

Dietary niche variation and its relationship to lizard population density

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Funding information

Israel Science Foundation, Grant/Award Number: 1005/12; Clore Israel Foundation

Handling Editor: Mariano Rodriguez-Cabal

Abstract

1. Insular species are predicted to broaden their niches, in response to having fewer competitors. They can thus exploit a greater proportion of the resource spectrum. In turn, broader niches are hypothesized to facilitate (or be a consequence of) increased population densities.
2. We tested whether insular lizards have broader dietary niches than mainland species, how it relates to competitor and predator richness, and the nature of the relationship between population density and dietary niche breadth.
3. We collected population density and dietary niche breadth data for 36 insular and 59 mainland lizard species, and estimated competitor and predator richness at the localities where diet data were collected. We estimated dietary niche shift by comparing island species to their mainland relatives. We controlled for phylogenetic relatedness, body mass and the size of the plots over which densities were estimated.
4. We found that island and mainland species had similar niche breadths. Dietary niche breadth was unrelated to competitor and predator richness, on both islands and the mainland. Population density was unrelated to dietary niche breadth across island and mainland populations.
5. Our results indicate that dietary generalism is not an effective way of increasing population density nor is it result of lower competitive pressure. A lower variety of resources on islands may prevent insular animals from increasing their niche breadths even in the face of few competitors.

KEY WORDS

diet, lizards, niche breadth, niche variation hypothesis, population density

1 | INTRODUCTION

Insular populations undergo different levels of niche shift in adapting to their environment (Grant, 1998). A phenomenon whereby insular populations expand their niches through expansion of intra-population variation, usually thought to derive through release from interspecific competition, is often termed the “niche variation hypothesis” (Bolnick, Svanbäck, Araújo, & Persson, 2007; Soule & Stewart, 1970; Van Valen, 1965; although the term also have other, related meanings, see, e.g.

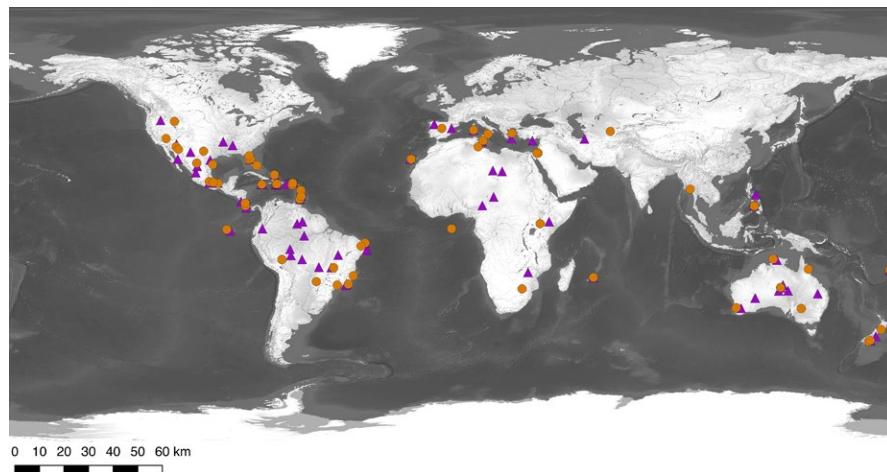
Costa, Mesquita, Colli, & Vitt, 2008; Kavanagh & Burns, 2014). Insular species are hypothesized to have wider niches than mainland ones because they are, presumably, free to exploit resources that on the mainland would be used by their competitors (Dunham, Tinkle, & Gibbons, 1978; Soule & Stewart, 1970).

The niche variation hypothesis has received mixed support from many studies (reviewed in Bolnick et al., 2007; Costa et al., 2008; Meiri, Dayan, & Simberloff, 2005). Parent and Crespi (2009), for example, found the expected negative relationship between morphological

manifestations of niche and the number of competitors in land snails on the Galapagos Islands. Bolnick et al. (2010) found that niche breadth in freshwater fish increased following a release from inter-specific competition. Meiri et al. (2005), however, found similar or even higher morphological variability in mainland settings, which they ascribed to the influence of gene flow. Kavanagh and Burns (2014) found no evidence for increased sexual size dimorphism (SSD) in island plants compared to mainland ones.

