principle components from weighted with small body sizes removed (A & B) PCA with size frequencies (Fig. A5).

Trait Frequencies	PC1	PC2	PC3	PC4
C	-0.54	-0.37	-0.44	0.08
D	0.60	-0.23	0.03	0.70
E	0.59	-0.08	-0.35	-0.66
F	-0.04	-0.46	0.79	-0.27
G	-0.04	0.77	0.23	0.02

Table 15: Loadings for first four principle components from total unweighted PCA with all trait frequencies combined (Fig. A6).

Trait Frequencies	PC1	PC2	PC3	PC4
A	-0.24	-0.02	0.01	0.38
B	-0.15	0.21	0.37	-0.05
C	-0.22	-0.23	-0.13	-0.40
D	-0.05	-0.16	-0.10	-0.17
E	0.04	0.38	-0.29	0.13
F	0.20	-0.33	0.11	0.10
G	0.35	-0.04	-0.15	-0.13
Browser	0.25	0.03	0.39	0.11
Carnivore	0.26	0.16	0.30	0.25
Folivore	-0.27	-0.22	-0.13	0.19
Granivore	0.20	0.25	-0.24	-0.21
Grazer	-0.15	0.26	0.00	-0.20
Herbivore	0.30	-0.20	-0.09	-0.06
Mixed Feeder	-0.18	-0.28	0.15	-0.25
Omnivore	0.16	-0.08	0.23	-0.34
Ambulatory	0.16	-0.15	-0.19	0.28
Aquatic/ Semi-Aquatic	0.02	-0.28	0.07	0.23
Arboreal/Scansorial	0.33	-0.03	-0.19	-0.16
Cursorial	-0.22	0.05	0.29	-0.23

Fossorial	-0.03	0.42	0.10	-0.01
Non-Cursorial	-0.29	-0.06	-0.06	0.17
Semi-Fossorial	-0.24	-0.02	0.01	0.38

Table 16: Loadings for first four principle components from total unweighted PCA with locomotion frequencies (Fig. A7).

Trait Frequency	PC1	PC2	PC3	PC4
Ambulatory	0.02	0.56	-0.35	0.44
Aquatic/Semi-Aquatic	0.48	-0.27	0.01	-0.17
Arboreal/Scansorial	0.27	-0.49	-0.49	-0.12
Cursorial	0.51	0.38	0.17	0.09
Fossorial	-0.42	-0.04	-0.62	0.05
Non-Cursorial	-0.32	0.31	0.11	-0.76
Semi-Fossorial	-0.39	-0.36	0.46	0.42

Table 17: Loadings for first four principle components from total unweighted PCA with diet frequencies (Fig. A8).

Trait Frequency	PC1	PC2	PC3	PC4
Browser	0.49	0.22	-0.13	-0.29
Carnivore	0.50	-0.05	-0.29	0.03
Folivore	-0.35	-0.44	0.24	0.09
Granivore	-0.38	0.40	0.01	0.33
Grazer	0.17	-0.41	0.57	-0.41
Herbivore	-0.18	-0.42	-0.58	-0.08
Mixed Feeder	0.34	0.09	0.39	0.55
Omnivore	-0.26	0.49	0.15	-0.57

Table 18: Loadings for first four principle components from total unweighted PCA with size frequencies (Fig. A9).

Trait Frequency	PC1	PC2	PC3	PC4
A	-0.46	0.07	0.38	0.58
B	-0.40	-0.22	-0.60	-0.12
C	-0.22	0.52	-0.07	-0.57
D	0.06	0.51	0.42	-0.11
E	0.01	-0.57	0.43	-0.26
F	0.45	0.25	-0.35	0.47
G	0.61	-0.13	0.08	-0.17

Table 19: Loadings for first four principle components from total weighted PCA with all trait frequencies combined (Fig. A10).

Trait Frequencies	PC1	PC2	PC3	PC4
A	-0.29	-0.12	0.22	0.30
B	-0.02	0.30	-0.44	0.02
C	0.07	0.19	0.20	-0.38
D	-0.17	-0.37	0.07	-0.10
E	-0.15	-0.35	0.11	-0.33
F	-0.06	0.20	0.28	-0.24
G	0.38	-0.19	0.05	0.07
Ambulatory	0.32	-0.11	0.05	0.01
Aquatic/ Semi-Aquatic	0.02	0.01	0.24	0.06
Arboreal/Scansorial	0.07	0.36	0.05	-0.38
Cursorial	0.39	-0.18	0.01	0.06
Fossorial	-0.18	-0.01	-0.33	-0.05
Non-Cursorial	-0.20	-0.35	-0.20	-0.10
Semi-Fossorial	-0.22	-0.02	0.23	0.39
Browser	0.01	-0.11	-0.09	-0.20
Carnivore	-0.07	-0.24	-0.30	-0.34
Folivore	-0.27	-0.11	-0.10	0.13
Granivore	-0.15	0.09	0.42	-0.09
Grazer	0.30	-0.20	0.01	0.08

Herbivore	0.07	0.28	-0.25	0.28
Mixed Feeder	0.36	-0.14	0.06	0.06
Omnivore	-0.04	0.06	0.06	0.01

Table 20: Loadings for first four principle components from total weighted PCA with locomotion frequencies (Fig. A11).

Trait Frequencies	PC1	PC2	PC3	PC4
Ambulatory	0.51	0.33	-0.21	0.07
Aquatic/ Semi-Aquatic	0.10	0.18	0.46	-0.85
Arboreal/Scansorial	0.21	-0.75	0.17	-0.04
Cursorial	0.56	0.28	-0.22	0.00
Fossorial	-0.35	-0.09	-0.52	-0.19
Non-Cursorial	-0.39	0.23	-0.35	-0.31
Semi-Fossorial	-0.33	0.40	0.52	0.39

Table 21: Loadings for first four principle components from total weighted PCA with diet frequencies (Fig. A12).

Trait Frequencies	PC1	PC2	PC3	PC4
Browser	0.28	0.42	0.10	-0.01
Carnivore	0.25	0.33	-0.43	0.53
Folivore	-0.51	0.05	-0.27	0.37
Granivore	-0.47	0.03	0.60	0.06
Grazer	0.33	-0.46	0.10	0.28
Herbivore	-0.09	-0.36	-0.52	-0.54
Mixed Feeder	0.40	-0.44	0.25	0.18
Omnivore	0.31	0.43	0.15	-0.42

Table 22: Loadings for first four principle components from total weighted PCA with size frequencies (Fig. A13).

Trait Frequencies	PC1	PC2	PC3	PC4
A	0.45	-0.45	-0.03	-0.26
B	-0.47	-0.42	0.03	0.39
C	-0.10	0.51	0.54	0.26
D	0.55	0.04	-0.11	0.11
E	0.50	0.24	0.07	0.47
F	0.05	-0.04	0.67	-0.56
G	-0.15	0.56	-0.48	-0.40

Table 23: Loadings for first four principle components from unweighted with rodents and lagomorphs PCA with all trait frequencies (Fig. A14).

Trait Frequency	PC1	PC2	PC3	PC4
A	0.01	0.44	0.06	0.27
B	-0.26	-0.39	-0.15	-0.10
C	-0.29	0.23	0.05	-0.35
D	0.17	0.07	0.38	-0.36
E	0.21	-0.35	0.12	0.25
F	0.29	0.12	-0.27	0.06
G	0.41	0.07	-0.09	-0.14
Carnivore	-0.02	0.10	0.25	0.24
Folivore	0.29	-0.05	0.43	0.03
Granivore	0.06	0.36	-0.21	-0.23
Herbivore	-0.26	-0.15	0.18	0.01
Omnivore	-0.10	-0.22	-0.42	0.18
Aquatic/Semi-Aquatic	0.39	0.05	-0.08	-0.27
Arboreal/Scansorial	0.05	-0.26	-0.21	-0.40
Fossorial	-0.28	-0.04	0.40	-0.10
Non-Cursorial	0.31	-0.20	0.09	0.31
Semi-Fossorial	-0.16	0.36	-0.15	0.30

Table 24: Loadings for first four principle components from unweighted with no rodents and lagomorphs PCA with all trait frequencies (Fig. A15).

Trait Frequency	PC1	PC2	PC3	PC4
A	0.37	0.12	0.06	0.13
B	0.31	-0.15	-0.27	-0.21
C	-0.24	-0.28	0.17	-0.09
D	-0.11	-0.34	0.16	-0.13
E	-0.02	0.15	0.45	-0.02
F	-0.06	-0.37	-0.17	0.24
G	-0.31	0.28	-0.08	-0.06
Browser	0.11	0.03	-0.42	-0.42
Carnivore	0.33	0.21	0.08	0.09
Grazer	-0.22	0.24	-0.15	0.00
Mixed Feeder	-0.30	0.17	-0.15	-0.01
Omnivore	-0.14	-0.41	0.12	-0.02
Ambulatory	-0.14	-0.09	-0.22	-0.60
Arboreal/Scansorial	-0.09	-0.38	-0.03	0.21
Cursorial	-0.30	0.28	0.04	0.07
Fossorial	0.37	-0.03	0.09	-0.13
Non-Cursorial	0.18	-0.01	0.39	-0.38
Semi-Fossorial	0.18	-0.05	-0.42	0.32

FIGURES

Figure 1: Size frequency distribution of original North American taxa calculated using the 'PivotTable' and 'Histogram' analyses functions in Excel 2016. Taxa were separated by size ranges into lettered bins (A through G) to represent as equal of distribution as possible while minimizing the number of bins.

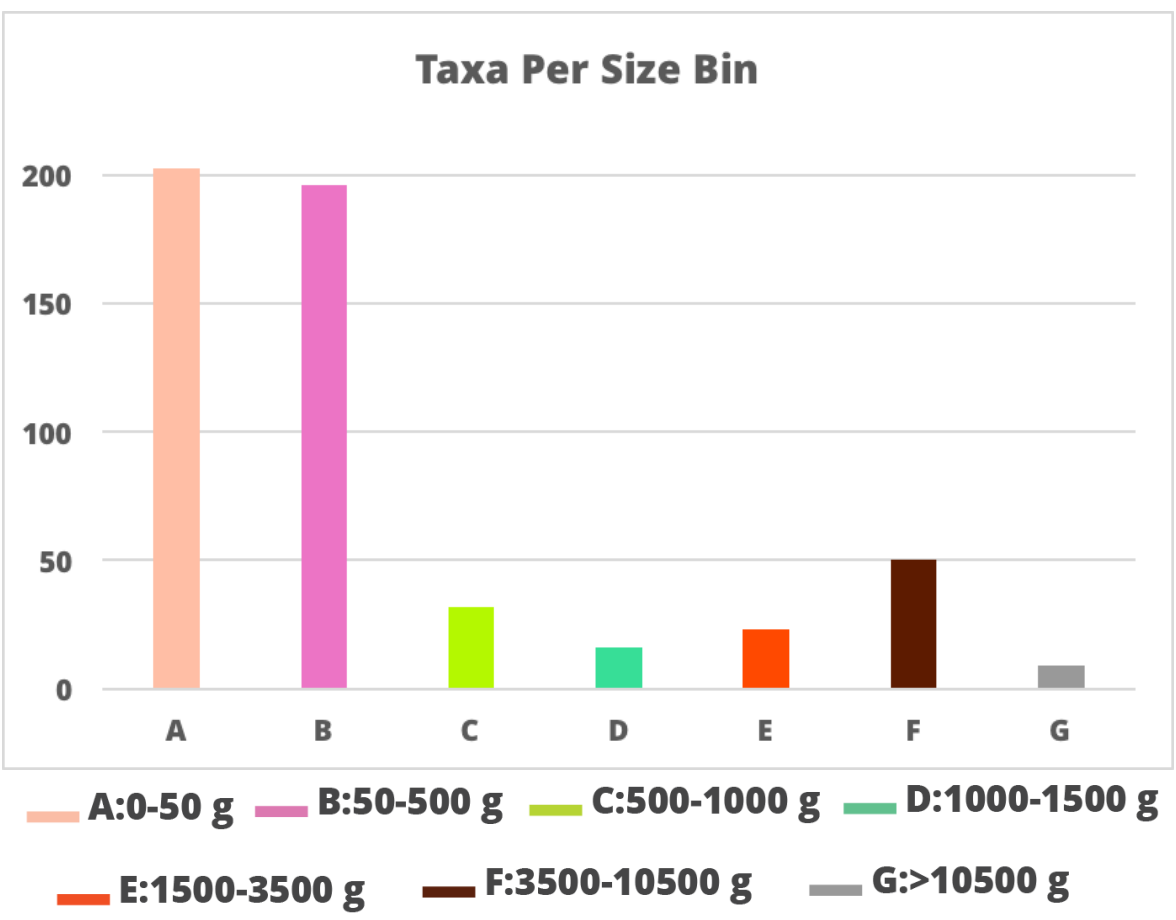


Figure 2: Explanatory scatter plot to illustrate PCA results, arrows, and the relationship of variables. Variables consist of trait frequencies and are plotted as arrows from their respective loadings on PC1 and PC2. The longer the arrow, the higher association that frequency has with both principle components. An arrow with a high association inside a biome's ellipse displays a trait frequency that best describes that biome, and the positions of arrows also indicate relationships between trait frequencies. Arrows that plot close together have a positive correlation with each other while arrows that plot in opposite directions have a negative or inverse correlation.

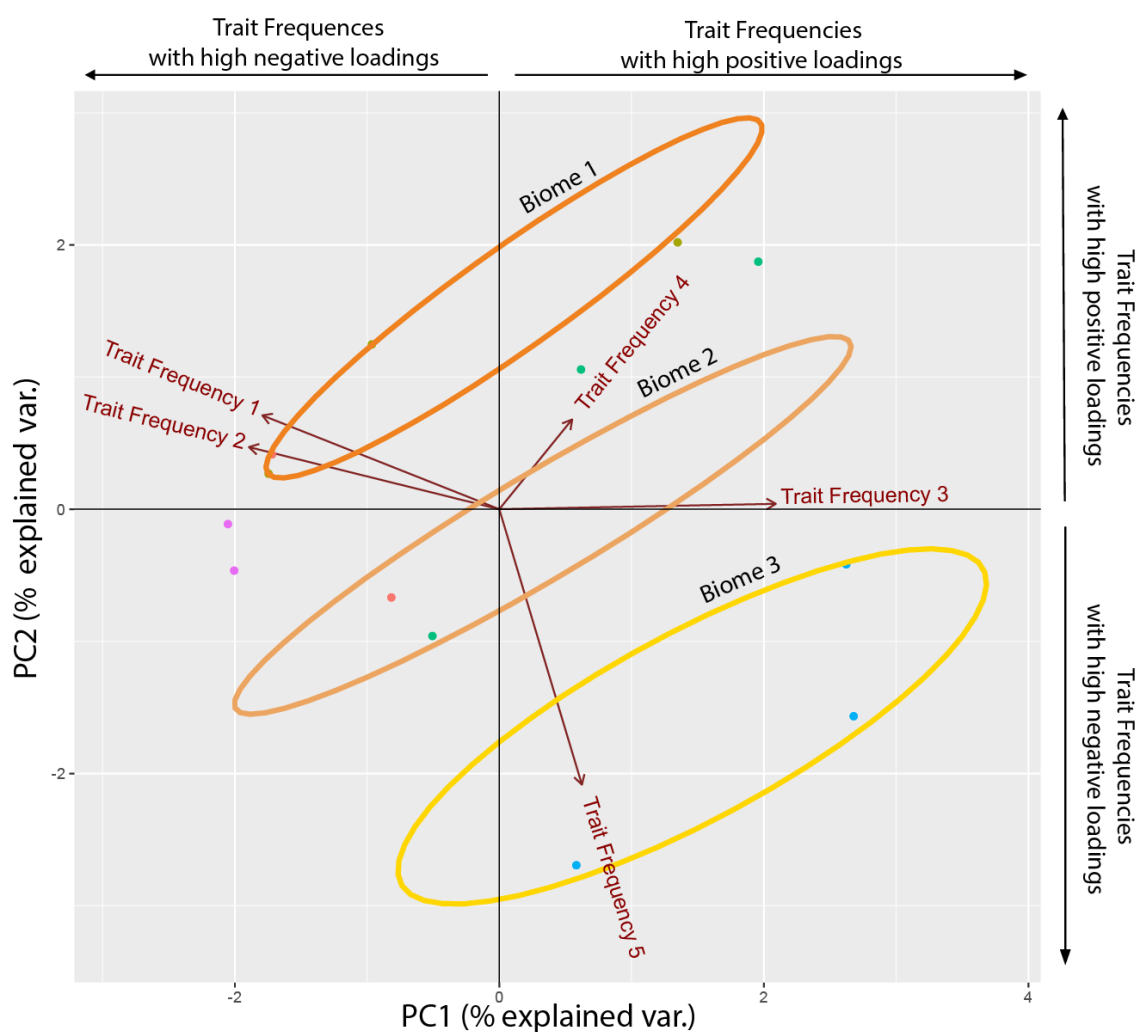


Figure 3: Scatter plot of Principle Component Analysis of all trait frequencies for total unweighted dataset with small body sizes removed. PC1 (31.5% variance) on x-axis, PC2 (24%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 7), displayed on PC1 and PC2 for positive and negative loadings.

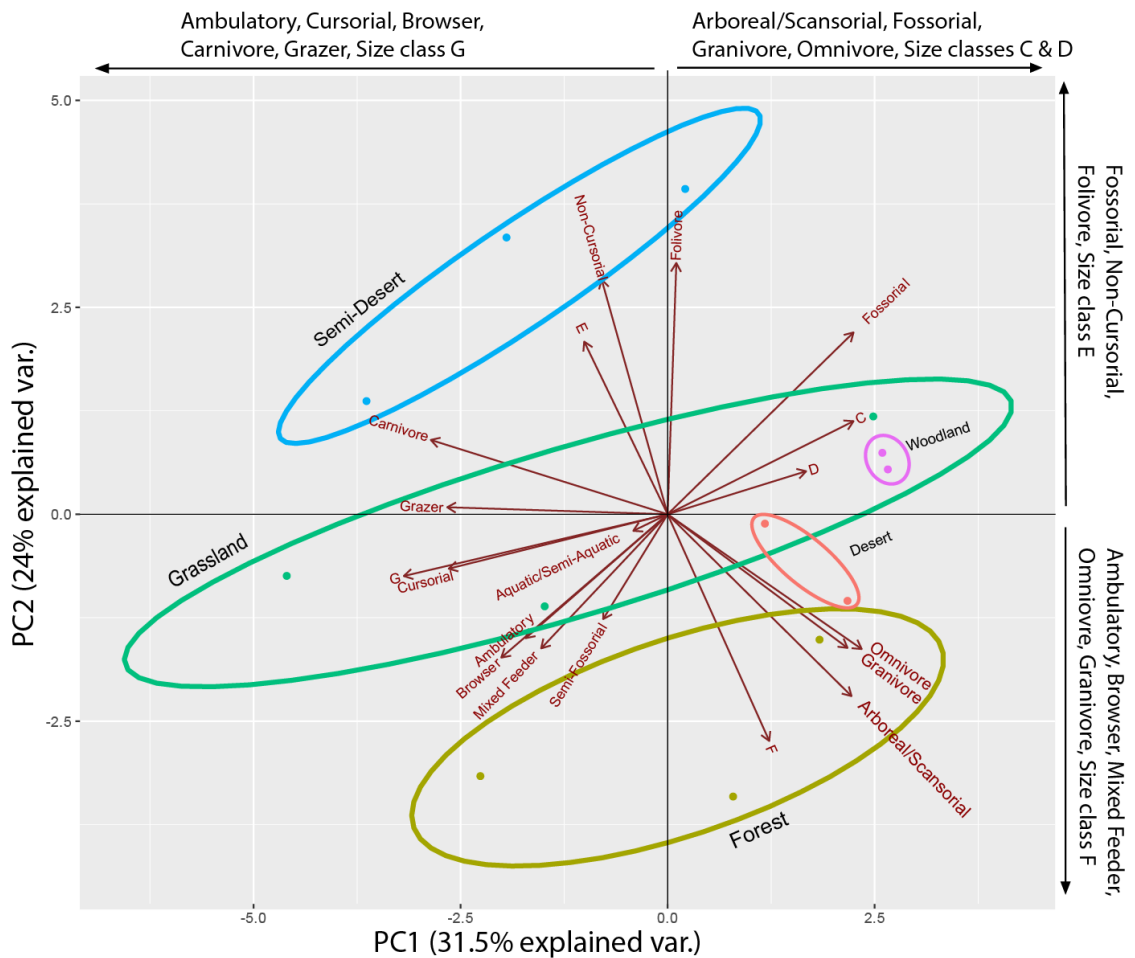


Figure 4: Scatter plot of Principle Component Analysis of locomotion frequencies for unweighted dataset with small sizes removed (A & B). PC1 (30.8% variance) on x-axis, PC2 (25.2%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 8), displayed on PC1 and PC2 for positive and negative loadings.

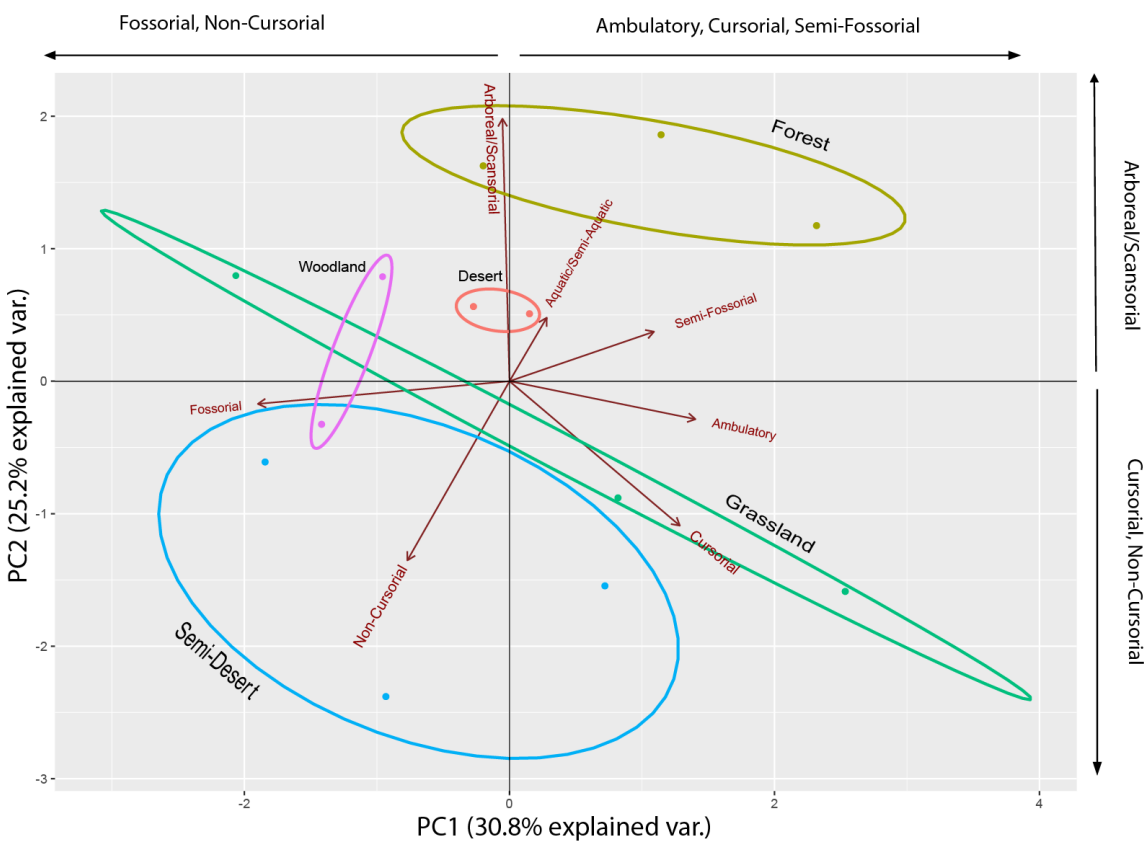


Figure 5: Scatter plot of Principle Component Analysis of dietary frequencies for unweighted dataset with small body sizes removed. PC1 (38% variance) on x-axis, PC2 (22.9%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 9), displayed on PC1 and PC2 for positive and negative loadings.

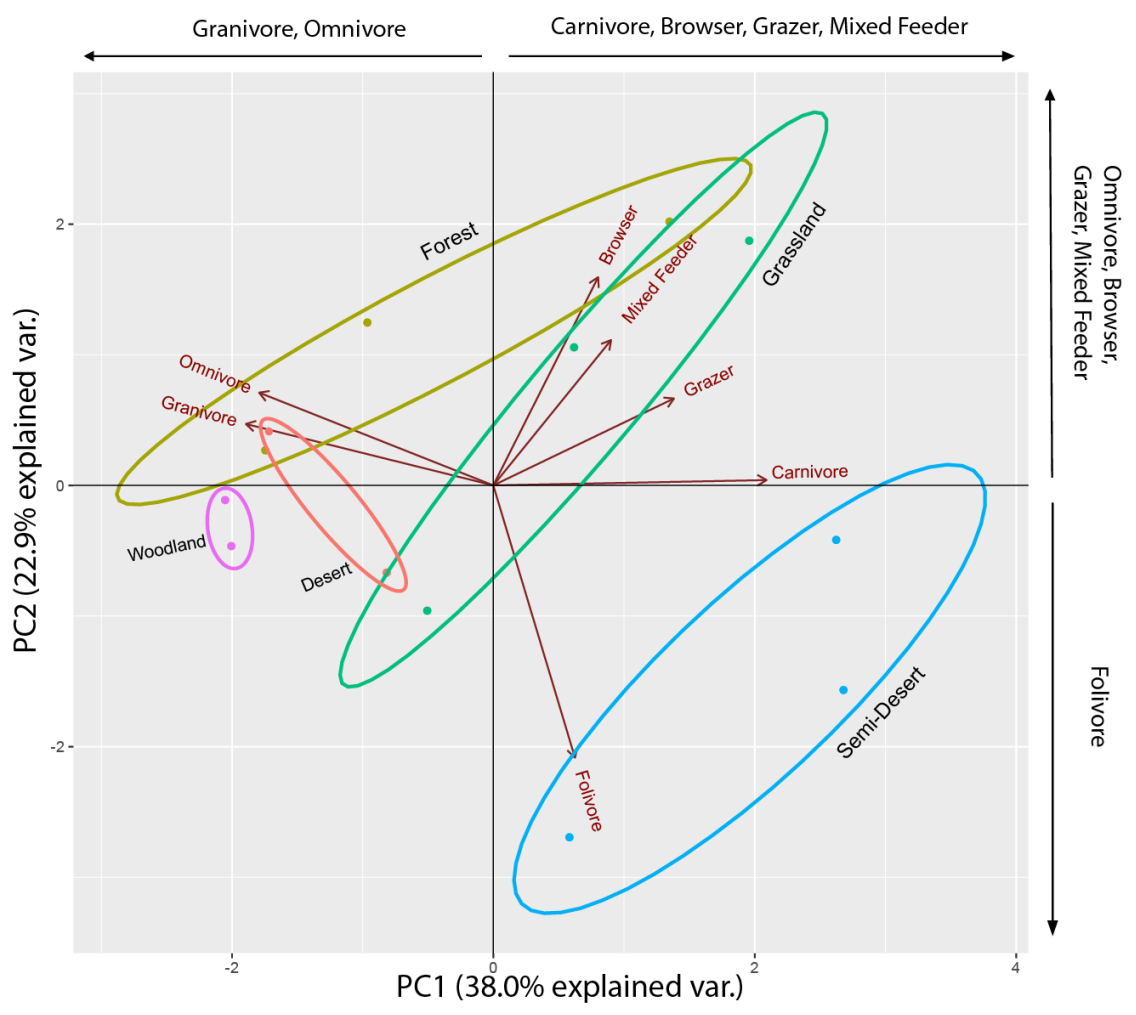


Figure 6: Scatter plot of Principle Component Analysis of all trait frequencies for weighted dataset with small body sizes removed (A & B). PC1 (28.4% variance) on x-axis, PC2 (20.7%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 10), displayed on PC1 and PC2 for positive and negative loadings.

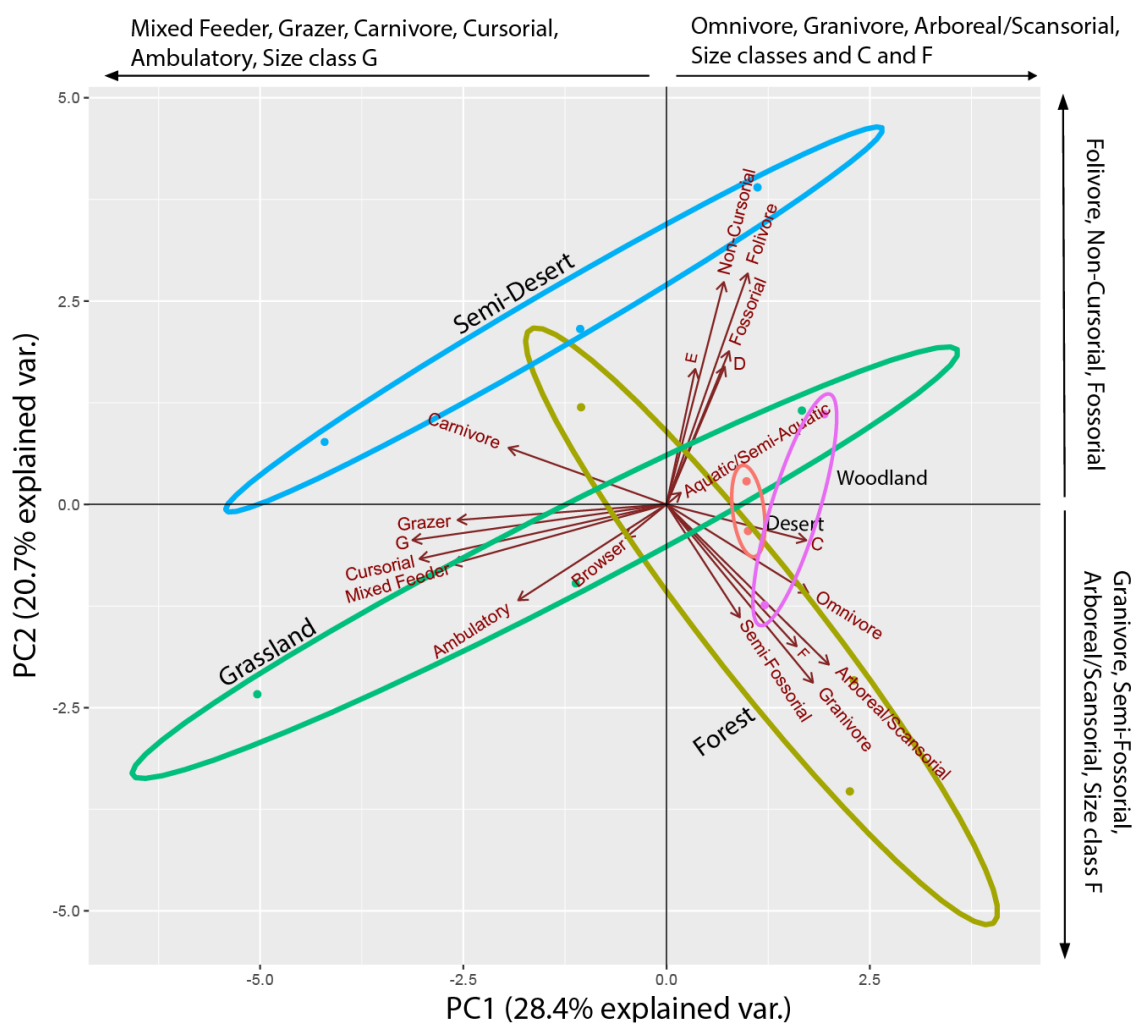


Figure 7: Scatter plot of Principle Component Analysis of locomotion frequencies for weighted dataset with small body sizes removed (A & B). PC1 (30.2% variance) on x-axis, PC2 (28.5%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 11), displayed on PC1 and PC2 for positive and negative loadings.

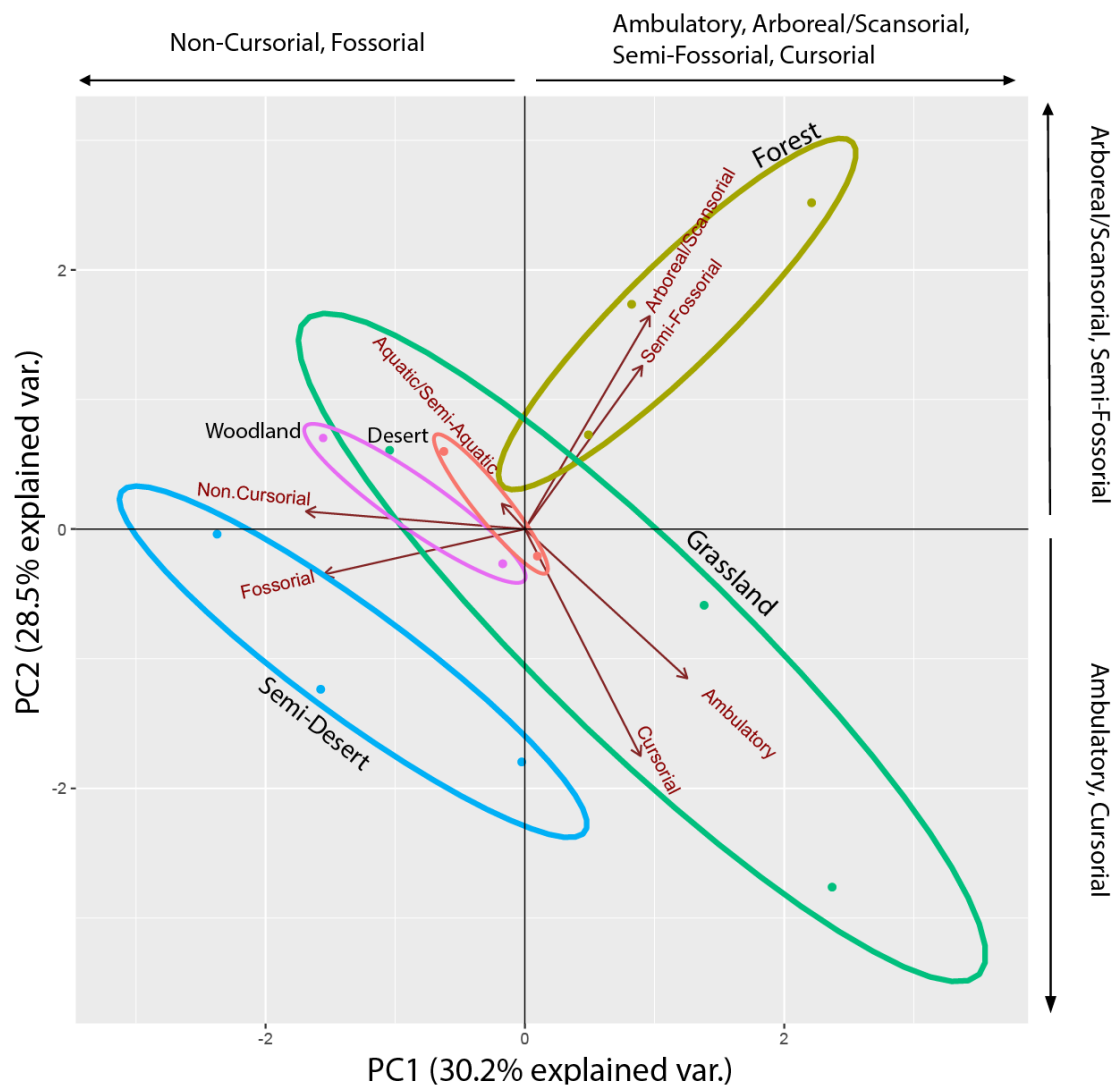


Figure 8: Stacked area charts for trait frequencies in total unweighted dataset. Biomes listed from closed (left) to open (right) on the x-axis, with percentage of composition on the y-axis.

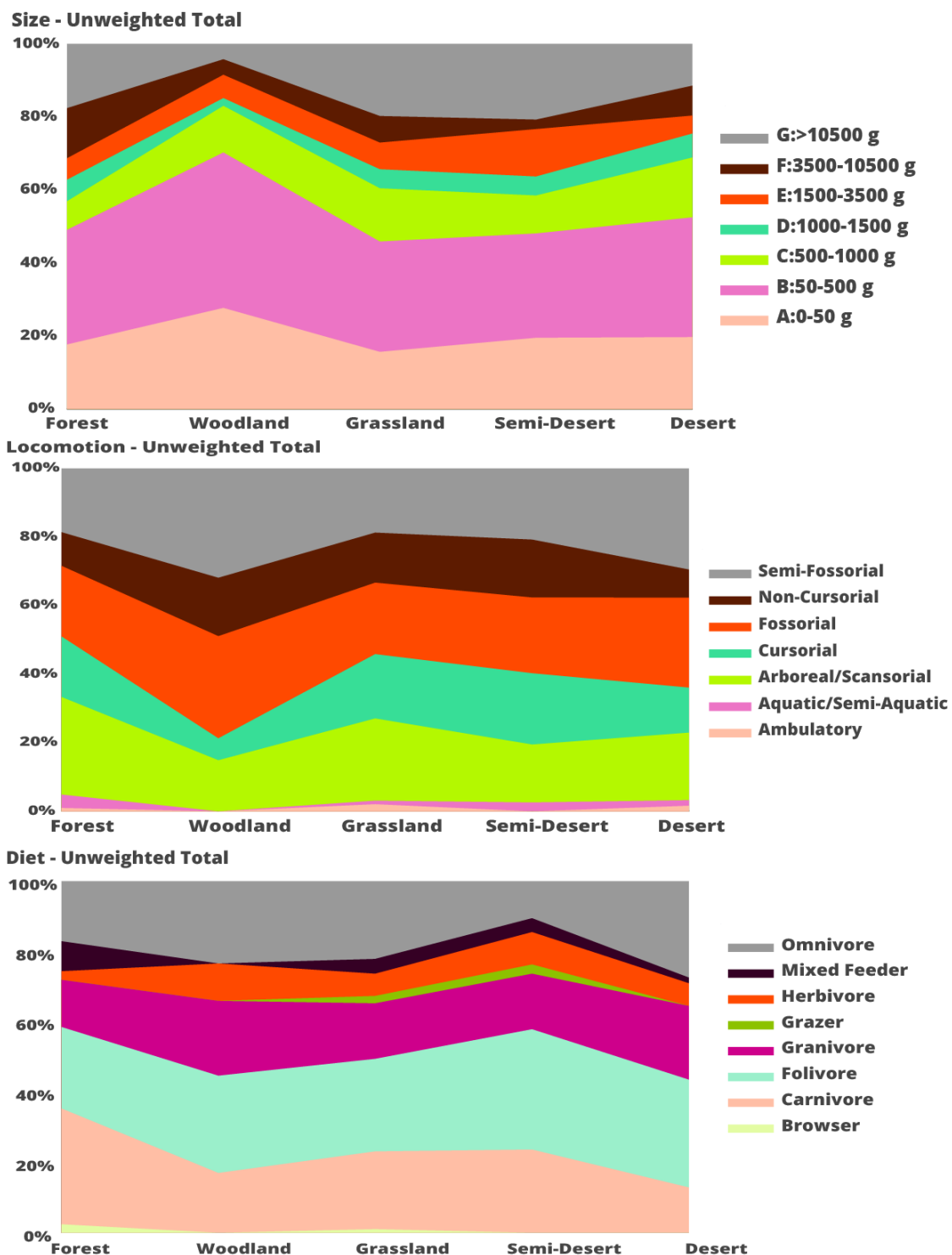


Figure 9: Stacked area charts for trait frequencies in unweighted dataset with size classes A and B removed. Biomes listed from closed (left) to open (right) on the x-axis, with percentage of composition on the y-axis.

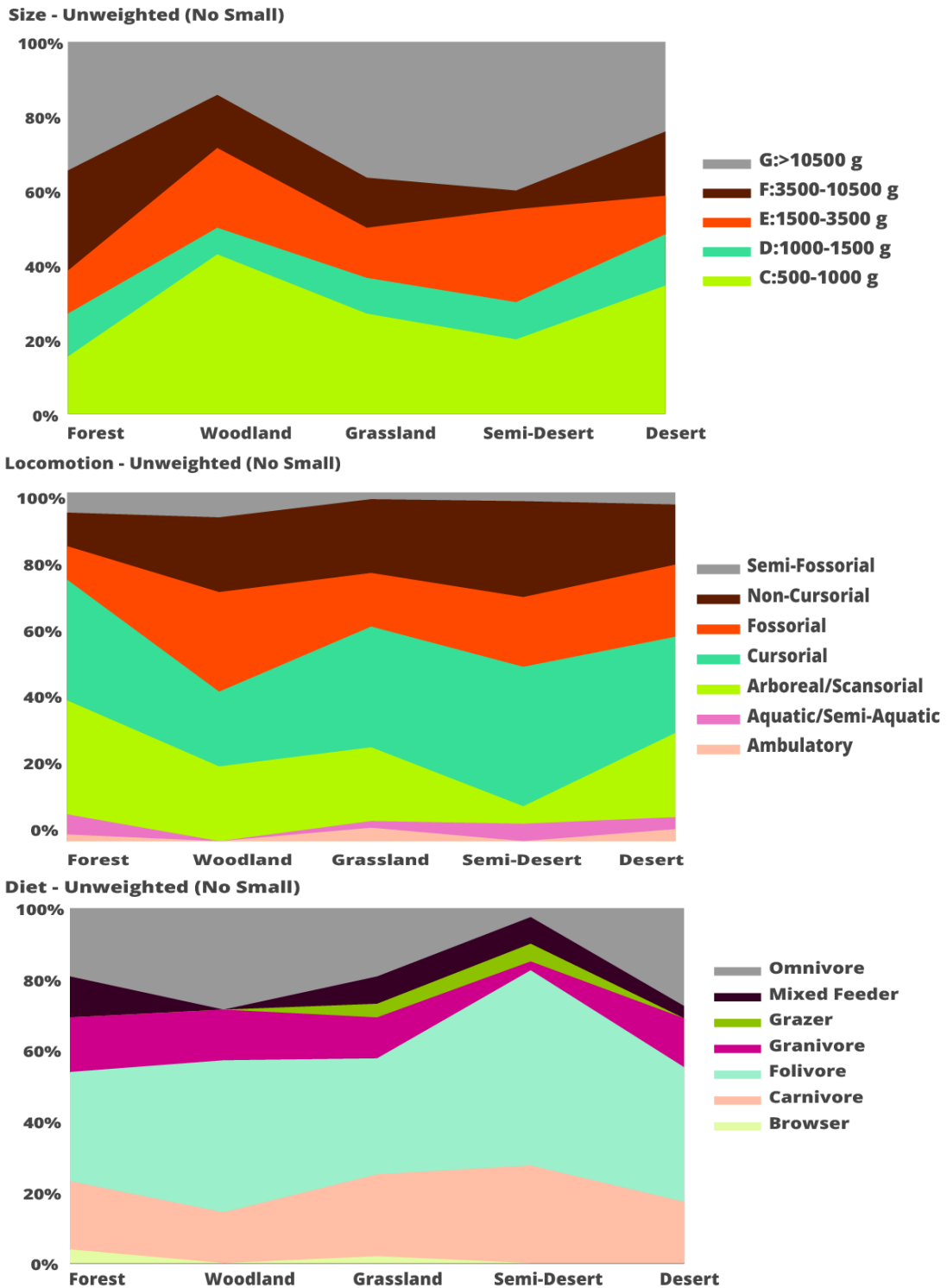


Figure 10: Stacked area charts for trait frequencies for total weighted dataset. Biomes listed from closed (left) to open (right) on the x-axis, with percentage of composition on the y-axis.

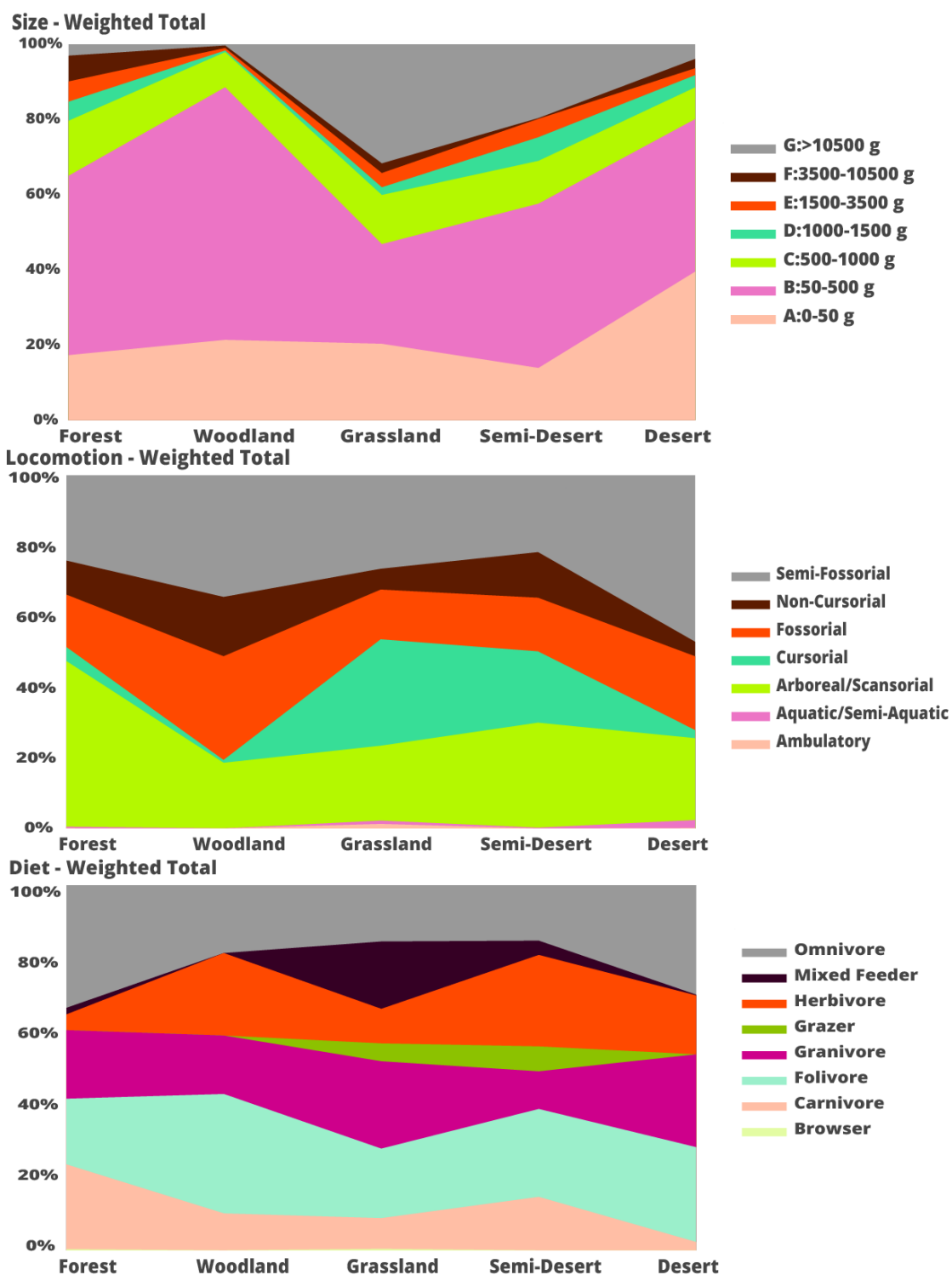
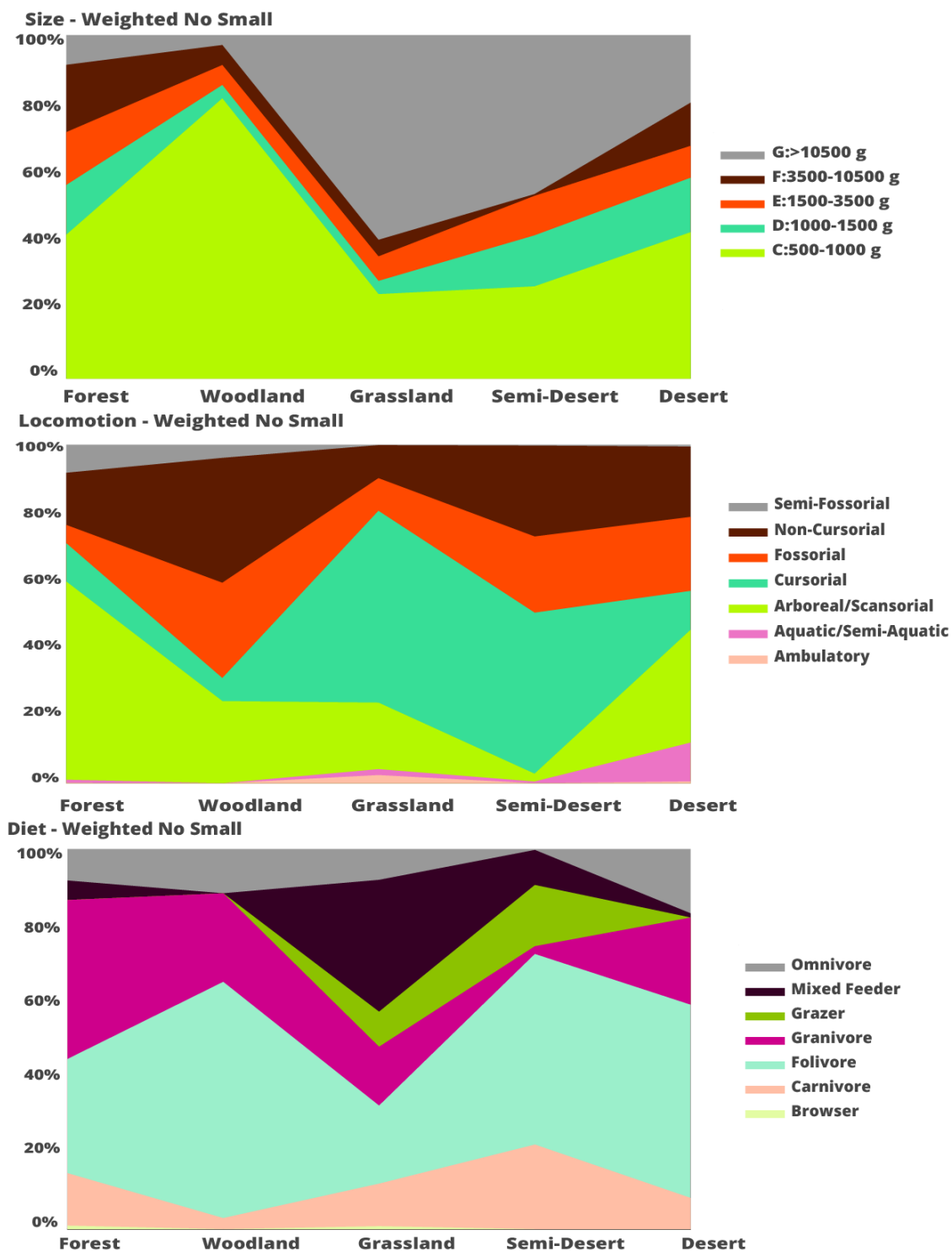


Figure 11: Stacked area charts for trait frequencies in unweighted dataset with small body sizes removed (A & B). Biomes listed from closed (left) to open (right) on the x-axis, with percentage of composition on the y-axis.



APPENDIX-A

Methods. R script for all statistical analyses ran in RStudio.

M1: Script to calculate cumulative proportions for cumulative stacked area charts and generate stacked area charts. Biomes (Forest, Woodland, Grassland, Semi-Desert, Desert) are used.

```

1 install.packages("plotly")
2 library("plotly")
3 install.packages("ggplot2")
4 library("ggplot2")
5 install.packages("RSelenium")
6 library("RSelenium")
7
8 ##Creating color-blind friendly color palette for consistent visual representation throughout
9 graphics
10 sizecolorpalette <- c("#FFBEA5", "#EC74C5", "#FF763F", "#FF4900", "#00D97C",
11 "#B4F800", "#999999")
12 locomotioncolorpalette <- c("#FFBEA5", "#EC74C5", "#FF763F", "#37DE97",
13 "#FF4900", "#00D97C", "#B4F800", "#999999", "#000000")
14 dietcolorpalette <- c("#E3FCA3", "#FFBEA5", "#9BEFCB", "#EC74C5", "#B4F800",
15 "#FF4900", "#00D97C", "#CE008B", "#405800", "#5D1B00", "#004025", "#350024",
16 "#999999")
17
18 ###Updated Habitats
19 ##Separating Habitats into Indiv. Columns and labeling absent vs present for each species
20 #Absent = 0; Present = 1
21
22 ##Historical Species Data
23 ##Unweighted New Biomes
24 taxabiome3=read.csv("Unweighted Total.csv")
25
26 taxabiome3$ForestBiome=rep(0,nrow(taxabiome3))
27 taxabiome3$ForestBiome[grep("Forest", taxabiome3$"BIOME")]=1
28
29 taxabiome3$WoodlandBiome=rep(0,nrow(taxabiome3))
30 taxabiome3$WoodlandBiome[grep("Woodland", taxabiome3$"BIOME")]=1
31
32 taxabiome3$GrasslandBiome=rep(0,nrow(taxabiome3))
33 taxabiome3$GrasslandBiome[grep("Grassland", taxabiome3$"BIOME")]=1
34
35 taxabiome3$SemiAridBiome=rep(0,nrow(taxabiome3))
36 taxabiome3$SemiAridBiome[grep("Semi-Arid", taxabiome3$"BIOME")]=1
37
38 taxabiome3$DesertBiome=rep(0,nrow(taxabiome3))

```

```

39 taxabiome3$DesertBiome[grep("Desert", taxabiome3$"BIOME")]=1
40
41 #calculation proportions for locomotion per habitat
42 biome3.taxa.results.loc=sapply(8:12, function(x) {
43   a=table(subset(taxabiome3, taxabiome3[,x]==1)[,"Locomotion"])
44 })
45 colnames(biome3.taxa.results.loc)=c("Forest","Woodland","Grassland","Semi-
46 Desert","Desert") #name headings of columns to appropriate habitat
47 biome3.taxa.loc=prop.table(biome3.taxa.results.loc, margin=2)*100
48 write.csv(biome3.taxa.loc, file = "unweighted total loc.csv")
49
50 #calculate proportions for diet per habitat
51 biome3.taxa.results.diet=sapply(8:12, function(x) {
52   c=table(subset(taxabiome3, taxabiome3[,x]==1)[,"Diet"])
53 })
54 colnames(biome3.taxa.results.diet)=c("Forest","Woodland","Grassland","Semi-
55 Desert","Desert") #name headings of columns to appropriate habitat
56 biome3.taxa.diet=prop.table(biome3.taxa.results.diet, margin=2)*100
57 write.csv(biome3.taxa.diet, file = "unweighted total diet.csv")
58
59 #calculate proportions for body size per habitat
60 biome3.taxa.results.size=sapply(8:12, function(x) {
61   e=table(subset(taxabiome3, taxabiome3[,x]==1)[,"Body.Class"])
62 })
63 colnames(biome3.taxa.results.size)=c("Forest","Woodland","Grassland","Semi-
64 Desert","Desert") #name headings of columns to appropriate habitat
65 biome3.taxa.size=prop.table(biome3.taxa.results.size, margin=2)*100
66 write.csv(biome3.taxa.size, file = "unweighted total size.csv")
67
68 ##calculate stacked area tables
69 #Locomotion
70 biome3.taxa.loc.stacked=sapply(8:12, function(x) {
71   b=table(subset(taxabiome3, taxabiome3[,x]==1)[,"Locomotion"])
72   cumsum(b/sum(b))
73 })
74 colnames(biome3.taxa.loc.stacked)=c("Forest","Woodland","Grassland","Semi-
75 Desert","Desert") #name headings of columns to appropriate habitat
76 biome3.taxa.loc.pct=biome3.taxa.loc.stacked*100
77 write.csv(biome3.taxa.loc.pct, file = "unweighted total loc stacked.csv")
78
79 #Diet
80 biome3.taxa.diet.stacked=sapply(8:12, function(x) {
81   d=table(subset(taxabiome3, taxabiome3[,x]==1)[,"Diet"])
82   cumsum(d/sum(d))
83 })
84 colnames(biome3.taxa.diet.stacked)=c("Forest","Woodland","Grassland","Semi-
85 Desert","Desert") #name headings of columns to appropriate habitat
86 biome3.taxa.diet.pct=biome3.taxa.diet.stacked*100
87 write.csv(biome3.taxa.diet.pct, file = "unweighted total diet stacked.csv")

```

```

88
89 #Size
90 biome3.taxa.size.stacked=sapply(8:12, function(x) {
91   f=table(subset(taxabiome3, taxabiome3[,x]==1)[,"Body.Class"])
92   cumsum(f/sum(f))
93 })
94 colnames(biome3.taxa.size.stacked)=c("Forest","Woodland","Grassland","Semi-
95 Desert","Desert") #name headings of columns to appropriate habitat
96 biome3.taxa.size.pct=biome3.taxa.size.stacked*100
97 write.csv(biome3.taxa.size.pct, file = "unweighted total size stacked.csv")
98
99 ##Stacked Area Charts
100 #diet
101 data.diet.taxa.biome3=data.frame(habitat=colnames(biome3.taxa.diet.pct),t(biome3.taxa.diet.
102 pct)[,8:1])
103 data.diet.taxa.biome3$habitat=factor(data.diet.taxa.biome3$habitat,
104 levels=data.diet.taxa.biome3$habitat)
105
106 plot.diet.taxa.biome3=plot_ly(data.diet.taxa.biome3, x=~habitat, y=~Omnivore,
107 name='Omnivore', type='scatter', mode='none', fill='tozeroy', fillcolor="#999999")%>%
108 add_trace(y=~Mixed.Feeder, name='Mixed Feeder', fillcolor='#350024')%>%
109 add_trace(y=~Herbivore, name='Herbivore', fillcolor='#FF4900')%>%
110 add_trace(y=~Grazer, name='Grazer', fillcolor='#8CC200')%>%
111 add_trace(y=~Granivore, name='Granivore', fillcolor='#CE008B')%>%
112 add_trace(y=~Folivore, name='Folivore', fillcolor='#9BEFCB')%>%
113 add_trace(y=~Carnivore, name='Carnivore', fillcolor='#FFBEA5')%>%
114 add_trace(y=~Browser, name='Browser', fillcolor='#E3FCA3')%>%
115 layout(title='Proportion of Diet - Unweighted',
116   xaxis=list(title="",
117     showgrid=F),
118   yaxis=list(title = "",
119     showgrid=F,
120     ticksuffix='%'),
121   autosize=F,
122   margin = unit(c(0,0,.1,0), "cm"))%>%
123 export(file = "taxadietbiome3.svg",
124   selenium = RSelenium::rsDriver(browser = "chrome"))
125
126 plot.diet.taxa.biome3
127
128 #locomotion for habitats
129 data.loc.taxa.biome3=data.frame(habitat=colnames(biome3.taxa.loc.pct),t(biome3.taxa.loc.pc
130 t)[,7:1])
131 data.loc.taxa.biome3$habitat=factor(data.loc.taxa.biome3$habitat,
132 levels=data.loc.taxa.biome3$habitat)
133
134 plot.loc.taxa.biome3=plot_ly(data.loc.taxa.biome3, x=~habitat, y=~Semi.Fossorial,
135 name='Semi-Fossorial', type='scatter', mode='none', fill='tozeroy', fillcolor="#999999")%>%
136 add_trace(y=~Non.Cursorial, name='Non-Cursorial', fillcolor='#5D1B00')%>%

```

```

137 add_trace(y=~Fossorial, name='Fossorial', fillcolor='#FF4900')%>%
138 add_trace(y=~Cursorial, name='Cursorial', fillcolor='#37DE97')%>%
139 add_trace(y=~Arboreal.Scansorial, name='Arboreal/Scansorial', fillcolor='#B4F800')%>%
140 add_trace(y=~Aquatic.Semi.Aquatic, name='Aquatic/Semi-Aquatic',
141 fillcolor='#EC74C5')%>%
142 add_trace(y=~Ambulatory, name='Ambulatory', fillcolor='#FFBEA5')%>%
143 layout(title='Proportion of Locomotion - Unweighted',
144         xaxis=list(title="",
145                   showgrid=F),
146         yaxis=list(title = "",
147                   showgrid=F,
148                   ticksuffix="%"),
149         autosize=F,
150         margin = unit(c(0,0,.2,0), "cm"))%>%
151 export(file = "taxalocbiome3.svg",
152        selenium = RSelenium::rsDriver(browser = "chrome"))
153 plot.loc.taxa.biome3
154
155 #size for habitats
156 data.size.taxa.biome3=data.frame(habitat=colnames(biome3.taxa.size.pct),t(biome3.taxa.size.
157 pct)[,7:1])
158 data.size.taxa.biome3$habitat=factor(data.size.taxa.biome3$habitat,
159 levels=data.size.taxa.biome3$habitat)
160
161 plot.size.taxa.biome3=plot_ly(data.size.taxa.biome3, x=~habitat, y=~G, name='G:>10500 g',
162 type='scatter', mode='none', fill='tozeroy', fillcolor='#999999')%>%
163 add_trace(y=~F, name='F:3500-10500 g', fillcolor='#5D1B00')%>%
164 add_trace(y=~E, name='E:1500-3500 g', fillcolor='#FF4900')%>%
165 add_trace(y=~D, name='D:1000-1500 g', fillcolor='#37DE97')%>%
166 add_trace(y=~C, name='C:500-1000 g', fillcolor='#B4F800')%>%
167 add_trace(y=~B, name='B:50-500 g', fillcolor='#EC74C5')%>%
168 add_trace(y=~A, name='A:0-50 g', fillcolor='#FFBEA5')%>%
169 layout(title='Proportion of Size - Unweighted',
170         xaxis=list(title="",
171                   showgrid=F),
172         yaxis=list(title = "",
173                   showgrid=F,
174                   ticksuffix='%'),
175         autosize=F,
176         margin = unit(c(0,0,.2,0), "cm"))%>%
177 export(file = "taxasizebiome3.svg",
178        selenium = RSelenium::rsDriver(browser = "chrome"))
179 plot.size.taxa.biome3
180
181 ##No Small Bodied Mammals
182 taxabiome5=read.csv("UnweightedNoA&B.csv")
183
184 taxabiome5$ForestBiome=rep(0,nrow(taxabiome5))
185 taxabiome5$ForestBiome[grep("Forest", taxabiome5$"BIOME")]=1

```

```

186
187 taxabiome5$WoodlandBiome=rep(0,nrow(taxabiome5))
188 taxabiome5$WoodlandBiome[grep("Woodland", taxabiome5$"BIOME")]=1
189
190 taxabiome5$GrasslandBiome=rep(0,nrow(taxabiome5))
191 taxabiome5$GrasslandBiome[grep("Grassland", taxabiome5$"BIOME")]=1
192
193 taxabiome5$SemiAridBiome=rep(0,nrow(taxabiome5))
194 taxabiome5$SemiAridBiome[grep("Semi-Arid", taxabiome5$"BIOME")]=1
195
196 taxabiome5$DesertBiome=rep(0,nrow(taxabiome5))
197 taxabiome5$DesertBiome[grep("Desert", taxabiome5$"BIOME")]=1
198
199 #calculation proportions for locomotion per habitat
200 biome5.taxa.results.loc=sapply(8:12, function(x) {
201   a=table(subset(taxabiome5, taxabiome5[,x]==1)[,"Locomotion"])
202 })
203 colnames(biome5.taxa.results.loc)=c("Forest", "Woodland", "Grassland", "Semi-
204 Desert", "Desert") #name headings of columns to appropriate habitat
205 biome5.taxa.loc=prop.table(biome5.taxa.results.loc, margin=2)*100
206 write.csv(biome5.taxa.loc, file = "unweighted no small loc.csv")
207
208 #calculate proportions for diet per habitat
209 biome5.taxa.results.diet=sapply(8:12, function(x) {
210   c=table(subset(taxabiome5, taxabiome5[,x]==1)[,"Diet"])
211 })
212 colnames(biome5.taxa.results.diet)=c("Forest", "Woodland", "Grassland", "Semi-
213 Desert", "Desert") #name headings of columns to appropriate habitat
214 biome5.taxa.diet=prop.table(biome5.taxa.results.diet, margin=2)*100
215 write.csv(biome5.taxa.diet, file = "unweighted no small diet.csv")
216
217 #calculate proportions for body size per habitat
218 biome5.taxa.results.size=sapply(8:12, function(x) {
219   e=table(subset(taxabiome5, taxabiome5[,x]==1)[,"Body.Class"])
220 })
221 colnames(biome5.taxa.results.size)=c("Forest", "Woodland", "Grassland", "Semi-
222 Desert", "Desert") #name headings of columns to appropriate habitat
223 biome5.taxa.size=prop.table(biome5.taxa.results.size, margin=2)*100
224 write.csv(biome5.taxa.size, file = "unweighted no small size.csv")
225
226 ##calculate stacked area tables
227 #Locomotion
228 biome5.taxa.loc.stacked=sapply(8:12, function(x) {
229   b=table(subset(taxabiome5, taxabiome5[,x]==1)[,"Locomotion"])
230   cumsum(b/sum(b))
231 })
232 colnames(biome5.taxa.loc.stacked)=c("Forest", "Woodland", "Grassland", "Semi-
233 Desert", "Desert") #name headings of columns to appropriate habitat
234 biome5.taxa.loc.pct=biome5.taxa.loc.stacked*100

```



```

235 write.csv(biome5.taxa.loc.pct, file = "unweighted no small loc stacked.csv")
236
237 #Diet
238 biome5.taxa.diet.stacked=sapply(8:12, function(x) {
239   d=table(subset(taxabiome5, taxabiome5[,x]==1)[,"Diet"])
240   cumsum(d/sum(d))
241 })
242 colnames(biome5.taxa.diet.stacked)=c("Forest", "Woodland", "Grassland", "Semi-
243 Desert", "Desert") #name headings of columns to appropriate habitat
244 biome5.taxa.diet.pct=biome5.taxa.diet.stacked*100
245 write.csv(biome5.taxa.diet.pct, file = "unweighted no small diet stacked.csv")
246
247 #Size
248 biome5.taxa.size.stacked=sapply(8:12, function(x) {
249   f=table(subset(taxabiome5, taxabiome5[,x]==1)[,"Body.Class"])
250   cumsum(f/sum(f))
251 })
252 colnames(biome5.taxa.size.stacked)=c("Forest", "Woodland", "Grassland", "Semi-
253 Desert", "Desert") #name headings of columns to appropriate habitat
254 biome5.taxa.size.pct=biome5.taxa.size.stacked*100
255 write.csv(biome5.taxa.size.pct, file = "unweighted no small size stacked.csv")
256
257 ##Stacked Area Charts
258 #diet for biomes
259 data.diet.taxa.biome5=data.frame(habitat=colnames(biome5.taxa.diet.pct),t(biome5.taxa.diet.
260 pct)[,7:1])
261 data.diet.taxa.biome5$habitat=factor(data.diet.taxa.biome5$habitat,
262 levels=data.diet.taxa.biome5$habitat)
263
264 plot.diet.taxa.biome5=plot_ly(data.diet.taxa.biome5, x=~habitat, y=~Omnivore,
265 name='Omnivore', type='scatter', mode='none', fill='tozeroy', fillcolor="#999999")%>%
266 add_trace(y=~Mixed.Feeder, name='Mixed Feeder', fillcolor='#350024')%>%
267 add_trace(y=~Grazer, name='Grazer', fillcolor='#8CC200')%>%
268 add_trace(y=~Granivore, name='Granivore', fillcolor='#CE008B')%>%
269 add_trace(y=~Folivore, name='Folivore', fillcolor='#9BEFCB')%>%
270 add_trace(y=~Carnivore, name='Carnivore', fillcolor='#FFBEA5')%>%
271 add_trace(y=~Browser, name='Browser', fillcolor='#E3FCA3')%>%
272 layout(title='Proportion of Diet - Unweighted (No Small)',
273   xaxis=list(title="",
274     showgrid=F),
275   yaxis=list(title = "",
276     showgrid=F,
277     ticksuffix='%'),
278   autosize=F,
279   margin = unit(c(0,0,.1,0), "cm"))%>%
280 export(file = "taxadietbiome5.svg",
281   selenium = R Selenium::rsDriver(browser = "chrome"))
282
283 plot.diet.taxa.biome5

```

```

284
285 #locomotion for habitats
286 data.loc.taxa.biome5=data.frame(habitat=colnames(biome5.taxa.loc.pct),t(biome5.taxa.loc.pct)[,7:1])
287
288 data.loc.taxa.biome5$habitat=factor(data.loc.taxa.biome5$habitat,
289 levels=data.loc.taxa.biome5$habitat)
290
291 plot.loc.taxa.biome5=plot_ly(data.loc.taxa.biome5, x=~habitat, y=~Semi.Fossorial,
292 name='Semi-Fossorial', type='scatter', mode='none', fill='tozeroy', fillcolor='#999999')%>%
293 add_trace(y=~Non.Cursorial, name='Non-Cursorial', fillcolor='#5D1B00')%>%
294 add_trace(y=~Fossorial, name='Fossorial', fillcolor='#FF4900')%>%
295 add_trace(y=~Cursorial, name='Cursorial', fillcolor='#37DE97')%>%
296 add_trace(y=~Arboreal.Scansorial, name='Arboreal/Scansorial', fillcolor='#B4F800')%>%
297 add_trace(y=~Aquatic.Semi.Aquatic, name='Aquatic/Semi-Aquatic',
298 fillcolor='#EC74C5')%>%
299 add_trace(y=~Ambulatory, name='Ambulatory', fillcolor='#FFBEA5')%>%
300 layout(title='Proportion of Locomotion - Unweighted (No Small)',
301 xaxis=list(title="",
302 showgrid=F),
303 yaxis=list(title = "",
304 showgrid=F,
305 ticksuffix="%"),
306 autosize=F,
307 margin = unit(c(0,0,.2,0), "cm"))%>%
308 export(file = "taxalocbiome5.svg",
309 selenium = RSelenium::rsDriver(browser = "chrome"))
310 plot.loc.taxa.biome5
311
312 #size for habitats
313 data.size.taxa.biome5=data.frame(habitat=colnames(biome5.taxa.size.pct),t(biome5.taxa.size.pct)[,5:1])
314
315 data.size.taxa.biome5$habitat=factor(data.size.taxa.biome5$habitat,
316 levels=data.size.taxa.biome5$habitat)
317
318 plot.size.taxa.biome5=plot_ly(data.size.taxa.biome5, x=~habitat, y=~G, name='G:>10500 g',
319 type='scatter', mode='none', fill='tozeroy', fillcolor='#999999')%>%
320 add_trace(y=~F, name='F:3500-10500 g', fillcolor='#5D1B00')%>%
321 add_trace(y=~E, name='E:1500-3500 g', fillcolor='#FF4900')%>%
322 add_trace(y=~D, name='D:1000-1500 g', fillcolor='#37DE97')%>%
323 add_trace(y=~C, name='C:500-1000 g', fillcolor='#B4F800')%>%
324 layout(title='Proportion of Size - Unweighted (No Small)',
325 xaxis=list(title="",
326 showgrid=F),
327 yaxis=list(title = "",
328 showgrid=F,
329 ticksuffix='%'),
330 autosize=F,
331 margin = unit(c(0,0,.2,0), "cm"))%>%
332 export(file = "taxasizebiome5.svg",

```

```

333     selenium = RSelenium::rsDriver(browser = "chrome")
334 plot.size.taxa.biome5
335
336 ##Historical Occurrence, New Habitats
337 #Weighted
338 histbiome3=read.csv("WeightedTotal.csv")
339
340 histbiome3$ForestBiome=rep(0,nrow(histbiome3))
341 histbiome3$ForestBiome[grep("Forest", histbiome3$"BIOME")]=1
342
343 histbiome3$WoodlandBiome=rep(0,nrow(histbiome3))
344 histbiome3$WoodlandBiome[grep("Woodland", histbiome3$"BIOME")]=1
345
346 histbiome3$GrasslandBiome=rep(0,nrow(histbiome3))
347 histbiome3$GrasslandBiome[grep("Grassland", histbiome3$"BIOME")]=1
348
349 histbiome3$SemiAridBiome=rep(0,nrow(histbiome3))
350 histbiome3$SemiAridBiome[grep("Semi-Arid", histbiome3$"BIOME")]=1
351
352 histbiome3$DesertBiome=rep(0,nrow(histbiome3))
353 histbiome3$DesertBiome[grep("Desert", histbiome3$"BIOME")]=1
354
355 ##Calculate proportion of diet, locomotion and body size per habitat
356 #calculation proportions for locomotion per habitat
357 biome3.hist.results.loc=sapply(9:13, function(x) {
358   a=table(subset(histbiome3, histbiome3[,x]==1)[,"Locomotion"])
359 })
360 colnames(biome3.hist.results.loc)=c("Forest","Woodland","Grassland","Semi-
361 Desert","Desert") #name headings of columns to appropriate habitat
362 biome3.hist.loc=prop.table(biome3.hist.results.loc, margin=2)*100
363 write.csv(biome3.hist.loc, file = "weighted total loc.csv")
364
365 #calculate proportions for diet per habitat
366 biome3.hist.results.diet=sapply(9:13, function(x) {
367   c=table(subset(histbiome3, histbiome3[,x]==1)[,"Diet"])
368 })
369 colnames(biome3.hist.results.diet)=c("Forest","Woodland","Grassland","Semi-
370 Desert","Desert") #name headings of columns to appropriate habitat
371 biome3.hist.diet=prop.table(biome3.hist.results.diet, margin=2)*100
372 write.csv(biome3.hist.diet, file = "weighted total diet.csv")
373
374 #calculate proportions for body size per habitat
375 biome3.hist.results.size=sapply(9:13, function(x) {
376   e=table(subset(histbiome3, histbiome3[,x]==1)[,"Body.Class"])
377 })
378 colnames(biome3.hist.results.size)=c("Forest","Woodland","Grassland","Semi-
379 Desert","Desert") #name headings of columns to appropriate habitat
380 biome3.hist.size=prop.table(biome3.hist.results.size, margin=2)*100
381 write.csv(biome3.hist.size, file = "weighted total size.csv")

```

```

382
383 ##calculate stacked area tables
384 #Locomotion
385 biome3.hist.loc.stacked=sapply(9:13, function(x) {
386   b=table(subset(histbiome3, histbiome3[,x]==1)[, "Locomotion"])
387   cumsum(b/sum(b))
388 })
389 colnames(biome3.hist.loc.stacked)=c("Forest", "Woodland", "Grassland", "Semi-
390 Desert", "Desert") #name headings of columns to appropriate habitat
391 biome3.hist.loc.pct=biome3.hist.loc.stacked*100
392 write.csv(biome3.hist.loc.pct, file = "weighted total loc stacked.csv")
393
394 #Diet
395 biome3.hist.diet.stacked=sapply(9:13, function(x) {
396   d=table(subset(histbiome3, histbiome3[,x]==1)[, "Diet"])
397   cumsum(d/sum(d))
398 })
399 colnames(biome3.hist.diet.stacked)=c("Forest", "Woodland", "Grassland", "Semi-
400 Desert", "Desert") #name headings of columns to appropriate habitat
401 biome3.hist.diet.pct=biome3.hist.diet.stacked*100
402 write.csv(biome3.hist.diet.pct, file = "weighted total diet stacked.csv")
403
404 #Size
405 biome3.hist.size.stacked=sapply(9:13, function(x) {
406   f=table(subset(histbiome3, histbiome3[,x]==1)[, "Body.Class"])
407   cumsum(f/sum(f))
408 })
409 colnames(biome3.hist.size.stacked)=c("Forest", "Woodland", "Grassland", "Semi-
410 Desert", "Desert") #name headings of columns to appropriate habitat
411 biome3.hist.size.pct=biome3.hist.size.stacked*100
412 write.csv(biome3.hist.size.pct, file = "weighted total size stacked.csv")
413
414 ##Stacked Area Charts
415 data.diet.hist.biome3=data.frame(habitat=colnames(biome3.hist.diet.pct),t(biome3.hist.diet.p
416 ct)[,8:1])
417 data.diet.hist.biome3$habitat=factor(data.diet.hist.biome3$habitat,
418 levels=data.diet.hist.biome3$habitat)
419
420 plot.diet.hist.biome3=plot_ly(data.diet.hist.biome3, x=~habitat, y=~Omnivore,
421 name='Omnivore', type='scatter', mode='none', fill='tozeroy', fillcolor="#999999")%>%
422 add_trace(y=~Mixed.Feeder, name='Mixed Feeder', fillcolor='#350024')%>%
423 add_trace(y=~Herbivore, name='Herbivore', fillcolor='#FF4900')%>%
424 add_trace(y=~Grazer, name='Grazer', fillcolor='#8CC200')%>%
425 add_trace(y=~Granivore, name='Granivore', fillcolor='#CE008B')%>%
426 add_trace(y=~Folivore, name='Folivore', fillcolor='#9BEFCB')%>%
427 add_trace(y=~Carnivore, name='Carnivore', fillcolor='#FFBEA5')%>%
428 add_trace(y=~Browser, name='Browser', fillcolor='#E3FCA3')%>%
429 layout(title='Proportion of Diet - Weighted by Occurrence',
430         xaxis=list(title="",

```

```

431         showgrid=F),
432     yaxis=list(title = "",
433         showgrid=F,
434         ticksuffix='%'),
435     autosize=F,
436     margin = unit(c(0,0,.1,0), "cm"))%>%
437     export(file = "histdietbiome3.svg",
438         selenium = RSelenium::rsDriver(browser = "chrome"))
439 plot.diet.hist.biome3
440
441 #locomotion for habitats
442 data.loc.hist.biome3=data.frame(habitat=colnames(biome3.hist.loc.pct),t(biome3.hist.loc.pct)
443 [,7:1])
444 data.loc.hist.biome3$habitat=factor(data.loc.hist.biome3$habitat,
445 levels=data.loc.hist.biome3$habitat)
446
447 plot.loc.hist.biome3=plot_ly(data.loc.hist.biome3, x=~habitat, y=~Semi.Fossorial,
448 name='Semi-Fossorial', type='scatter', mode='none', fill='tozeroy', fillcolor='#999999')%>%
449 add_trace(y=~Non.Cursorial, name='Non-Cursorial', fillcolor='#5D1B00')%>%
450 add_trace(y=~Fossorial, name='Fossorial', fillcolor='#FF4900')%>%
451 add_trace(y=~Cursorial, name='Cursorial', fillcolor='#37DE97')%>%
452 add_trace(y=~Arboreal.Scansorial, name='Arboreal/Scansorial', fillcolor='#B4F800')%>%
453 add_trace(y=~Aquatic.Semi.Aquatic, name='Aquatic/Semi-Aquatic',
454 fillcolor='#EC74C5')%>%
455 add_trace(y=~Ambulatory, name='Ambulatory', fillcolor='#FFBEA5')%>%
456 layout(title='Proportion of Locomotion - Weighted by Occurrence',
457     xaxis=list(title="",
458         showgrid=F),
459     yaxis=list(title = "",
460         showgrid=F,
461         ticksuffix="%"),
462     autosize=F,
463     margin = unit(c(0,0,.2,0), "cm"))%>%
464     export(file = "histlocbiome3.svg",
465         selenium = RSelenium::rsDriver(browser = "chrome"))
466 plot.loc.hist.biome3
467
468 #size for habitats
469 data.size.hist.biome3=data.frame(habitat=colnames(biome3.hist.size.pct),t(biome3.hist.size.p
470 ct)[,7:1])
471 data.size.hist.biome3$habitat=factor(data.size.hist.biome3$habitat,
472 levels=data.size.hist.biome3$habitat)
473
474 plot.size.hist.biome3=plot_ly(data.size.hist.biome3, x=~habitat, y=~G, name='G:>10500 g',
475 type='scatter', mode='none', fill='tozeroy', fillcolor='#999999')%>%
476 add_trace(y=~F, name='F:3500-10500 g', fillcolor='#5D1B00')%>%
477 add_trace(y=~E, name='E:1500-3500 g', fillcolor='#FF4900')%>%
478 add_trace(y=~D, name='D:1000-1500 g', fillcolor='#37DE97')%>%
479 add_trace(y=~C, name='C:500-1000 g', fillcolor='#B4F800')%>%

```

```

480 add_trace(y=~B, name='B:50-500 g', fillcolor='#EC74C5')%>%
481 add_trace(y=~A, name='A:0-50 g', fillcolor='#FFBEA5')%>%
482 layout(title='Proportion of Size - Weighted by Occurrence',
483         xaxis=list(title="",
484                   showgrid=F),
485         yaxis=list(title = "",
486                   showgrid=F,
487                   ticksuffix='%'),
488         autosize=F,
489         margin = unit(c(0,0,.2,0), "cm"))%>%
490 export(file = "histsizebiome3.svg",
491        selenium = RSelenium::rsDriver(browser = "chrome"))
492 plot.size.hist.biome3
493
494 ##Historical Occurrence, New Habitats
495 ##Weighted, No Small Bodied Mammals
496 histbiome5=read.csv("WeightedNoA&B.csv")
497
498 histbiome5$ForestBiome=rep(0,nrow(histbiome5))
499 histbiome5$ForestBiome[grep("Forest", histbiome5$"BIOME")]=1
500
501 histbiome5$WoodlandBiome=rep(0,nrow(histbiome5))
502 histbiome5$WoodlandBiome[grep("Woodland", histbiome5$"BIOME")]=1
503
504 histbiome5$GrasslandBiome=rep(0,nrow(histbiome5))
505 histbiome5$GrasslandBiome[grep("Grassland", histbiome5$"BIOME")]=1
506
507 histbiome5$SemiAridBiome=rep(0,nrow(histbiome5))
508 histbiome5$SemiAridBiome[grep("Semi-Arid", histbiome5$"BIOME")]=1
509
510 histbiome5$DesertBiome=rep(0,nrow(histbiome5))
511 histbiome5$DesertBiome[grep("Desert", histbiome5$"BIOME")]=1
512
513 ##Calculate proportion of diet, locomotion and body size per habitat
514
515 #calculation proportions for locomotion per habitat
516 biome5.hist.results.loc=sapply(9:13, function(x) {
517   a=table(subset(histbiome5, histbiome5[,x]==1)[,"Locomotion"])
518 })
519 colnames(biome5.hist.results.loc)=c("Forest", "Woodland", "Grassland", "Semi-
520 Desert", "Desert") #name headings of columns to appropriate habitat
521 biome5.hist.loc=prop.table(biome5.hist.results.loc, margin=2)*100
522 write.csv(biome5.hist.loc, file = "weighted no small loc.csv")
523
524 #calculate proportions for diet per habitat
525 biome5.hist.results.diet=sapply(9:13, function(x) {
526   c=table(subset(histbiome5, histbiome5[,x]==1)[,"Diet"])
527 })

```

```

528 colnames(biome5.hist.results.diet)=c("Forest","Woodland", "Grassland","Semi-
529 Desert","Desert")#name headings of columns to appropriate habitat
530 biome5.hist.diet=prop.table(biome5.hist.results.diet, margin=2)*100
531 write.csv(biome5.hist.diet, file = "weighted no small diet.csv")
532
533 #calculate proportions for body size per habitat
534 biome5.hist.results.size=sapply(9:13, function(x) {
535   e=table(subset(histbiome5, histbiome5[,x]==1)[,"Body.Class"])
536 })
537 colnames(biome5.hist.results.size)=c("Forest","Woodland", "Grassland","Semi-
538 Desert","Desert")#name headings of columns to appropriate habitat
539 biome5.hist.size=prop.table(biome5.hist.results.size, margin=2)*100
540 write.csv(biome5.hist.size, file = "weighted no small size.csv")
541
542 ##calculate stacked area tables
543 #Locomotion
544 biome5.hist.loc.stacked=sapply(9:13, function(x) {
545   b=table(subset(histbiome5, histbiome5[,x]==1)[,"Locomotion"])
546   cumsum(b/sum(b))
547 })
548 colnames(biome5.hist.loc.stacked)=c("Forest","Woodland","Grassland","Semi-
549 Desert","Desert") #name headings of columns to appropriate habitat
550 biome5.hist.loc.pct=biome5.hist.loc.stacked*100
551 write.csv(biome5.hist.loc.pct, file = "weighted no small loc stacked.csv")
552
553 #Diet
554 biome5.hist.diet.stacked=sapply(9:13, function(x) {
555   d=table(subset(histbiome5, histbiome5[,x]==1)[,"Diet"])
556   cumsum(d/sum(d))
557 })
558 colnames(biome5.hist.diet.stacked)=c("Forest","Woodland","Grassland","Semi-
559 Desert","Desert") #name headings of columns to appropriate habitat
560 biome5.hist.diet.pct=biome5.hist.diet.stacked*100
561 write.csv(biome5.hist.diet.pct, file = "weighted no small diet stacked.csv")
562
563 #Size
564 biome5.hist.size.stacked=sapply(9:13, function(x) {
565   f=table(subset(histbiome5, histbiome5[,x]==1)[,"Body.Class"])
566   cumsum(f/sum(f))
567 })
568 colnames(biome5.hist.size.stacked)=c("Forest","Woodland","Grassland","Semi-
569 Desert","Desert") #name headings of columns to appropriate habitat
570 biome5.hist.size.pct=biome5.hist.size.stacked*100
571 write.csv(biome5.hist.size.pct, file = "weighted no small size stacked.csv")
572
573 ##Stacked Area Charts
574
575 data.diet.hist.biome5=data.frame(habitat=colnames(biome5.hist.diet.pct),t(biome5.hist.diet.p
576 ct)[,8:1])

```

```

577 data.diet.hist.biome5$habitat=factor(data.diet.hist.biome5$habitat,
578 levels=data.diet.hist.biome5$habitat)
579
580 plot.diet.hist.biome5=plot_ly(data.diet.hist.biome5, x=~habitat, y=~Omnivore,
581 name='Omnivore', type='scatter', mode='none', fill='tozeroy', fillcolor="#999999")%>%
582 add_trace(y=~Mixed.Feeder, name='Mixed Feeder', fillcolor='#350024')%>%
583 add_trace(y=~Grazer, name='Grazer', fillcolor='#8CC200')%>%
584 add_trace(y=~Granivore, name='Granivore', fillcolor='#CE008B')%>%
585 add_trace(y=~Folivore, name='Folivore', fillcolor='#9BEFCB')%>%
586 add_trace(y=~Carnivore, name='Carnivore', fillcolor='#FFBEA5')%>%
587 add_trace(y=~Browser, name='Browser', fillcolor='#E3FCA3')%>%
588 layout(title='Proportion of Diet - Weighted by Occurrence (No Small)',
589 xaxis=list(title="",
590 showgrid=F),
591 yaxis=list(title = "",
592 showgrid=F,
593 ticksuffix='%'),
594 autosize=F,
595 margin = unit(c(0,0,.1,0), "cm"))%>%
596 export(file = "histdietbiome5.svg",
597 selenium = RSelenium::rsDriver(browser = "chrome"))
598 plot.diet.hist.biome5
599
600 #locomotion for habitats
601 data.loc.hist.biome5=data.frame(habitat=colnames(biome5.hist.loc.pct),t(biome5.hist.loc.pct)
602 [,7:1])
603 data.loc.hist.biome5$habitat=factor(data.loc.hist.biome5$habitat,
604 levels=data.loc.hist.biome5$habitat)
605
606 plot.loc.hist.biome5=plot_ly(data.loc.hist.biome5, x=~habitat, y=~Semi.Fossorial,
607 name='Semi-Fossorial', type='scatter', mode='none', fill='tozeroy', fillcolor='#999999')%>%
608 add_trace(y=~Non.Cursorial, name='Non-Cursorial', fillcolor='#5D1B00')%>%
609 add_trace(y=~Fossorial, name='Fossorial', fillcolor='#FF4900')%>%
610 add_trace(y=~Cursorial, name='Cursorial', fillcolor='#37DE97')%>%
611 add_trace(y=~Arboreal.Scansorial, name='Arboreal/Scansorial', fillcolor='#B4F800')%>%
612 add_trace(y=~Aquatic.Semi.Aquatic, name='Aquatic/Semi-Aquatic',
613 fillcolor='#EC74C5')%>%
614 add_trace(y=~Ambulatory, name='Ambulatory', fillcolor='#FFBEA5')%>%
615 layout(title='Proportion of Locomotion - Weighted by Occurrence (No Small)',
616 xaxis=list(title="",
617 showgrid=F),
618 yaxis=list(title = "",
619 showgrid=F,
620 ticksuffix="%"),
621 autosize=F,
622 margin = unit(c(0,0,.2,0), "cm"))%>%
623 export(file = "histlocbiome5.svg",
624 selenium = RSelenium::rsDriver(browser = "chrome"))
625 plot.loc.hist.biome5

```



```
626
627 #size for habitats
628 data.size.hist.biome5=data.frame(habitat=colnames(biome5.hist.size.pct),t(biome5.hist.size.p
629 ct)[,5:1])
630 data.size.hist.biome5$habitat=factor(data.size.hist.biome5$habitat,
631 levels=data.size.hist.biome5$habitat)
632
633 plot.size.hist.biome5=plot_ly(data.size.hist.biome5, x=~habitat, y=~G, name='G:>10500 g',
634 type='scatter', mode='none', fill='tozeroy', fillcolor='#999999')%>%
635 add_trace(y=~F, name='F:3500-10500 g', fillcolor='#5D1B00')%>%
636 add_trace(y=~E, name='E:1500-3500 g', fillcolor='#FF4900')%>%
637 add_trace(y=~D, name='D:1000-1500 g', fillcolor='#37DE97')%>%
638 add_trace(y=~C, name='C:500-1000 g', fillcolor='#B4F800')%>%
639 layout(title='Proportion of Size - Weighted by Occurrence (No Small)',
640         xaxis=list(title="",
641                   showgrid=F),
642         yaxis=list(title = "",
643                   showgrid=F,
644                   ticksuffix='%'),
645         autosize=F,
646         margin = unit(c(0,0,.2,0), "cm"))%>%
647 export(file = "histsizebiome5.svg",
648        selenium = RSelenium::rsDriver(browser = "chrome"))
649 plot.size.hist.biome5
```

M2: Script to calculate trait frequency proportions for principle component analyses.

Ecocodes are used for sub-sampling points.

```

1 ##Unweighted, Total
2 taxaecocode=read.csv("Unweighted Total.csv")
3
4 taxaecocode$'340'=rep(0,nrow(taxaecocode))
5 taxaecocode$'340'[grep("-340", taxaecocode$"ECOCODE")]=1
6
7 taxaecocode$'332'=rep(0,nrow(taxaecocode))
8 taxaecocode$'332'[grep("-332", taxaecocode$"ECOCODE")]=1
9
10 taxaecocode$'331'=rep(0,nrow(taxaecocode))
11 taxaecocode$'331'[grep("-331", taxaecocode$"ECOCODE")]=1
12
13 taxaecocode$'323'=rep(0,nrow(taxaecocode))
14 taxaecocode$'323'[grep("-323", taxaecocode$"ECOCODE")]=1
15
16 taxaecocode$'321'=rep(0,nrow(taxaecocode))
17 taxaecocode$'321'[grep("-321", taxaecocode$"ECOCODE")]=1
18
19 taxaecocode$'314'=rep(0,nrow(taxaecocode))
20 taxaecocode$'314'[grep("-314", taxaecocode$"ECOCODE")]=1
21
22 taxaecocode$'311'=rep(0,nrow(taxaecocode))
23 taxaecocode$'311'[grep("-311", taxaecocode$"ECOCODE")]=1
24
25 taxaecocode$'251'=rep(0,nrow(taxaecocode))
26 taxaecocode$'251'[grep("-251", taxaecocode$"ECOCODE")]=1
27
28 taxaecocode$'263'=rep(0,nrow(taxaecocode))
29 taxaecocode$'263'[grep("-263", taxaecocode$"ECOCODE")]=1
30
31 taxaecocode$'262'=rep(0,nrow(taxaecocode))
32 taxaecocode$'262'[grep("-262", taxaecocode$"ECOCODE")]=1
33
34 taxaecocode$'230'=rep(0,nrow(taxaecocode))
35 taxaecocode$'230'[grep("-230", taxaecocode$"ECOCODE")]=1
36
37 taxaecocode$'221'=rep(0,nrow(taxaecocode))
38 taxaecocode$'221'[grep("-221", taxaecocode$"ECOCODE")]=1
39
40 taxaecocode$'211'=rep(0,nrow(taxaecocode))
41 taxaecocode$'211'[grep("-211", taxaecocode$"ECOCODE")]=1
42
43 ##Calculate proportion of diet, locomotion and body size per habitat
44 #calculation proportions for locomotion per habitat

```

```

45 ecocode.taxa.results.loc=sapply(8:20, function(x) {
46   a=table(subset(taxaecocode, taxaecocode[,x]==1)[,"Locomotion"])
47 })
48 colnames(ecocode.taxa.results.loc)=c("Semi-Desert","Semi-Desert","Semi-
49 Desert","Desert","Desert","Grassland","Grassland","Grassland","Woodland","Woodland","F
50 orest","Forest","Forest") #name headings of columns to appropriate habitat
51 ecocode.taxa.loc=prop.table(ecocode.taxa.results.loc, margin=2)
52 unweighted.total.loc=t(ecocode.taxa.loc)
53 write.csv(unweighted.total.loc, file = "unweighted.total.loc.csv")
54
55 #calculate proportions for diet per habitat
56 ecocode.taxa.results.diet=sapply(8:20, function(x) {
57   c=table(subset(taxaecocode, taxaecocode[,x]==1)[,"Diet"])
58 })
59 colnames(ecocode.taxa.results.diet)=c("Semi-Desert","Semi-Desert","Semi-
60 Desert","Desert","Desert","Grassland","Grassland","Grassland","Woodland","Woodland","F
61 orest","Forest","Forest")#name headings of columns to appropriate habitat
62 ecocode.taxa.diet=prop.table(ecocode.taxa.results.diet, margin=2)
63 unweighted.total.diet=t(ecocode.taxa.diet)
64 write.csv(unweighted.total.diet, file = "unweighted.total.diet.csv")
65
66 #calculate proportions for body size per habitat
67 ecocode.taxa.results.size=sapply(8:20, function(x) {
68   e=table(subset(taxaecocode, taxaecocode[,x]==1)[,"Body.Class"])
69 })
70 colnames(ecocode.taxa.results.size)=c("Semi-Desert","Semi-Desert","Semi-
71 Desert","Desert","Desert","Grassland","Grassland","Grassland","Woodland","Woodland","F
72 orest","Forest","Forest")#name headings of columns to appropriate habitat
73 ecocode.taxa.size=prop.table(ecocode.taxa.results.size, margin=2)
74 unweighted.total.size=t(ecocode.taxa.size)
75 write.csv(unweighted.total.size, file = "unweighted.total.size.csv")
76
77 unweighted.ecocode<-rbind(ecocode.taxa.size, ecocode.taxa.diet, ecocode.taxa.loc)
78 unweighted.total<-t(unweighted.ecocode)
79 write.csv(unweighted.total, file = "unweighted.total.csv")
80
81 ##Unweighted, No Small
82 taxaecocodenosmall=read.csv("UnweightedNoA&B.csv")
83
84 taxaecocodenosmall$'340'=rep(0,nrow(taxaecocodenosmall))
85 taxaecocodenosmall$'340'[grep("-340", taxaecocodenosmall$"ECOCODE")]=1
86
87 taxaecocodenosmall$'332'=rep(0,nrow(taxaecocodenosmall))
88 taxaecocodenosmall$'332'[grep("-332", taxaecocodenosmall$"ECOCODE")]=1
89
90 taxaecocodenosmall$'331'=rep(0,nrow(taxaecocodenosmall))
91 taxaecocodenosmall$'331'[grep("-331", taxaecocodenosmall$"ECOCODE")]=1
92
93 taxaecocodenosmall$'323'=rep(0,nrow(taxaecocodenosmall))

```

```

94 taxaecocodenosmall$'323'[grep("-323", taxaecocodenosmall$"ECOCODE")]=1
95
96 taxaecocodenosmall$'321'=rep(0,nrow(taxaecocodenosmall))
97 taxaecocodenosmall$'321'[grep("-321", taxaecocodenosmall$"ECOCODE")]=1
98
99 taxaecocodenosmall$'314'=rep(0,nrow(taxaecocodenosmall))
100 taxaecocodenosmall$'314'[grep("-314", taxaecocodenosmall$"ECOCODE")]=1
101
102 taxaecocodenosmall$'311'=rep(0,nrow(taxaecocodenosmall))
103 taxaecocodenosmall$'311'[grep("-311", taxaecocodenosmall$"ECOCODE")]=1
104
105 taxaecocodenosmall$'251'=rep(0,nrow(taxaecocodenosmall))
106 taxaecocodenosmall$'251'[grep("-251", taxaecocodenosmall$"ECOCODE")]=1
107
108 taxaecocodenosmall$'263'=rep(0,nrow(taxaecocodenosmall))
109 taxaecocodenosmall$'263'[grep("-263", taxaecocodenosmall$"ECOCODE")]=1
110
111 taxaecocodenosmall$'262'=rep(0,nrow(taxaecocodenosmall))
112 taxaecocodenosmall$'262'[grep("-262", taxaecocodenosmall$"ECOCODE")]=1
113
114 taxaecocodenosmall$'230'=rep(0,nrow(taxaecocodenosmall))
115 taxaecocodenosmall$'230'[grep("-230", taxaecocodenosmall$"ECOCODE")]=1
116
117 taxaecocodenosmall$'221'=rep(0,nrow(taxaecocodenosmall))
118 taxaecocodenosmall$'221'[grep("-221", taxaecocodenosmall$"ECOCODE")]=1
119
120 taxaecocodenosmall$'211'=rep(0,nrow(taxaecocodenosmall))
121 taxaecocodenosmall$'211'[grep("-211", taxaecocodenosmall$"ECOCODE")]=1
122
123 ##Calculate proportion of diet, locomotion and body size per habitat
124
125 #calculation proportions for locomotion per habitat
126 ecocode.taxanosmall.results.loc=sapply(8:20, function(x) {
127   a=table(subset(taxaecocodenosmall, taxaecocodenosmall[,x]==1)[,"Locomotion"])
128 })
129 colnames(ecocode.taxanosmall.results.loc)=c("Semi-Desert", "Semi-Desert", "Semi-
130 Desert", "Desert", "Desert", "Grassland", "Grassland", "Grassland", "Woodland", "Woodland", "F
131 orest", "Forest", "Forest") #name headings of columns to appropriate habitat
132 ecocode.taxanosmall.loc=prop.table(ecocode.taxanosmall.results.loc, margin=2)
133 unweighted.nosmall.loc=t(ecocode.taxanosmall.loc)
134 write.csv(unweighted.nosmall.loc, file = "unweighted.nosmall.loc.csv")
135
136 #calculate proportions for diet per habitat
137 ecocode.taxanosmall.results.diet=sapply(8:20, function(x) {
138   c=table(subset(taxaecocodenosmall, taxaecocodenosmall[,x]==1)[,"Diet"])
139 })
140 colnames(ecocode.taxanosmall.results.diet)=c("Semi-Desert", "Semi-Desert", "Semi-
141 Desert", "Desert", "Desert", "Grassland", "Grassland", "Grassland", "Woodland", "Woodland", "F
142 orest", "Forest", "Forest")#name headings of columns to appropriate habitat

```

```

143 ecocode.taxanosmall.diet=prop.table(ecocode.taxanosmall.results.diet, margin=2)
144 unweighted.nosmall.diet=t(ecocode.taxanosmall.diet)
145 write.csv(unweighted.nosmall.diet, file = "unweighted.nosmall.diet.csv")
146
147 #calculate proportions for body size per habitat
148 ecocode.taxanosmall.results.size=sapply(8:20, function(x) {
149   e=table(subset(taxaecocodenosmall, taxaecocodenosmall[,x]==1)[, "Body.Class"])
150 })
151 colnames(ecocode.taxanosmall.results.size)=c("Semi-Desert", "Semi-Desert", "Semi-
152 Desert", "Desert", "Desert", "Grassland", "Grassland", "Grassland", "Woodland", "Woodland", "F
153 orest", "Forest", "Forest")#name headings of columns to appropriate habitat
154 ecocode.taxanosmall.size=prop.table(ecocode.taxanosmall.results.size, margin=2)
155 unweighted.nosmall.size=t(ecocode.taxanosmall.size)
156 write.csv(unweighted.nosmall.size, file = "unweighted.nosmall.size.csv")
157
158 taxanosmall.ecocode<-rbind(ecocode.taxanosmall.size, ecocode.taxanosmall.loc,
159 ecocode.taxanosmall.diet)
160 unweighted.nosmall <-t(taxanosmall.ecocode)
161 write.csv(unweighted.nosmall, file = "unweighted.nosmall.csv")
162
163 ##Weighted, Total
164 weightecocode=read.csv("WeightedTotal.csv")
165
166 weightecocode$'340'=rep(0,nrow(weightecocode))
167 weightecocode$'340'[grep("-340", weightecocode$"ECOCODE")]=1
168
169 weightecocode$'332'=rep(0,nrow(weightecocode))
170 weightecocode$'332'[grep("-332", weightecocode$"ECOCODE")]=1
171
172 weightecocode$'331'=rep(0,nrow(weightecocode))
173 weightecocode$'331'[grep("-331", weightecocode$"ECOCODE")]=1
174
175 weightecocode$'323'=rep(0,nrow(weightecocode))
176 weightecocode$'323'[grep("-323", weightecocode$"ECOCODE")]=1
177
178 weightecocode$'321'=rep(0,nrow(weightecocode))
179 weightecocode$'321'[grep("-321", weightecocode$"ECOCODE")]=1
180
181 weightecocode$'314'=rep(0,nrow(weightecocode))
182 weightecocode$'314'[grep("-314", weightecocode$"ECOCODE")]=1
183
184 weightecocode$'311'=rep(0,nrow(weightecocode))
185 weightecocode$'311'[grep("-311", weightecocode$"ECOCODE")]=1
186
187 weightecocode$'251'=rep(0,nrow(weightecocode))
188 weightecocode$'251'[grep("-251", weightecocode$"ECOCODE")]=1
189
190 weightecocode$'263'=rep(0,nrow(weightecocode))
191 weightecocode$'263'[grep("-263", weightecocode$"ECOCODE")]=1

```

```

192
193 weightecocode$'262'=rep(0,nrow(weightecocode))
194 weightecocode$'262'[grep("-262", weightecocode$"ECOCODE")]=1
195
196 weightecocode$'230'=rep(0,nrow(weightecocode))
197 weightecocode$'230'[grep("-230", weightecocode$"ECOCODE")]=1
198
199 weightecocode$'221'=rep(0,nrow(weightecocode))
200 weightecocode$'221'[grep("-221", weightecocode$"ECOCODE")]=1
201
202 weightecocode$'211'=rep(0,nrow(weightecocode))
203 weightecocode$'211'[grep("-211", weightecocode$"ECOCODE")]=1
204
205 ##Calculate proportion of diet, locomotion and body size per habitat
206 #calculation proportions for locomotion per habitat
207 ecocode.weight.results.loc=sapply(9:21, function(x) {
208   a=table(subset(weightecocode, weightecocode[,x]==1),"Locomotion")
209 })
210 colnames(ecocode.weight.results.loc)=c("Semi-Desert","Semi-Desert","Semi-
211 Desert","Desert","Desert","Grassland","Grassland","Grassland","Woodland","Woodland","F
212 orest","Forest","Forest") #name headings of columns to appropriate habitat
213 ecocode.weight.loc=prop.table(ecocode.weight.results.loc, margin=2)
214 weighted.total.loc=t(ecocode.weight.loc)
215 write.csv(weighted.total.loc, file = "weighted.total.loc.csv")
216
217 #calculate proportions for diet per habitat
218 ecocode.weight.results.diet=sapply(9:21, function(x) {
219   c=table(subset(weightecocode, weightecocode[,x]==1),"Diet")
220 })
221 colnames(ecocode.weight.results.diet)=c("Semi-Desert","Semi-Desert","Semi-
222 Desert","Desert","Desert","Grassland","Grassland","Grassland","Woodland","Woodland","F
223 orest","Forest","Forest")#name headings of columns to appropriate habitat
224 ecocode.weight.diet=prop.table(ecocode.weight.results.diet, margin=2)
225 weighted.total.diet=t(ecocode.weight.diet)
226 write.csv(weighted.total.diet, file = "weighted.total.diet.csv")
227
228 #calculate proportions for body size per habitat
229 ecocode.weight.results.size=sapply(9:21, function(x) {
230   e=table(subset(weightecocode, weightecocode[,x]==1),"Body.Class")
231 })
232 colnames(ecocode.weight.results.size)=c("Semi-Desert","Semi-Desert","Semi-
233 Desert","Desert","Desert","Grassland","Grassland","Grassland","Woodland","Woodland","F
234 orest","Forest","Forest")#name headings of columns to appropriate habitat
235 ecocode.weight.size=prop.table(ecocode.weight.results.size, margin=2)
236 weighted.total.size=t(ecocode.weight.size)
237 write.csv(weighted.total.size, file = "weighted.total.size.csv")
238
239 weight.ecocode<-rbind(ecocode.weight.size, ecocode.weight.loc, ecocode.weight.diet)
240 weighted.total <-t(weight.ecocode)

```

```

241 write.csv(weighted.total, file = "weighted.total.csv")
242
243 ##Weighted, No Small
244 weightecocodenosmall=read.csv("WeightedNoA&B.csv")
245
246 weightecocodenosmall$'340'=rep(0,nrow(weightecocodenosmall))
247 weightecocodenosmall$'340'[grep("-340", weightecocodenosmall$"ECOCODE")]=1
248
249 weightecocodenosmall$'332'=rep(0,nrow(weightecocodenosmall))
250 weightecocodenosmall$'332'[grep("-332", weightecocodenosmall$"ECOCODE")]=1
251
252 weightecocodenosmall$'331'=rep(0,nrow(weightecocodenosmall))
253 weightecocodenosmall$'331'[grep("-331", weightecocodenosmall$"ECOCODE")]=1
254
255 weightecocodenosmall$'323'=rep(0,nrow(weightecocodenosmall))
256 weightecocodenosmall$'323'[grep("-323", weightecocodenosmall$"ECOCODE")]=1
257
258 weightecocodenosmall$'321'=rep(0,nrow(weightecocodenosmall))
259 weightecocodenosmall$'321'[grep("-321", weightecocodenosmall$"ECOCODE")]=1
260
261 weightecocodenosmall$'314'=rep(0,nrow(weightecocodenosmall))
262 weightecocodenosmall$'314'[grep("-314", weightecocodenosmall$"ECOCODE")]=1
263
264 weightecocodenosmall$'311'=rep(0,nrow(weightecocodenosmall))
265 weightecocodenosmall$'311'[grep("-311", weightecocodenosmall$"ECOCODE")]=1
266
267 weightecocodenosmall$'251'=rep(0,nrow(weightecocodenosmall))
268 weightecocodenosmall$'251'[grep("-251", weightecocodenosmall$"ECOCODE")]=1
269
270 weightecocodenosmall$'263'=rep(0,nrow(weightecocodenosmall))
271 weightecocodenosmall$'263'[grep("-263", weightecocodenosmall$"ECOCODE")]=1
272
273 weightecocodenosmall$'262'=rep(0,nrow(weightecocodenosmall))
274 weightecocodenosmall$'262'[grep("-262", weightecocodenosmall$"ECOCODE")]=1
275
276 weightecocodenosmall$'230'=rep(0,nrow(weightecocodenosmall))
277 weightecocodenosmall$'230'[grep("-230", weightecocodenosmall$"ECOCODE")]=1
278
279 weightecocodenosmall$'221'=rep(0,nrow(weightecocodenosmall))
280 weightecocodenosmall$'221'[grep("-221", weightecocodenosmall$"ECOCODE")]=1
281
282 weightecocodenosmall$'211'=rep(0,nrow(weightecocodenosmall))
283 weightecocodenosmall$'211'[grep("-211", weightecocodenosmall$"ECOCODE")]=1
284
285 ##Calculate proportion of diet, locomotion and body size per habitat
286 #calculation proportions for locomotion per habitat
287 ecocode.weightnosmall.results.loc=sapply(9:21, function(x) {
288   a=table(subset(weightecocodenosmall, weightecocodenosmall[,x]==1)[,"Locomotion"])
289 })

```

```

290 colnames(ecocode.weightnosmall.results.loc)=c("Semi-Desert","Semi-Desert","Semi-
291 Desert","Desert","Desert","Grassland","Grassland","Grassland","Woodland","Woodland","F
292 orest","Forest","Forest") #name headings of columns to appropriate habitat
293 ecocode.weightnosmall.loc=prop.table(ecocode.weightnosmall.results.loc, margin=2)
294 weighted.nosmall.loc=t(ecocode.weightnosmall.loc)
295 write.csv(weighted.nosmall.loc, file = "weighted.nosmall.loc.csv")
296
297 #calculate proportions for diet per habitat
298 ecocode.weightnosmall.results.diet=sapply(9:21, function(x) {
299   c=table(subset(weightecocodenosmall, weightecocodenosmall[,x]==1), "Diet")
300 })
301 colnames(ecocode.weightnosmall.results.diet)=c("Semi-Desert","Semi-Desert","Semi-
302 Desert","Desert","Desert","Grassland","Grassland","Grassland","Woodland","Woodland","F
303 orest","Forest","Forest")#name headings of columns to appropriate habitat
304 ecocode.weightnosmall.diet=prop.table(ecocode.weightnosmall.results.diet, margin=2)
305 weighted.nosmall.diet=t(ecocode.weightnosmall.diet)
306 write.csv(weighted.nosmall.diet, file = "weighted.nosmall.diet.csv")
307
308 #calculate proportions for body size per habitat
309 ecocode.weightnosmall.results.size=sapply(9:21, function(x) {
310   e=table(subset(weightecocodenosmall, weightecocodenosmall[,x]==1), "Body.Class")
311 })
312 colnames(ecocode.weightnosmall.results.size)=c("Semi-Desert","Semi-Desert","Semi-
313 Desert","Desert","Desert","Grassland","Grassland","Grassland","Woodland","Woodland","F
314 orest","Forest","Forest")#name headings of columns to appropriate habitat
315 ecocode.weightnosmall.size=prop.table(ecocode.weightnosmall.results.size, margin=2)
316 weighted.nosmall.size=t(ecocode.weightnosmall.size)
317 write.csv(weighted.nosmall.size, file = "weighted.nosmall.size.csv")
318
319 weightnosmall.ecocode<-rbind(ecocode.weightnosmall.size, ecocode.weightnosmall.loc,
320 ecocode.weightnosmall.diet)
321 weighted.nosmall <-t(weightnosmall.ecocode)
322 write.csv(weighted.nosmall, file = "weighted.nosmall.csv")
323
324 ##Unweighted, Rodents
325 rodentecocode=read.csv("Unweighted Rodents.csv")
326
327 rodentecocode$'340'=rep(0,nrow(rodentecocode))
328 rodentecocode$'340'[grep("-340", rodentecocode$"ECOCODE")]=1
329
330 rodentecocode$'332'=rep(0,nrow(rodentecocode))
331 rodentecocode$'332'[grep("-332", rodentecocode$"ECOCODE")]=1
332
333 rodentecocode$'331'=rep(0,nrow(rodentecocode))
334 rodentecocode$'331'[grep("-331", rodentecocode$"ECOCODE")]=1
335
336 rodentecocode$'323'=rep(0,nrow(rodentecocode))
337 rodentecocode$'323'[grep("-323", rodentecocode$"ECOCODE")]=1
338

```



```

339 rodentecocode$'321'=rep(0,nrow(rodentecocode))
340 rodentecocode$'321'[grep("-321", rodentecocode$"ECOCODE")]=1
341
342 rodentecocode$'314'=rep(0,nrow(rodentecocode))
343 rodentecocode$'314'[grep("-314", rodentecocode$"ECOCODE")]=1
344
345 rodentecocode$'311'=rep(0,nrow(rodentecocode))
346 rodentecocode$'311'[grep("-311", rodentecocode$"ECOCODE")]=1
347
348 rodentecocode$'251'=rep(0,nrow(rodentecocode))
349 rodentecocode$'251'[grep("-251", rodentecocode$"ECOCODE")]=1
350
351 rodentecocode$'263'=rep(0,nrow(rodentecocode))
352 rodentecocode$'263'[grep("-263", rodentecocode$"ECOCODE")]=1
353
354 rodentecocode$'262'=rep(0,nrow(rodentecocode))
355 rodentecocode$'262'[grep("-262", rodentecocode$"ECOCODE")]=1
356
357 rodentecocode$'230'=rep(0,nrow(rodentecocode))
358 rodentecocode$'230'[grep("-230", rodentecocode$"ECOCODE")]=1
359
360 rodentecocode$'221'=rep(0,nrow(rodentecocode))
361 rodentecocode$'221'[grep("-221", rodentecocode$"ECOCODE")]=1
362
363 rodentecocode$'211'=rep(0,nrow(rodentecocode))
364 rodentecocode$'211'[grep("-211", rodentecocode$"ECOCODE")]=1
365
366 ##Calculate proportion of diet, locomotion and body size per habitat
367 #calculation proportions for locomotion per habitat
368 ecocode.rodent.results.loc=sapply(8:20, function(x) {
369   a=table(subset(rodentecocode, rodentecocode[,x]==1)[, "Locomotion"])
370 })
371 colnames(ecocode.rodent.results.loc)=c("Semi-Desert", "Semi-Desert", "Semi-
372 Desert", "Desert", "Desert", "Grassland", "Grassland", "Grassland", "Woodland", "Woodland", "F
373 orest", "Forest", "Forest") #name headings of columns to appropriate habitat
374 ecocode.rodent.loc=prop.table(ecocode.rodent.results.loc, margin=2)
375 unweighted.rodent.total.loc=t(ecocode.rodent.loc)
376 write.csv(unweighted.rodent.total.loc, file = "unweighted.rodent.loc.csv")
377
378 #calculate proportions for diet per habitat
379 ecocode.rodent.results.diet=sapply(8:20, function(x) {
380   c=table(subset(rodentecocode, rodentecocode[,x]==1)[, "Diet"])
381 })
382 colnames(ecocode.rodent.results.diet)=c("Semi-Desert", "Semi-Desert", "Semi-
383 Desert", "Desert", "Desert", "Grassland", "Grassland", "Grassland", "Woodland", "Woodland", "F
384 orest", "Forest", "Forest") #name headings of columns to appropriate habitat
385 ecocode.rodent.diet=prop.table(ecocode.rodent.results.diet, margin=2)
386 unweighted.rodent.total.diet=t(ecocode.rodent.diet)
387 write.csv(unweighted.rodent.total.diet, file = "unweighted.rodent.diet.csv")

```

```

388
389 #calculate proportions for body size per habitat
390 ecocode.rodent.results.size=sapply(8:20, function(x) {
391   e=table(subset(rodentecocode, rodentecocode[,x]==1)[,"Body.Class"])
392 })
393 colnames(ecocode.rodent.results.size)=c("Semi-Desert", "Semi-Desert", "Semi-
394 Desert", "Desert", "Desert", "Grassland", "Grassland", "Grassland", "Woodland", "Woodland", "F
395 orest", "Forest", "Forest")#name headings of columns to appropriate habitat
396 ecocode.rodent.size=prop.table(ecocode.rodent.results.size, margin=2)
397 unweighted.rodent.total.size=t(ecocode.rodent.size)
398 write.csv(unweighted.rodent.total.size, file = "unweighted.rodent.size.csv")
399
400 unweighted.rodent.ecocode<-rbind(ecocode.rodent.size, ecocode.rodent.diet,
401 ecocode.rodent.loc)
402 unweighted.rodent.total<-t(unweighted.rodent.ecocode)
403 write.csv(unweighted.rodent.total, file = "unweighted.rodent.csv")
404
405 ##Unweighted, Rodents
406 norodentecocode=read.csv("Unweighted No Rodents.csv")
407
408 norodentecocode$'340'=rep(0,nrow(norodentecocode))
409 norodentecocode$'340'[grep("-340", norodentecocode$"ECOCODE")]=1
410
411 norodentecocode$'332'=rep(0,nrow(norodentecocode))
412 norodentecocode$'332'[grep("-332", norodentecocode$"ECOCODE")]=1
413
414 norodentecocode$'331'=rep(0,nrow(norodentecocode))
415 norodentecocode$'331'[grep("-331", norodentecocode$"ECOCODE")]=1
416
417 norodentecocode$'323'=rep(0,nrow(norodentecocode))
418 norodentecocode$'323'[grep("-323", norodentecocode$"ECOCODE")]=1
419
420 norodentecocode$'321'=rep(0,nrow(norodentecocode))
421 norodentecocode$'321'[grep("-321", norodentecocode$"ECOCODE")]=1
422
423 norodentecocode$'314'=rep(0,nrow(norodentecocode))
424 norodentecocode$'314'[grep("-314", norodentecocode$"ECOCODE")]=1
425
426 norodentecocode$'311'=rep(0,nrow(norodentecocode))
427 norodentecocode$'311'[grep("-311", norodentecocode$"ECOCODE")]=1
428
429 norodentecocode$'251'=rep(0,nrow(norodentecocode))
430 norodentecocode$'251'[grep("-251", norodentecocode$"ECOCODE")]=1
431
432 norodentecocode$'263'=rep(0,nrow(norodentecocode))
433 norodentecocode$'263'[grep("-263", norodentecocode$"ECOCODE")]=1
434
435 norodentecocode$'262'=rep(0,nrow(norodentecocode))
436 norodentecocode$'262'[grep("-262", norodentecocode$"ECOCODE")]=1

```

```

437
438 norodentecocode$'230'=rep(0,nrow(norodentecocode))
439 norodentecocode$'230'[grep("-230", norodentecocode$"ECOCODE")]=1
440
441 norodentecocode$'221'=rep(0,nrow(norodentecocode))
442 norodentecocode$'221'[grep("-221", norodentecocode$"ECOCODE")]=1
443
444 norodentecocode$'211'=rep(0,nrow(norodentecocode))
445 norodentecocode$'211'[grep("-211", norodentecocode$"ECOCODE")]=1
446
447 ##Calculate proportion of diet, locomotion and body size per habitat
448 #calculation proportions for locomotion per habitat
449 ecocode.norodent.results.loc=sapply(8:20, function(x) {
450   a=table(subset(norodentecocode, norodentecocode[,x]==1)[, "Locomotion"])
451 })
452 colnames(ecocode.norodent.results.loc)=c("Semi-Desert", "Semi-Desert", "Semi-
453 Desert", "Desert", "Desert", "Grassland", "Grassland", "Grassland", "Woodland", "Woodland", "F
454 orest", "Forest", "Forest") #name headings of columns to appropriate habitat
455 ecocode.norodent.loc=prop.table(ecocode.norodent.results.loc, margin=2)
456 unweighted.norodent.total.loc=t(ecocode.norodent.loc)
457 write.csv(unweighted.norodent.total.loc, file = "unweighted.norodent.loc.csv")
458
459 #calculate proportions for diet per habitat
460 ecocode.norodent.results.diet=sapply(8:20, function(x) {
461   c=table(subset(norodentecocode, norodentecocode[,x]==1)[, "Diet"])
462 })
463 colnames(ecocode.norodent.results.diet)=c("Semi-Desert", "Semi-Desert", "Semi-
464 Desert", "Desert", "Desert", "Grassland", "Grassland", "Grassland", "Woodland", "Woodland", "F
465 orest", "Forest", "Forest") #name headings of columns to appropriate habitat
466 ecocode.norodent.diet=prop.table(ecocode.norodent.results.diet, margin=2)
467 unweighted.norodent.total.diet=t(ecocode.norodent.diet)
468 write.csv(unweighted.norodent.total.diet, file = "unweighted.norodent.diet.csv")
469
470 #calculate proportions for body size per habitat
471 ecocode.norodent.results.size=sapply(8:20, function(x) {
472   e=table(subset(norodentecocode, norodentecocode[,x]==1)[, "Body.Class"])
473 })
474 colnames(ecocode.norodent.results.size)=c("Semi-Desert", "Semi-Desert", "Semi-
475 Desert", "Desert", "Desert", "Grassland", "Grassland", "Grassland", "Woodland", "Woodland", "F
476 orest", "Forest", "Forest") #name headings of columns to appropriate habitat
477 ecocode.norodent.size=prop.table(ecocode.norodent.results.size, margin=2)
478 unweighted.norodent.total.size=t(ecocode.norodent.size)
479 write.csv(unweighted.norodent.total.size, file = "unweighted.norodent.size.csv")
480
481 unweighted.norodent.ecocode<-rbind(ecocode.norodent.size, ecocode.norodent.diet,
482 ecocode.norodent.loc)
483 unweighted.norodent.total<-t(unweighted.norodent.ecocode)
484 write.csv(unweighted.norodent.total, file = "unweighted.norodent.csv")

```

M3: Script to generate principle component analyses charts from the trait frequency

proportions.

```

1 install.packages('svglite')
2 library('svglite')
3 install.packages("ggplot2")
4 install.packages("ggbiplot")
5 library('ggplot2')
6 library('ggbiplot')
7 install.packages("devtools")
8 library('devtools')
9 install_github("vqv/ggbiplot")
10
11 ##Principle Components
12 #Unweighted-Total
13 unweightedtotal=read.csv("unweighted.total.csv")
14 data.class <- unweightedtotal[,1]
15 data.pca <- prcomp(unweightedtotal[,2:24], scale. = TRUE)
16 unweighted.total.pca <- data.pca
17 unweighted.total.pca.loadings <-print(unweighted.total.pca)
18 print(unweighted.total.pca$x)
19 #PC1 and PC2
20 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
21             groups = data.class, ellipse = TRUE, circle = TRUE)
22 g <- g + scale_color_discrete(name = "")
23 g <- g + theme(legend.direction = 'horizontal',
24             legend.position = 'top')
25 print(g)
26 unweightedtotalpca<-g
27 ggsave(filename = "unweighted.total.svg",plot=unweightedtotalpca, width = 10, height = 8)
28
29 #Unweighted-No Small
30 unweightedtotalnosmall =read.csv("unweighted.nosmall.csv")
31 data.class <- unweightedtotalnosmall[,1]
32 data.pca <- prcomp(unweightedtotalnosmall[,2:21], scale. = TRUE)
33 unweighted.total.nosmall.pca <- data.pca
34 unweighted.total.nosmall.pca.loadings <-print(unweighted.total.nosmall.pca)
35 print(unweighted.total.nosmall.pca$x)
36 #PC1 and PC2
37 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
38             groups = data.class, ellipse = TRUE, circle = TRUE)
39 g <- g + scale_color_discrete(name = "")
40 g <- g + theme(legend.direction = 'horizontal',
41             legend.position = 'top')
42 print(g)
43 unweightedtotalnosmallpcanew <-g

```

```

44 ggsave(filename = "unweighted.nosmall.new.svg",plot=unweightedtotalnosmallpca,
45 width = 10, height = 8)
46
47 #Weighted-Total
48 weightedtotal =read.csv("weighted.total.csv")
49 data.class <- weightedtotal[,1]
50 data.pca <- prcomp(weightedtotal[,2:24], scale. = TRUE)
51 weight.total.pca <- data.pca
52 weight.total.pca.loadings <-print(weight.total.pca)
53 #PC1 and PC2
54 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
55             groups = data.class, ellipse = TRUE, circle = TRUE)
56 g <- g + scale_color_discrete(name = "")
57 g <- g + theme(legend.direction = 'horizontal',
58             legend.position = 'top')
59 print(g)
60 weightedtotalpca <- g
61 ggsave(filename = "weighted.total.svg",plot=weightedtotalpca, width = 10, height = 8)
62
63 #Weighted-No Small
64 weightednosmall =read.csv("weighted.nosmall.csv")
65 data.class <- weightednosmall[,1]
66 data.pca <- prcomp(weightednosmall[,2:21], scale. = TRUE)
67 weight.nosmall.pca <- data.pca
68 weight.nosmall.pca.loadings <-print(weight.nosmall.pca)
69 print(weight.nosmall.pca$x)
70 #PC1 and PC2
71 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
72             groups = data.class, ellipse = TRUE, circle = TRUE)
73 g <- g + scale_color_discrete(name = "")
74 g <- g + theme(legend.direction = 'horizontal',
75             legend.position = 'top')
76 print(g)
77 weightednosmall<-g
78 ggsave(filename = "weighted.nosmall.svg",plot=weightednosmall, width = 10, height = 8)
79
80 ##Taxonomically Grouping
81 #Unweighted-Rodents
82 unweightedrodent=read.csv("unweighted.rodent.csv")
83 data.class <- unweightedrodent[,1]
84 data.pca <- prcomp(unweightedrodent[,2:19], scale. = TRUE)
85 unweighted.rodent.pca <- data.pca
86 unweighted.rodent.pca.loadings <-print(unweighted.rodent.pca)
87 unweighted.rodent.scores<- print(unweighted.rodent.pca$x)
88 #PC1 and PC2
89 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
90             groups = data.class, ellipse = TRUE, circle = TRUE)
91 g <- g + scale_color_discrete(name = "")
92 g <- g + theme(legend.direction = 'horizontal',

```

```

93     legend.position = 'top')
94 print(g)
95 unweightedrodentpca2<-g
96 ggsave(filename = "unweighted.rodent2.svg",plot=unweightedrodentpca2, width = 10, height
97 = 8)
98
99 #Unweighted No Rodents
100 unweightednorodent=read.csv("unweighted.norodent.csv")
101 data.class <- unweightednorodent[,1]
102 data.pca <- prcomp(unweightednorodent[,2:19], scale. = TRUE)
103 unweighted.norodent.pca <- data.pca
104 unweighted.norodent.pca.loadings <-print(unweighted.norodent.pca)
105 #PC1 and PC2
106 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
107     groups = data.class, ellipse = TRUE, circle = TRUE)
108 g <- g + scale_color_discrete(name = "")
109 g <- g + theme(legend.direction = 'horizontal',
110     legend.position = 'top')
111 print(g)
112 unweightednorodentpca<-g
113 ggsave(filename = "unweighted.norodent.svg",plot=unweightednorodentpca, width = 10,
114 height = 8)
115
116 ###Individual Traits
117 #Unweighted-Locomotion
118 unweightedtotalloc =read.csv("unweighted.total.loc.csv")
119 data.class <- unweightedtotalloc[,1]
120 data.pca <- prcomp(unweightedtotalloc[,2:8], scale. = TRUE)
121 unweighted.total.loc.pca <- data.pca
122 unweighted.total.loc.pca.loadings <-print(unweighted.total.loc.pca)
123 #PC1 and PC2
124 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
125     groups = data.class, ellipse = TRUE, circle = TRUE)
126 g<- g + scale_color_discrete(name = "")
127 g <- g + theme(legend.direction = 'horizontal',
128     legend.position = 'top')
129 print(g)
130 unweightttotallocpca<-g
131 ggsave(filename = "unweighted.total.loc.svg",plot=unweightttotallocpca, width = 10, height =
132 8)
133
134 #Unweighted-Diet
135 unweightedtotaldiet =read.csv("unweighted.total.diet.csv")
136 data.class <- unweightedtotaldiet[,1]
137 data.pca <- prcomp(unweightedtotaldiet[,2:10], scale. = TRUE)
138 unweighted.total.diet.pca <- data.pca
139 unweighted.total.diet.pca.loadings <-print(unweighted.total.diet.pca)
140 #PC1 and PC2
141 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,

```

```
142     groups = data.class, ellipse = TRUE, circle = TRUE)
143 g<- g + scale_color_discrete(name = "")
144 g <- g + theme(legend.direction = 'horizontal',
145     legend.position = 'top')
146 print(g)
147 unweighttotaldietpca<-g
148 ggsave(filename = "unweighted.total.diet.svg",plot=unweighttotaldietpca, width = 10, height
149 = 8)
150
151 #Unweighted-Size
152 unweightedtotalsize =read.csv("unweighted.total.size.csv")
153 data.class <- unweightedtotalsize[,1]
154 data.pca <- prcomp(unweightedtotalsize[,2:8], scale. = TRUE)
155 unweighted.total.size.pca <- data.pca
156 unweighted.total.size.pca.loadings <-print(unweighted.total.size.pca)
157 #PC1 and PC2
158 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
159     groups = data.class, ellipse = TRUE, circle = TRUE)
160 g<- g + scale_color_discrete(name = "")
161 g <- g + theme(legend.direction = 'horizontal',
162     legend.position = 'top')
163 print(g)
164 unweighttotalsizepca<-g
165 ggsave(filename = "unweighted.total.size.svg",plot=unweighttotalsizepca, width = 10, height
166 = 8)
167
168 #Unweighted-No Small - Loc
169 unweightednosmallloc =read.csv("unweighted.nosmall.loc.csv")
170 data.class <- unweightednosmallloc[,1]
171 data.pca <- prcomp(unweightednosmallloc[,2:8], scale. = TRUE)
172 unweighted.nosmall.loc.pca <- data.pca
173 unweighted.nosmall.loc.pca.loadings <-print(unweighted.nosmall.loc.pca)
174 #PC1 and PC2
175 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
176     groups = data.class, ellipse = TRUE, circle = TRUE)
177 g<- g + scale_color_discrete(name = "")
178 g <- g + theme(legend.direction = 'horizontal',
179     legend.position = 'top')
180 print(g)
181 unweightnosmalllocpca<-g
182 ggsave(filename = "unweighted.nosmall.loc.svg",plot=unweightnosmalllocpca, width = 10,
183 height = 8)
184
185 #Unweighted-No Small - Diet
186 unweightednosmalldiet =read.csv("unweighted.nosmall.diet.csv")
187 data.class <- unweightednosmalldiet[,1]
188 data.pca <- prcomp(unweightednosmalldiet[,2:9], scale. = TRUE)
189 unweighted.nosmall.diet.pca <- data.pca
190 unweighted.nosmall.diet.pca.loadings <-print(unweighted.nosmall.diet.pca)
```

```

191 #PC1 and PC2
192 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
193               groups = data.class, ellipse = TRUE, circle = TRUE)
194 g<- g + scale_color_discrete(name = "")
195 g <- g + theme(legend.direction = 'horizontal',
196               legend.position = 'top')
197 print(g)
198 unweightnosmalldietpca<-g
199 ggsave(filename = "unweighted.nosmall.diet.svg",plot=unweightnosmalldietpca, width = 10,
200 height = 8)
201
202 #Unweighted-No Small - Size
203 unweightednosmallsize =read.csv("unweighted.nosmall.size.csv")
204 data.class <- unweightednosmallsize[,1]
205 data.pca <- prcomp(unweightednosmallsize[,2:6], scale. = TRUE)
206 unweighted.nosmall.size.pca <- data.pca
207 unweighted.nosmall.size.pca.loadings <-print(unweighted.nosmall.size.pca)
208 #PC1 and PC2
209 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
210               groups = data.class, ellipse = TRUE, circle = TRUE)
211 g<- g + scale_color_discrete(name = "")
212 g <- g + theme(legend.direction = 'horizontal',
213               legend.position = 'top')
214 print(g)
215 unweightnosmallsizepca<-g
216 ggsave(filename = "unweighted.nosmall.size.svg",plot=unweightnosmallsizepca, width = 10,
217 height = 8)
218
219 ##Weighted
220 #Weighted-Locomotion
221 weightedtotalloc =read.csv("weighted.total.loc.csv")
222 data.class <- weightedtotalloc[,1]
223 data.pca <- prcomp(weightedtotalloc[,2:8], scale. = TRUE)
224 weighted.total.loc.pca <- data.pca
225 weighted.total.loc.pca.loadings <-print(weighted.total.loc.pca)
226 #PC1 and PC2
227 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
228               groups = data.class, ellipse = TRUE, circle = TRUE)
229 g<- g + scale_color_discrete(name = "")
230 g <- g + theme(legend.direction = 'horizontal',
231               legend.position = 'top')
232 print(g)
233 weighttotallocpca<-g
234 ggsave(filename = "weighted.total.loc.svg",plot=weighttotallocpca, width = 10, height = 8)
235
236 #Unweighted-Diet
237 weightedtotaldiet =read.csv("weighted.total.diet.csv")
238 data.class <- weightedtotaldiet[,1]
239 data.pca <- prcomp(weightedtotaldiet[,2:10], scale. = TRUE)

```



```

240 weighted.total.diet.pca <- data.pca
241 weighted.total.diet.pca.loadings <-print(weighted.total.diet.pca)
242 #PC1 and PC2
243 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
244             groups = data.class, ellipse = TRUE, circle = TRUE)
245 g<- g + scale_color_discrete(name = "")
246 g <- g + theme(legend.direction = 'horizontal',
247             legend.position = 'top')
248 print(g)
249 weighttotaldietpca<-g
250 ggsave(filename = "weighted.total.diet.svg",plot=weighttotaldietpca, width = 10, height = 8)
251
252 #Weighted-Size
253 weightedtotalsize =read.csv("weighted.total.size.csv")
254 data.class <- weightedtotalsize[,1]
255 data.pca <- prcomp(weightedtotalsize[,2:8], scale. = TRUE)
256 weighted.total.size.pca <- data.pca
257 weighted.total.size.pca.loadings <-print(weighted.total.size.pca)
258 #PC1 and PC2
259 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
260             groups = data.class, ellipse = TRUE, circle = TRUE)
261 g<- g + scale_color_discrete(name = "")
262 g <- g + theme(legend.direction = 'horizontal',
263             legend.position = 'top')
264 print(g)
265 weighttotalsizepca<-g
266 ggsave(filename = "weighted.total.size.svg",plot=weighttotalsizepca, width = 10, height = 8)
267
268 #Weighted-No Small - Loc
269 weightednosmallloc =read.csv("weighted.nosmall.loc.csv")
270 data.class <- weightednosmallloc[,1]
271 data.pca <- prcomp(weightednosmallloc[,2:8], scale. = TRUE)
272 weighted.nosmall.loc.pca <- data.pca
273 weighted.nosmall.loc.pca.loadings <-print(weighted.nosmall.loc.pca)
274 #PC1 and PC2
275 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
276             groups = data.class, ellipse = TRUE, circle = TRUE)
277 g<- g + scale_color_discrete(name = "")
278 g <- g + theme(legend.direction = 'horizontal',
279             legend.position = 'top')
280 print(g)
281 weightnosmalllocpca<-g
282 ggsave(filename = "weighted.nosmall.loc.svg",plot=weightnosmalllocpca, width = 10, height
283 = 8)
284
285 #Weighted-No Small - Diet
286 weightednosmalldiet =read.csv("weighted.nosmall.diet.csv")
287 data.class <- weightednosmalldiet[,1]
288 data.pca <- prcomp(weightednosmalldiet[,2:9], scale. = TRUE)

```

```
289 weighted.nosmall.diet.pca <- data.pca
290 weighted.nosmall.diet.pca.loadings <- print(weighted.nosmall.diet.pca)
291 #PC1 and PC2
292 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
293             groups = data.class, ellipse = TRUE, circle = TRUE)
294 g <- g + scale_color_discrete(name = "")
295 g <- g + theme(legend.direction = 'horizontal',
296             legend.position = 'top')
297 print(g)
298 weightnosmalldietpca <- g
299 ggsave(filename = "weighted.nosmall.diet.svg", plot = weightnosmalldietpca, width = 10,
300 height = 8)
301
302 #Weighted-No Small - Size
303 weightednosmallsize = read.csv("weighted.nosmall.size.csv")
304 data.class <- weightednosmallsize[,1]
305 data.pca <- prcomp(weightednosmallsize[,2:6], scale. = TRUE)
306 weighted.nosmall.size.pca <- data.pca
307 weighted.nosmall.size.pca.loadings <- print(weighted.nosmall.size.pca)
308 #PC1 and PC2
309 g <- ggbiplot(data.pca, obs.scale = 1, var.scale = 1,
310             groups = data.class, ellipse = TRUE, circle = TRUE)
311 g <- g + scale_color_discrete(name = "")
312 g <- g + theme(legend.direction = 'horizontal',
313             legend.position = 'top')
314 print(g)
315 weightnosmallsizepca <- g
316 ggsave(filename = "weighted.nosmall.size.svg", plot = weightnosmallsizepca, width = 10,
317 height = 8)
```

APPENDIX-B

Table A1. Description of traits assigned to North American species.

Table A1a: Description of Diet categories. Percentages gathered from Wilman *et al.*, 2014.

Diet	Description
Browser	Predominantly leaves and branches/tree material
Grazer	Predominantly grass and sedges
Mixed Feeder	Equal parts grass/sedges, leaves, and branch/tree material
Frugivore	Fruit; 40-50% or more observed in diet
Granivore	Grains and seeds; 40-50% or more observed in diet
Folivore	Plant Material such as grass, ground vegetation, seedlings, weeds, lichen, moss, small plants, reeds, cultivated crops, forbs, vegetables, fungi, roots, tubers, legumes, bulbs, leaves, above ground vegetation, twigs, bark, shrubs, herbs, shoots, aquatic vegetation, aquatic plants; 40-50% observed in diet
Herbivore	Diet contains an equal mix of herbivorous materials so one majority cannot be determined
Omnivore	Diet contains a mix of invertebrates, vertebrates (incl. scavenging), and herbivorous material
Carnivore	Diet contains majority of vertebrate animals (mammals, reptiles, fish, and scavenging) or insects/invertebrate animals.

Table A1b: Description of Locomotion categories. Gathered from NatureServe and Walkers Mammals of the World 6th Ed. (Nowak 1999a; Nowak 1999b)

Locomotion	Description
Ambulatory	Plantigrade; Moves slowly unless provoked
Aquatic/Semi-Aquatic	Majority of life in water; hunts in water or on land
Arboreal/Scansorial	Majority of life in trees / Terrestrial and climbs trees to nest or eat
Cursorial	Digitigrade and unguligrade
Fossorial	Lives majority of life in burrows; hunts in burrows
Non-Cursorial	Spends majority of life on the ground but is neither cursorial nor ambulatory
Semi-Fossorial	Spends inactive time in burrows; hunts on surface and in burrows

Table A1c: Description of Body Class categories.

Body Class	Body Mass Range
A	0 – 50 g
B	50 – 500 g
C	500 - 1000 g
D	1000 – 1500 g
E	1500 - 3500 g
F	3500 - 10500 g
G	>10500 g

Table A2: List of original and updated taxonomic names. An 'x' indicates whether the original species name was replaced with the updated name.

Original Taxa	Updated Taxa	Replaced
<i>Alces alces</i>	<i>Alces americanus</i>	
<i>Alopex lagopus</i>	<i>Vulpes lagopus</i>	
<i>Lepus floridanus</i>	<i>Sylvilagus floridanus</i>	x
<i>Lepus nuttalli</i>	<i>Sylvilagus nuttallii</i>	x
<i>Lepus palustris</i>	<i>Sylvilagus palustris</i>	x
<i>Lepus sylvaticus</i>	<i>Sylvilagus floridanus</i>	x
<i>Lynx subsolanus</i>	<i>Lynx canadensis</i>	x
<i>Marmosa canescens</i>	<i>Tlacuatzin canescens</i>	x
<i>Martes pennanti</i>	<i>Pekania pennanti</i>	
<i>Neurotrichus trowbridgei</i>	<i>Sorex trowbridgii</i>	x
<i>Perognathus apache</i>	<i>Perognathus flavescens</i>	x
<i>Perognathus californicus</i>	<i>Chaetodipus californicus</i>	
<i>Perognathus fallax</i>	<i>Chaetodipus fallax</i>	x
<i>Perognathus hispidus</i>	<i>Chaetodipus hispidus</i>	x
<i>Perognathus paradoxus</i>	<i>Chaetodipus hispidus</i>	x
<i>Perognathus penicillatus</i>	<i>Chaetodipus penicillatus</i>	x
<i>Perognathus spinatus</i>	<i>Chaetodipus spinatus</i>	x
<i>Sciurus hudsonius</i>	<i>Tamiasciurus hudsonicus</i>	x
<i>Spermophilus annulatus</i>	<i>Notocitellus annulatus</i>	
<i>Spermophilus beecheyi</i>	<i>Otospermophilus beecheyi</i>	

<i>Spermophilus columbianus</i>	<i>Uroditellus columbianus</i>	
<i>Spermophilus lateralis</i>	<i>Callospermophilus lateralis</i>	
<i>Spermophilus richardsonii</i>	<i>Uroditellus richardsonii</i>	
<i>Spermophilus spilosoma</i>	<i>Xerospermophilus spilosoma</i>	
<i>Spermophilus tridecemlineatus</i>	<i>Ictidomys tridecemlineatus</i>	
<i>Spermophilus variegatus</i>	<i>Otospermophilus variegatus</i>	
<i>Tamias amoenus</i>	<i>Neotamias amoenus</i>	
<i>Tamias cinereicollis</i>	<i>Neotamias cinereicollis</i>	
<i>Tamias dorsalis</i>	<i>Neotamias dorsalis</i>	
<i>Tamias merriami</i>	<i>Neotamias merriami</i>	
<i>Tamias minimus</i>	<i>Neotamias minimus</i>	
<i>Tamias obscurus</i>	<i>Neotamias obscurus</i>	
<i>Tamias ochrogenys</i>	<i>Neotamias ochrogenys</i>	
<i>Tamias quadrivittatus</i>	<i>Neotamias quadrivittatus</i>	
<i>Tamias speciosus</i>	<i>Neotamias speciosus</i>	
<i>Tamias townsendii</i>	<i>Neotamias townsendii</i>	
<i>Zapus insignis</i>	<i>Napaeozapus insignis</i>	x

Table A3: Definition of ecoregions (Bailey, 1995), ordered alphabetically.

Ecoregion	Description
Coastal	Needle leaf forest; Douglas-fir, red cedar, and spruce can grow to magnificent heights
Hot Continental	Winter deciduous forest, dominated by tall broadleaf trees that provide a continuous dense canopy in summer but shed leaves completely in winter; lower layers of small trees and shrubs are weakly developed; in spring, a ground cover of herbs quickly develops but greatly reduced after trees reach full foliage
Mediterranean	Transition between dry west coast desert and the wet west coast; Sclerophyll forest (Hard-leaved evergreen trees and shrubs); sclerophyll woodland and scrub
Prairie	Sub-humid continental climate; Deeply rooted tall grasses associated with subdominant broad-leaved herbs; trees and shrubs almost totally absent but may grow as woodland patches in valleys/depressions
Rainforest	Rainforest/selva type of vegetation unsurpassed in number of species and abundance of tree growth; broadleaf trees form a dense leaf canopy
Savanna	Alternation of wet and dry seasons; open expanses of tall grasses interspersed with hardy, drought-resistant shrubs and trees

Subarctic	A great belt of needle-leaf forest (boreal forest) and open lichen woodland (taiga); most trees are small
Subtropical	Forests; sandy coastal regions covered by second-growth forests of longleaf, loblolly, and slash pines; inland covered by deciduous forests
Temperate Desert	Sparse xerophytic vegetation typical of semi-desert
Temperate Steppe	Semi-arid continental regime where evaporation usually exceeds precipitation; short grasses that usually grow in sparsely distributed bunches; scattered shrubs and low trees; all gradations of cover are present, from semi-desert to woodland
Tropical/Subtropical Desert	Continental desert climates; dry-desert vegetation, xerophytic plants that are widely dispersed and provide negligible ground cover; in dry periods, vegetation limited to small hard-leaved or spiny shrubs, cacti, or hard grasses
Tropical/Subtropical Steppe	Semi-arid steppe climate; grasslands of short grasses and other herbs, with locally developed shrub-and woodland
Tundra	Grasses, sedges, lichens, and willow shrubs; moving south, birch-lichen woodland, then needle-leaf forest.
Warm Continental	Needle-leaf and mixed needle-leaf/deciduous forest

Table A4: Bailey's ecoregions (Bailey 1995) re-assigned to broader biome categories, ordered from closed to open.

Bailey's Ecoregions	Biomes
Subtropical	Forest
Warm Continental	Forest
Hot Continental	Forest
Mediterranean	Woodland
Prairie	Grassland
Tropical/Subtropical Steppe	Grassland
Temperate Desert	Semi-Desert
Temperate Steppe	Semi-Desert
Tropical/Subtropical Desert	Desert

Table A5: Temperate and Precipitation annual averages per biome, averaged from Bailey's ecoregion province climate data (Bailey 1995).

Biome	Temperature (°F)	Precipitation (mm)
Forest	56.6 °F	1100.666667
Woodland	57 °F	999.0666667
Grassland	57.6 °F	706.12
Semi-Desert	50.6 °F	412.75
Desert	62.5 °F	186.055

APPENDIX-C

Figure A1. Map of Bailey's Ecoregions (Rocky Mountain Research Station 1996).

Displaying the geographical ranges of Divisions, which were either trimmed or grouped into larger biomes (Table A4).

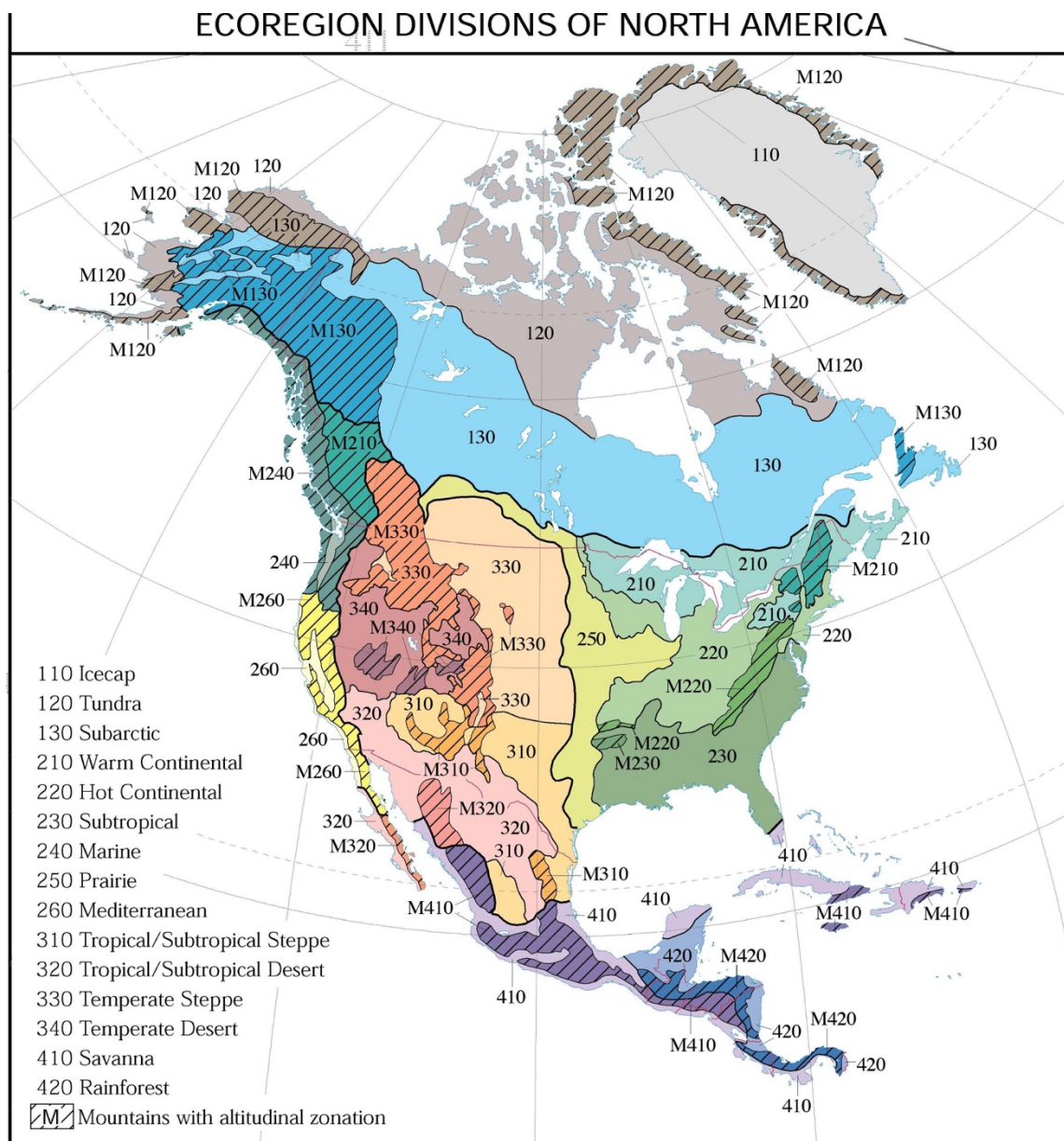


Figure A2. Historical sampling of data included in analyses. Circles indicate the distribution, spread, and density of the historical data collected by AMNH. Larger circles indicate more taxa are present, and smaller circles show less taxa in that region. The colors correspond to Bailey's Divisions, re-assigned to broader biomes (Table A4).

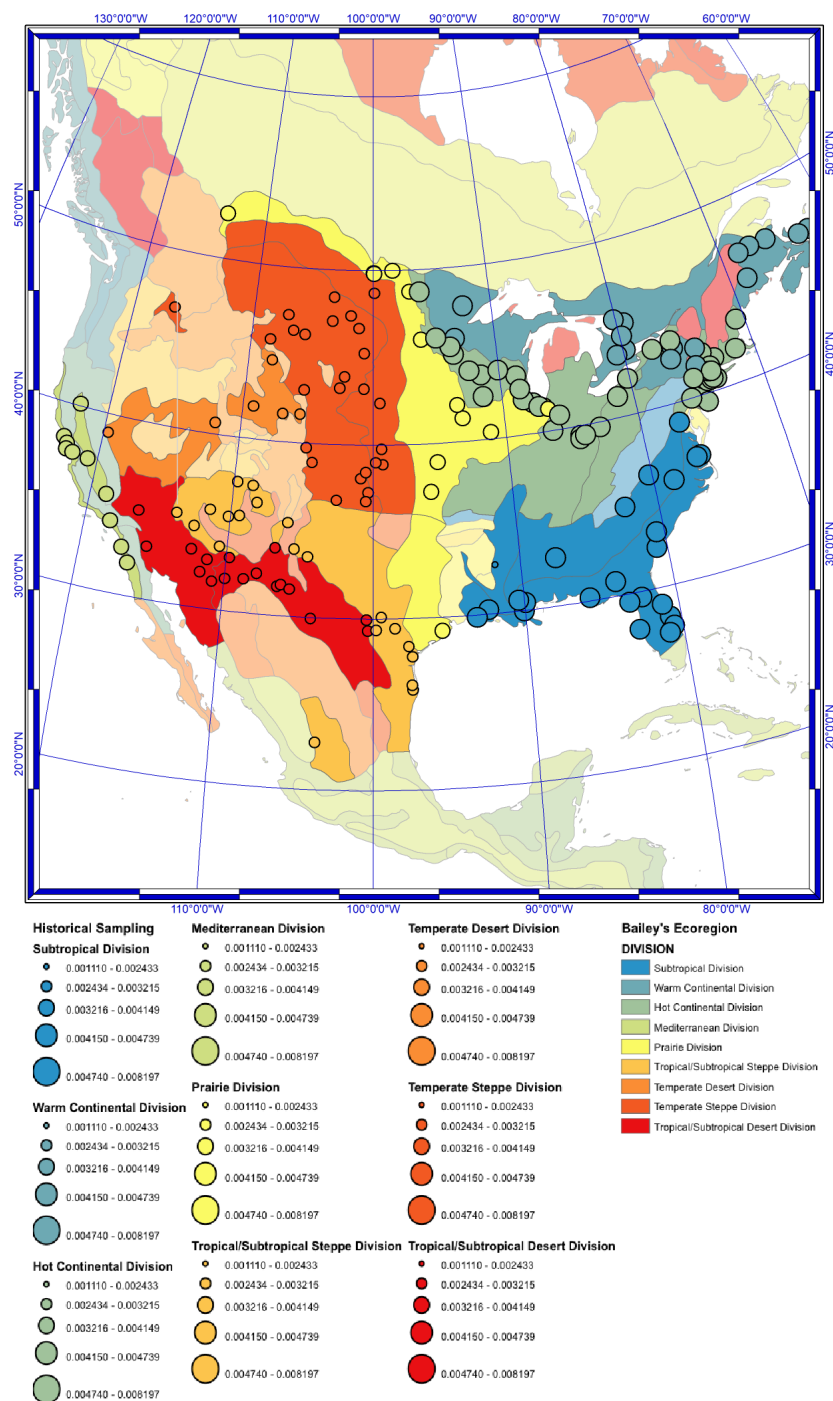


Figure A3: Scatter plot of Principle Component Analysis of size frequencies for unweighted dataset with small body sizes removed (A & B). PC1 (37.3% variance) on x-axis, PC2 (29.7%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 10), displayed on PC1 and PC2 for positive and negative loadings.

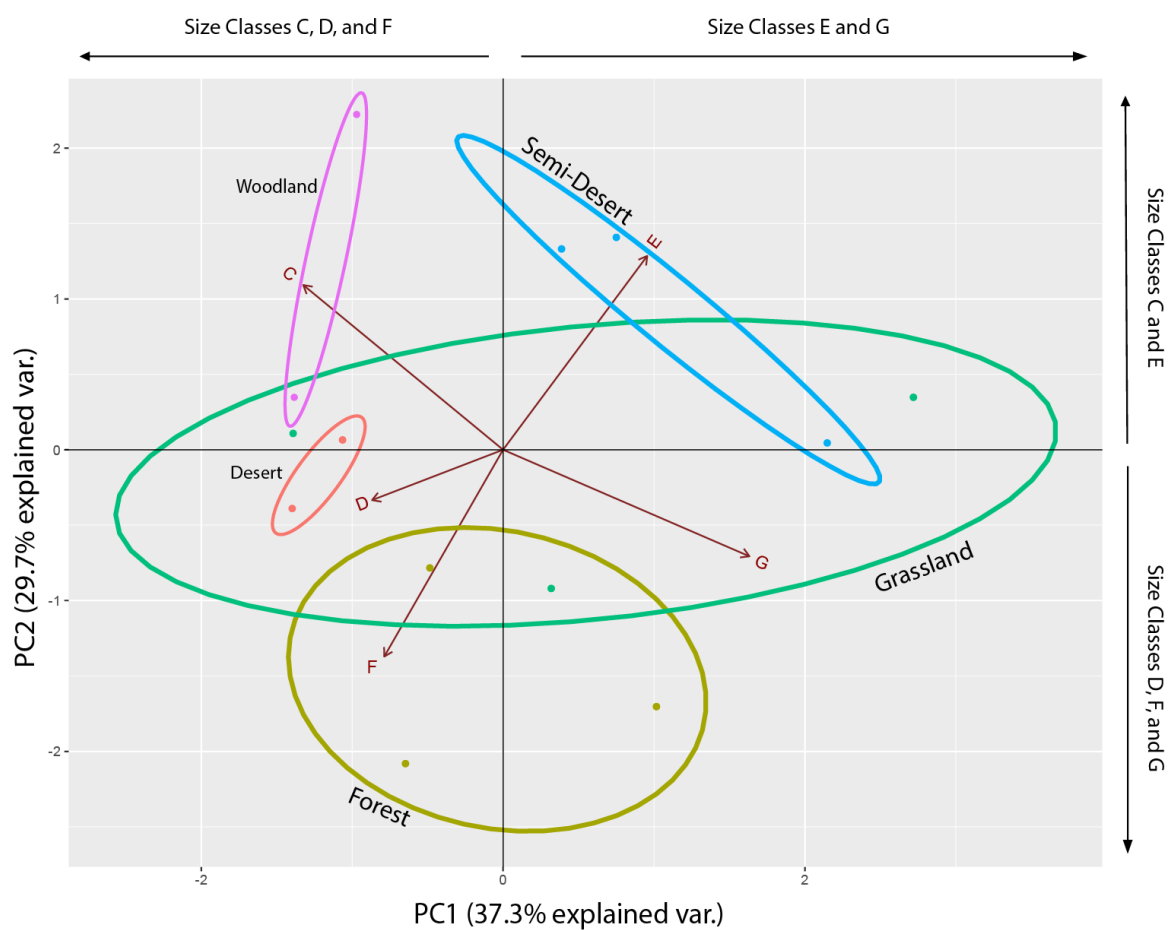


Figure A4: Scatter plot of Principle Component Analysis of diet frequencies for weighted dataset with small body sizes removed (A & B). PC1 (323.8% variance) on x-axis, PC2 (21.3%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 13), displayed on PC1 and PC2 for positive and negative loadings.

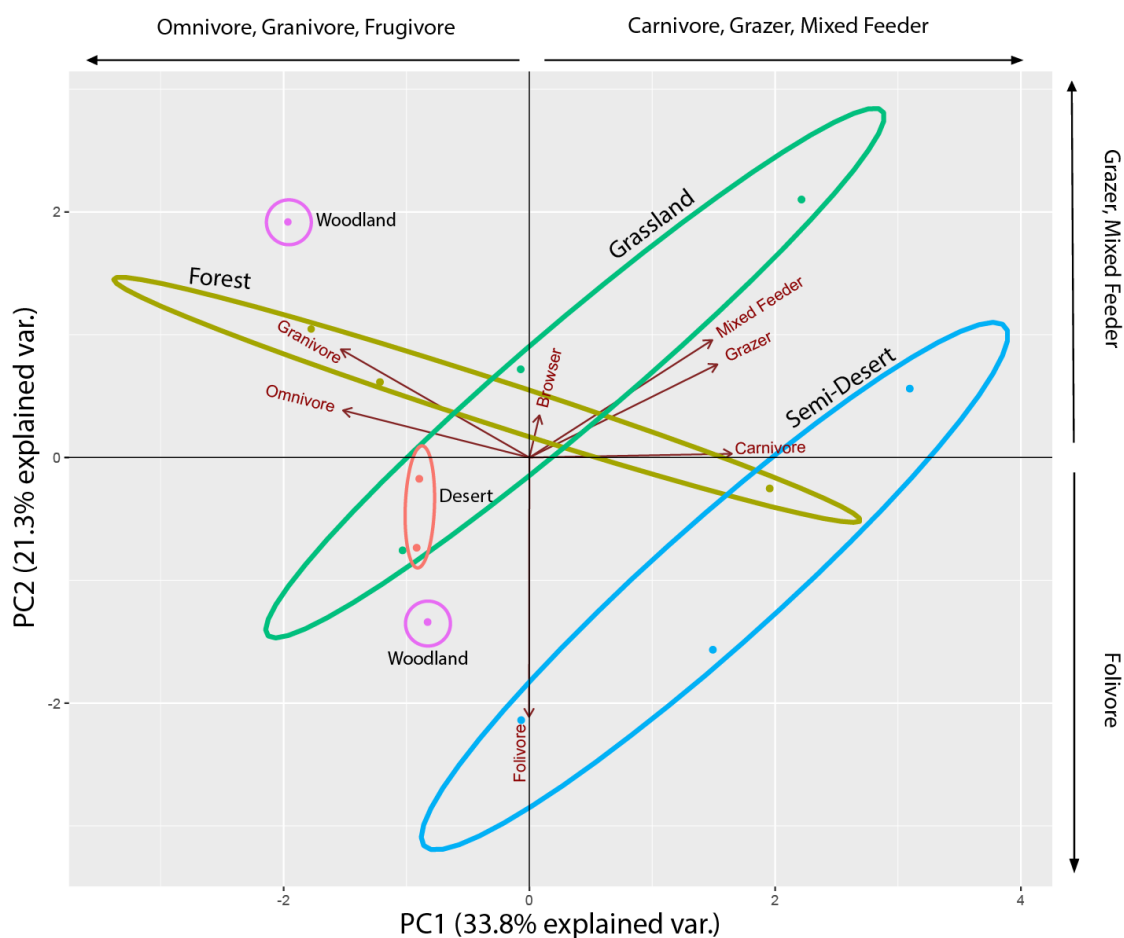


Figure A5: Scatter plot of Principle Component Analysis of size frequencies for weighted dataset with small body sizes removed (A & B). PC1 (40.8% variance) on x-axis, PC2 (31.7%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 14), displayed on PC1 and PC2 for positive and negative loadings.

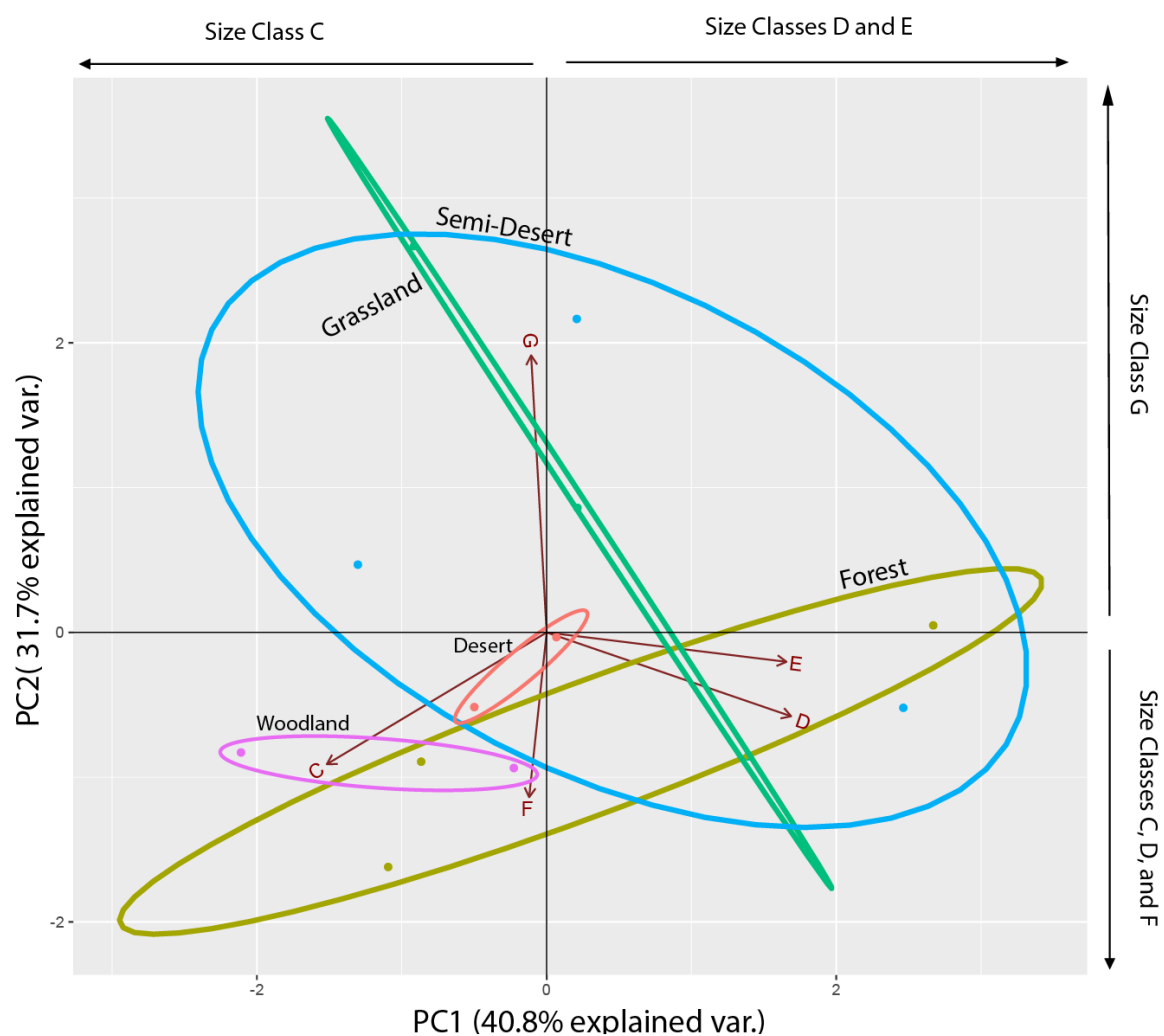


Figure A6: Scatter plot of Principle Component Analysis of all trait frequencies for total unweighted dataset. PC1 (29.3% variance) on x-axis, PC2 (17%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 15), displayed on PC1 and PC2 for positive and negative loadings.

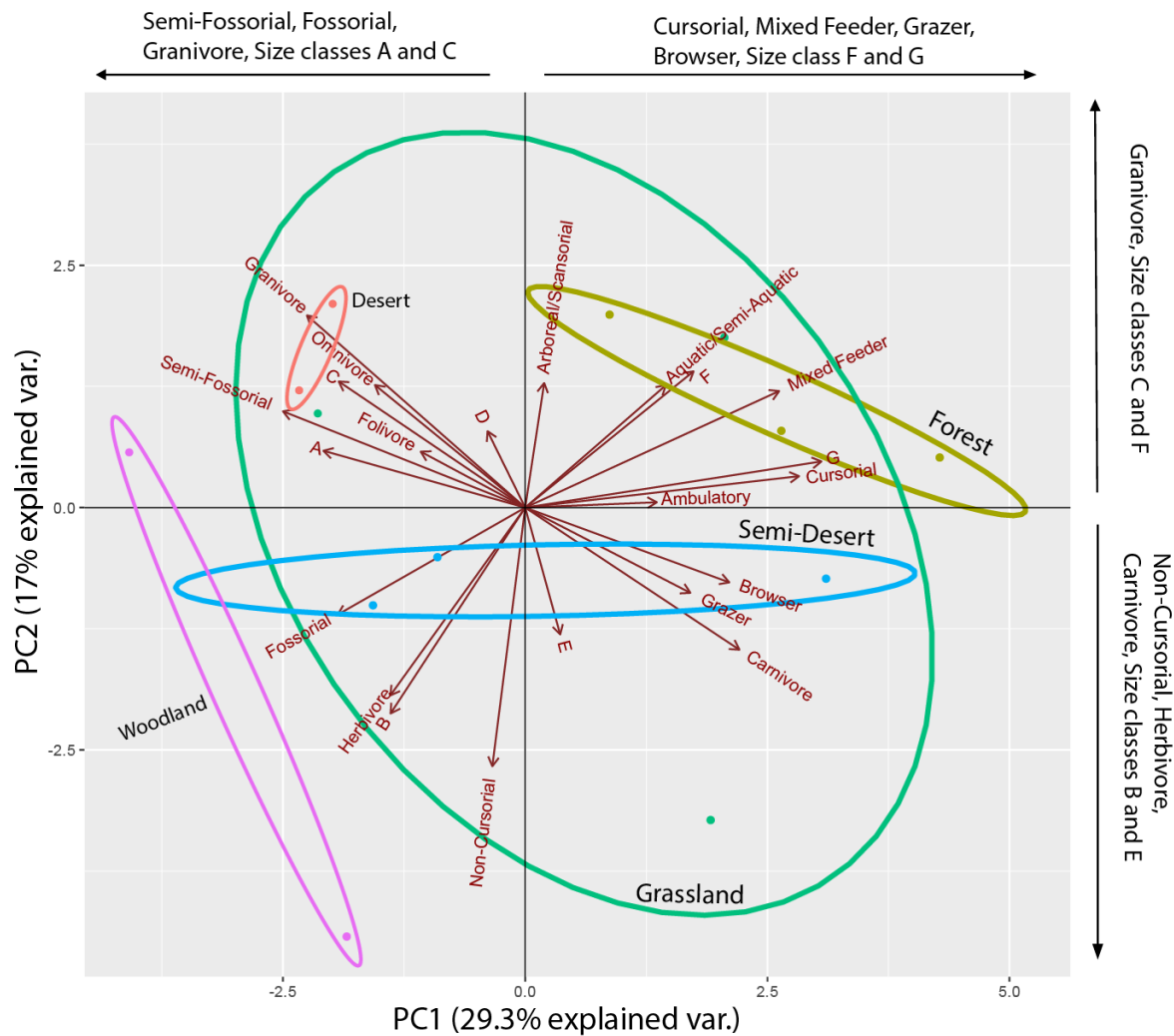


Figure A7: Scatter plot of Principle Component Analysis of locomotion frequencies for total unweighted dataset. PC1 (34.2% variance) on x-axis, PC2 (23.9%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 16), displayed on PC1 and PC2 for positive and negative loadings.

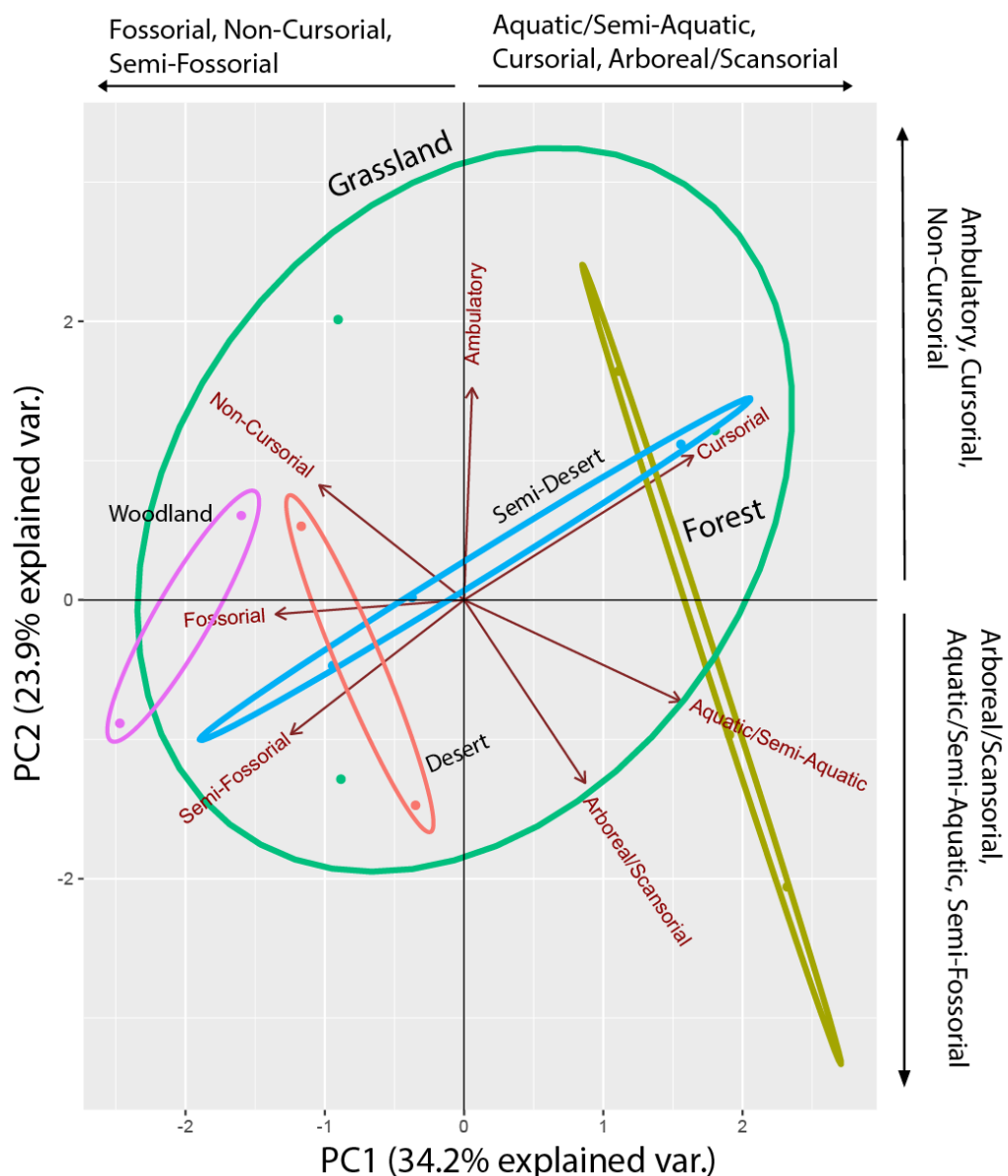


Figure A8: Scatter plot of Principle Component Analysis of diet frequencies for total unweighted dataset. PC1 (36% variance) on x-axis, PC2 (22.9%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 17), displayed on PC1 and PC2 for positive and negative loadings.

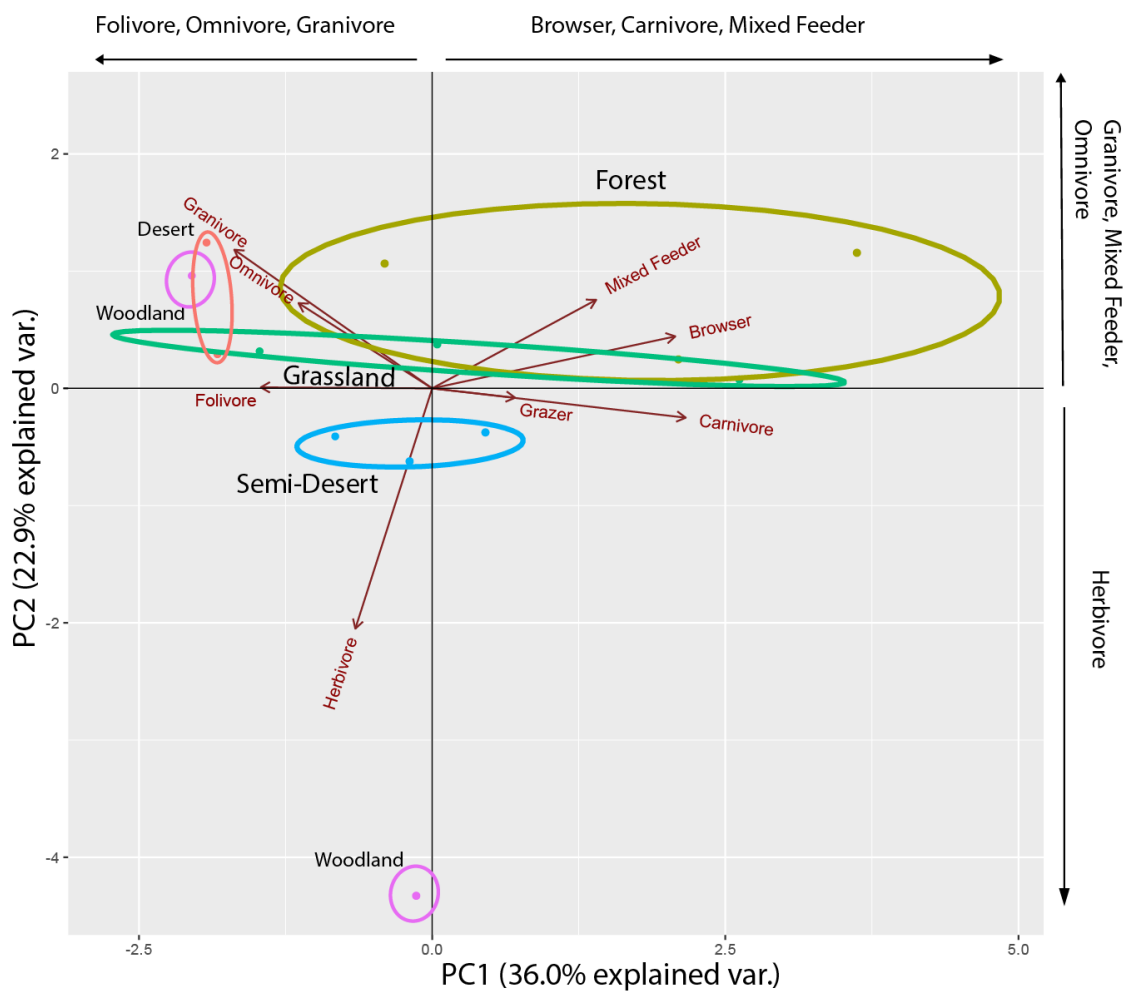


Figure A9: Scatter plot of Principle Component Analysis of size frequencies for total unweighted dataset. PC1 (31.1% variance) on x-axis, PC2 (25.4%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 18), displayed on PC1 and PC2 for positive and negative loadings.

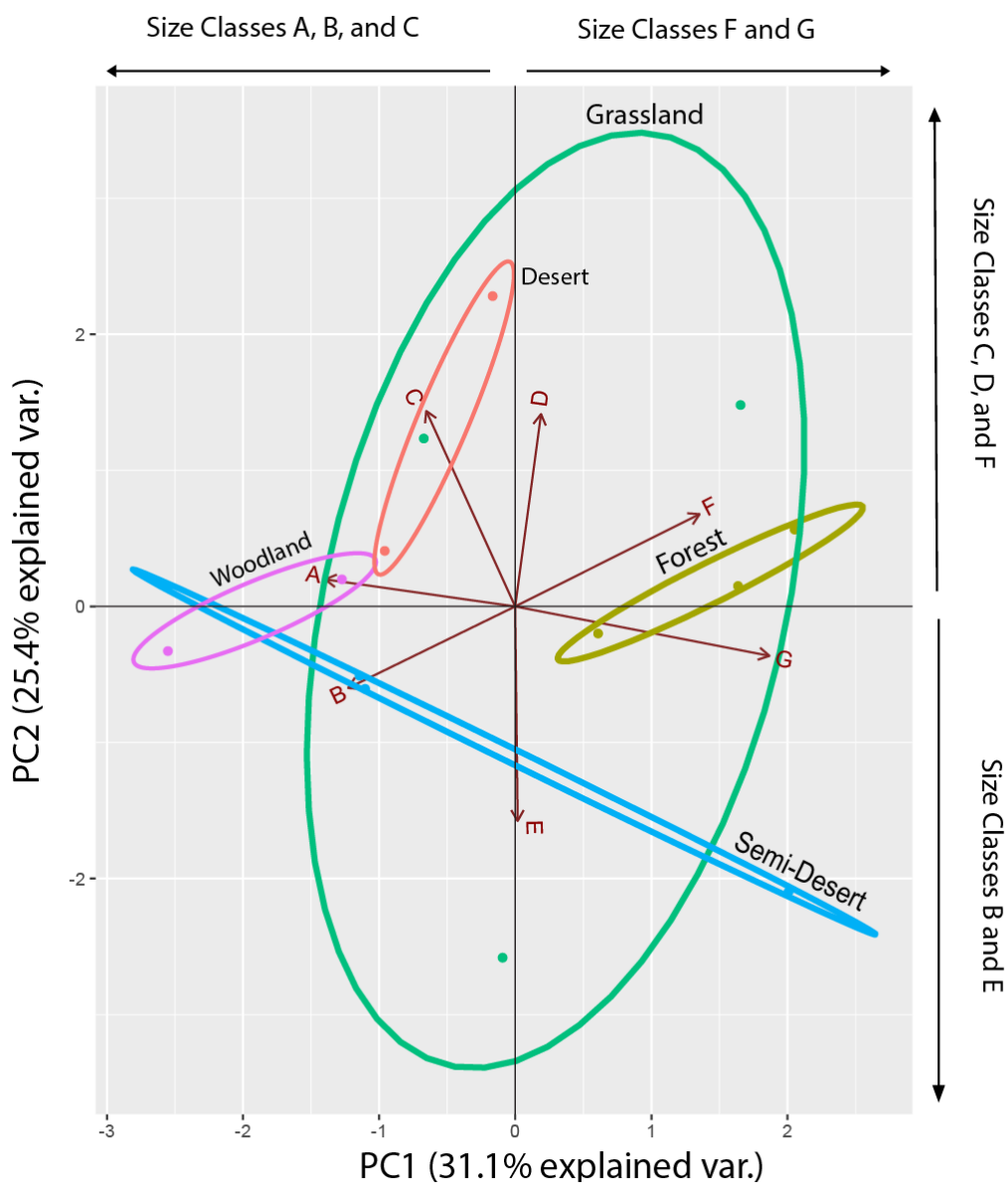


Figure A10: Scatter plot of Principle Component Analysis of all trait frequencies for total weighted dataset. PC1 (24.8% variance) on x-axis, PC2 (16.3%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 19), displayed on PC1 and PC2 for positive and negative loadings.

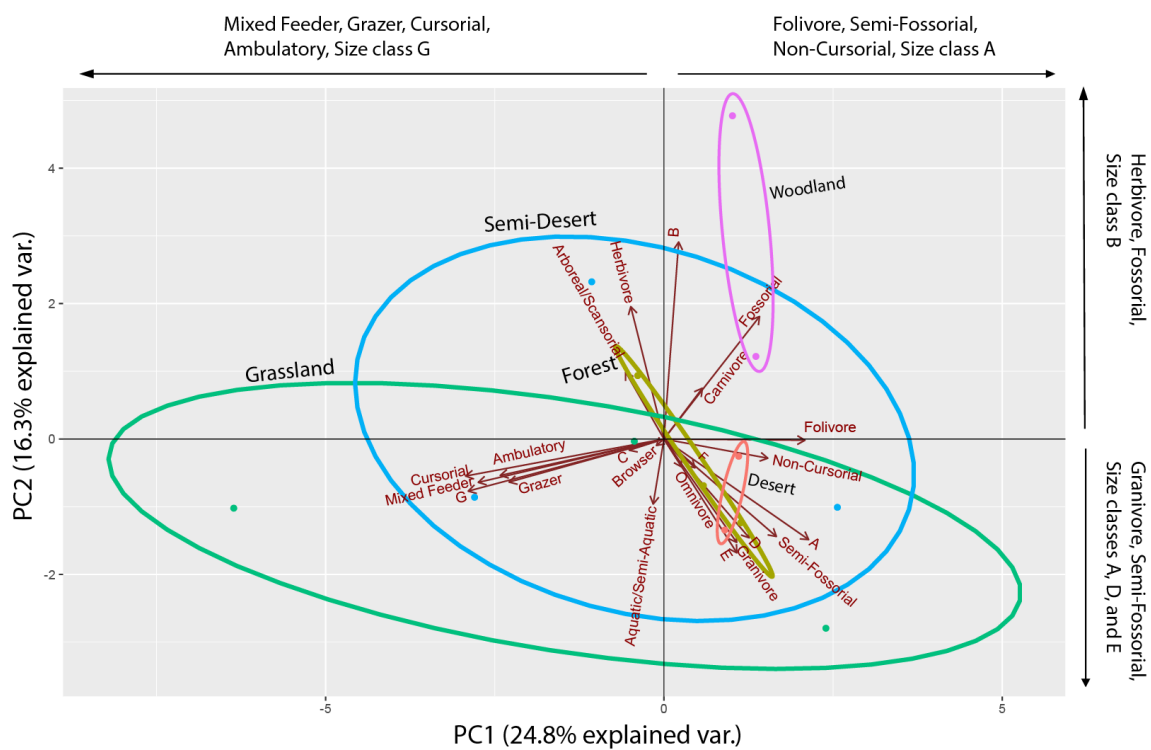


Figure A11: Scatter plot of Principle Component Analysis of locomotion frequencies for total weighted dataset. PC1 (32.8% variance) on x-axis, PC2 (21.1%) on y-axis.

Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 20), displayed on PC1 and PC2 for positive and negative loadings.

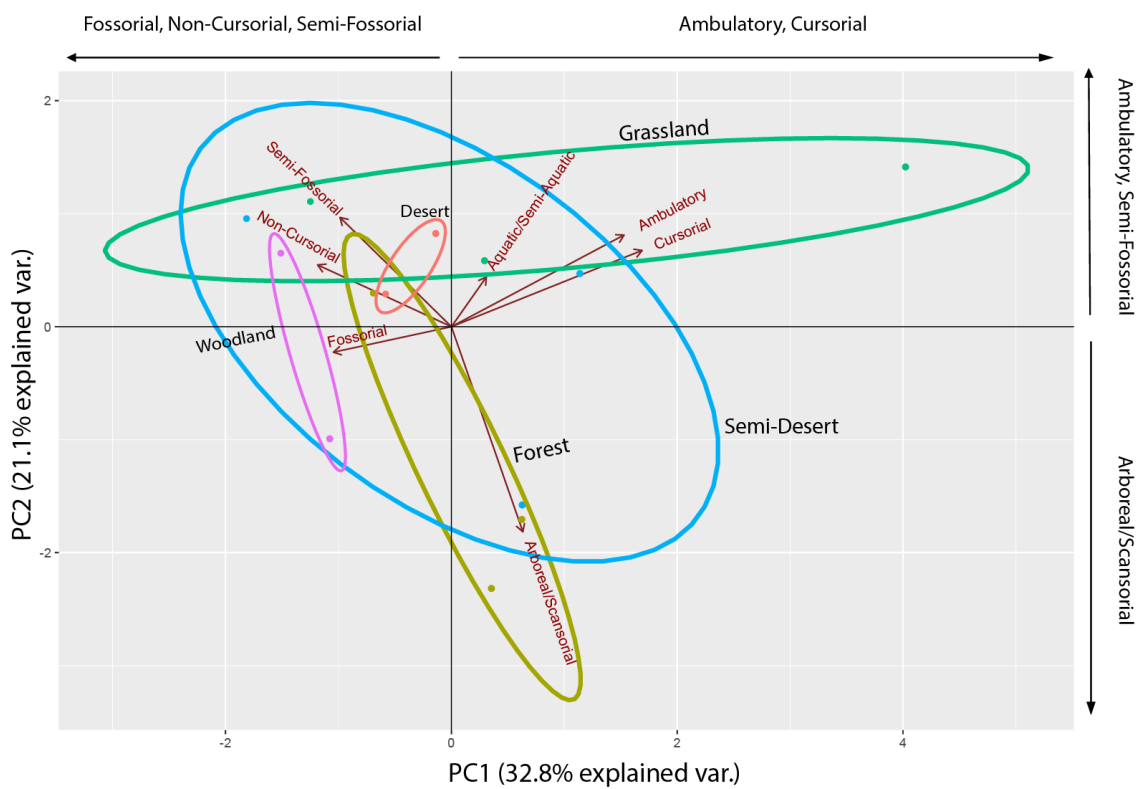


Figure A12: Scatter plot of Principle Component Analysis of dietary frequencies for total weighted dataset. PC1 (24.4% variance) on x-axis, PC2 (22%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 21), displayed on PC1 and PC2 for positive and negative loadings.

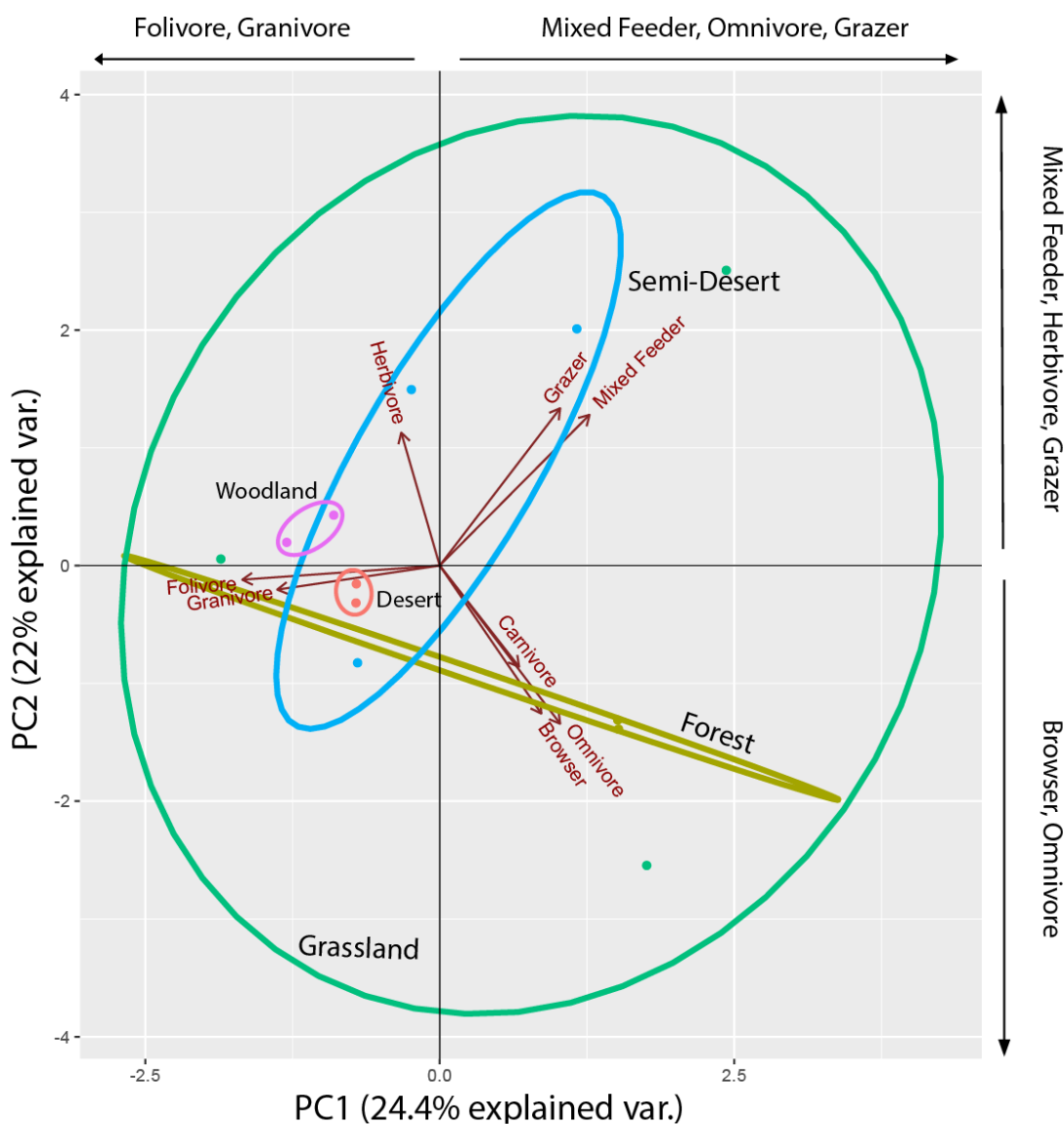


Figure A13: Scatter plot of Principle Component Analysis of size frequencies for total weighted dataset. PC1 (34.1% variance) on x-axis, PC2 (22.5%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 22), displayed on PC1 and PC2 for positive and negative loadings.

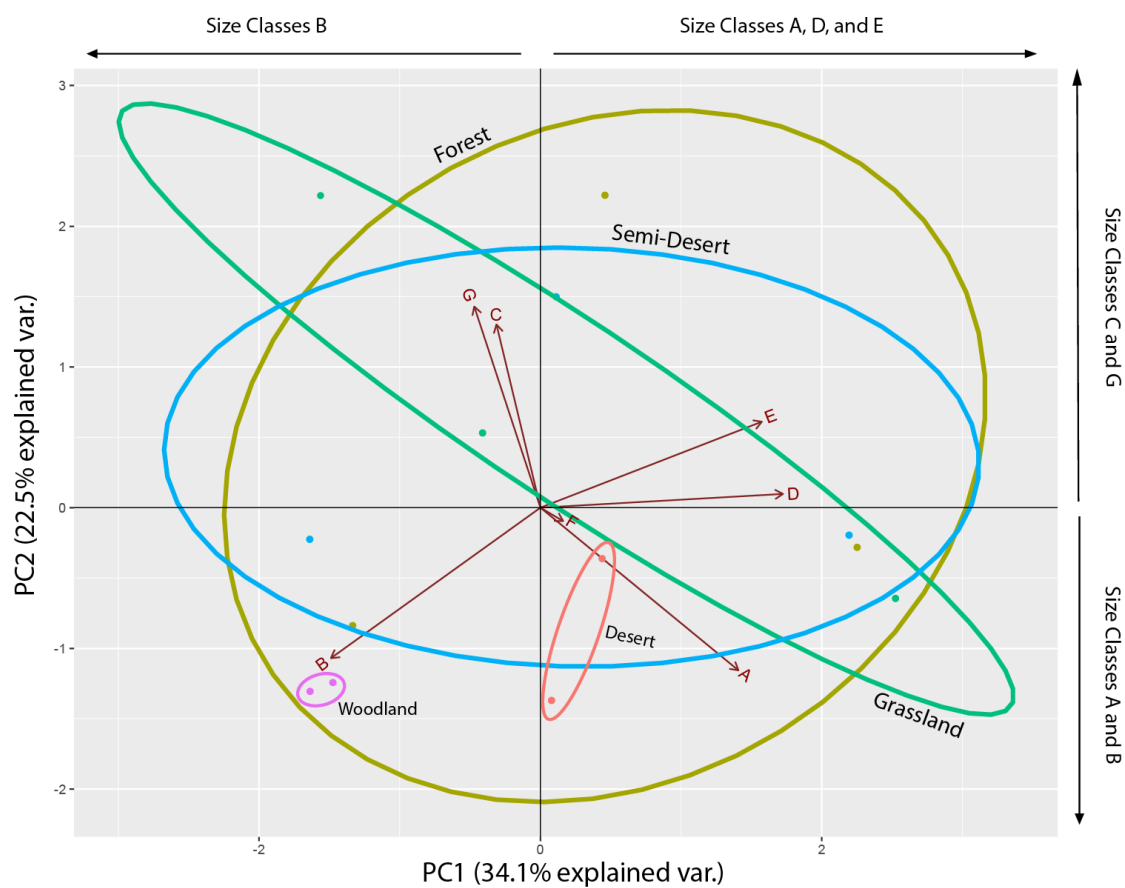


Figure A14: Scatter plot of Principle Component Analysis of rodents and lagomorphs for total unweighted dataset. PC1 (27.4% variance) on x-axis, PC2 (22.3%) on y-axis.

Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 23), displayed on PC1 and PC2 for positive and negative loadings.

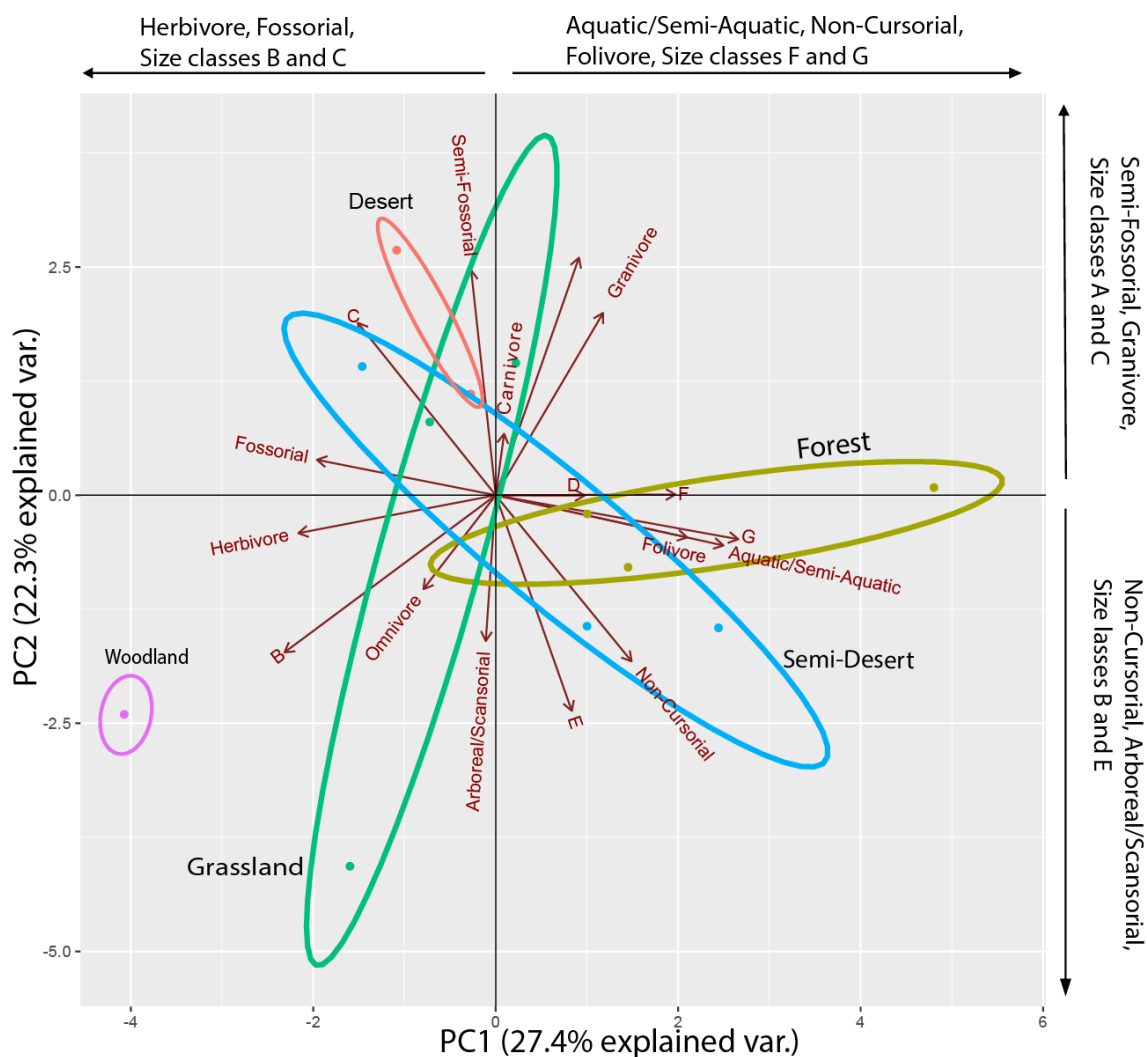


Figure A15: Scatter plot of Principle Component Analysis of non-rodent and lagomorphs for total unweighted dataset. PC1 (33.8% variance) on x-axis, PC2 (25.5%) on y-axis. Confidence ellipses representing 95% confidence intervals for Semi-Desert, Grassland and Forest. Non-Significant ellipses for Woodland and Desert. Trait frequencies with high loadings (cut-off 20%; Table 23), displayed on PC1 and PC2 for positive and negative loadings.