High population densities may indicate that a population is well adapted to its habitat and makes effective use of the available resources and in dealing with competition and predation (Kaspari, O'Donnell, & Kercher, 2000; MacArthur, Diamond, & Karr, 1972). Generalist species can make use of more resources, which allows them to divide the niche among individuals, or among males and females, facilitating increased population density (Angerbjorn, 1985; MacArthur et al., 1972; Van Valen, 1965). The relationship between population density and niche breadth may work both ways, species with high population density may experience higher intraspecific competition, forcing them to widen their niche (Bolnick & Svanback, 2007).

We tested whether dietary niches of island lizards are wider than those of mainland ones, reflecting the lower number of competitors on islands. In addition, we tested the hypothesis that niche breadth is positively correlated with population density (Van Valen, 1965). Lizards constitute an extremely variable group with a wide distribution across both islands and the mainland (Blackburn, 2006; Pianka, 1995). Although predominantly carnivorous, island lizards are known to often evolve herbivory, thereby increasing their dietary niches (Cooper & Vitt, 2002; Janzen, 1973; Meiri, 2008; Olesen & Valido, 2003). We hypothesized that insular lizard species would have broader dietary niches than mainland species due to decreased competition and predation. Moreover, we hypothesized that population density would be higher in species with broader dietary niches, especially on islands. This is because species with broader dietary niches can better exploit the different resources in their environment, thereby increasing population density (Bolnick et al., 2007).



2 | MATERIALS AND METHODS

2.1 | Data collection

We collected data from the primary literature on population density and diet for 59 mainland, and 36 insular species (localities in Figure 1; Data and sources in Appendix S1). We did not relate to whether the species was an island endemic as previous studies had shown no difference in population density between insular populations of endemic and non-endemic species (i.e. species that have both mainland and island populations; Novosolov et al., 2016).

For each species, we collected detailed dietary data (from the localities in Figure 1), which were divided into 44 categories based on what is commonly reported in the literature (Appendix S1; hereafter the "full" dataset). Thirty-nine categories referred to invertebrates (mainly arthropod orders), three categories to vegetation ("plant material," "flowers," and "fruit/seed"), one category of "non-identified," and one category to "vertebrates" (studies usually combine all vertebrate remains found in the diet when reporting dietary components). This focus on invertebrates can potentially mask major niche expansion, such as the evolution of herbivory. To avoid potential bias towards the consumption of a varied invertebrate diet, we condensed the dataset (Appendix S1; hereafter the "clumped" dataset) by combining the dietary categories based on animal phyla—(1) Annelida, (2) Arthropoda, (3) Mollusca and (4) Chordata, and further included the (5) "non-identified" category, as well as the three plant categories (categories 6–8). Statistical analyses were performed on both datasets.

We aimed to study the relationship between population density and diet, thus we limited our data search to the 192 species for which we already had reliable population density data from a previous study (Novosolov et al., 2016). First, we searched for dietary data in the papers Novosolov et al. (2016) used to obtain density data. We then used Google Scholar to search for dietary data using the words "diet" or "dietary niche" coupled with the scientific name of the species (from the list of species we had density data for) to find the dietary contents of the species of interest. We used only sources that reported dietary categories which are commonly used in the literature.

FIGURE 1 Map showing the localities from which data on population density (orange circle) and diet (purple triangle) were collected

For non-endemic island species, we used only data reported from an island population, to use these species as insular species in our study. We ended up with 94 species for which we had reliable dietary and population density data.

We used dietary data recorded from either stomach contents or faecal pellets. Faecal pellets are considered to be less reliable for dietary analysis (Pérez-Mellado, Pérez-Cembranos, Garrido, Luiselli, & Corti, 2011) because the food undergoes further processing in the intestines. However, we found no differences in dietary niche breadth between data based on stomach content and those based on faecal material (Appendix S2), and therefore retain both types of data.

We calculated dietary niche breadth based on either the volumetric or numeric proportion of different prey categories, preferring volumetric proportions where both were reported. When volumetric proportions were not available, we used numeric proportions. To make sure our results are not biased by the type of proportion we used, we compared niche breadths calculated using the two methods. The differences in niche breadth was not significant (Appendix S2). To calculate our niche breadth, we used the inverse of Simpson's (Simpson, 1949) diversity measure (Pianka, 1973):

$$\text{Niche Breadth} = \sum_{i=1}^n p_i^2$$

where p is the proportional use of each diet category i . Niche breadth values range from 1 (exclusive use of a single diet category) to n (use of all diet categories). We set the minimum sample size (i.e. minimum number of stomachs used to quantify diet) to nine following Bolnick et al. (2003). An analysis with a minimum sample size of two gave similar results (Appendix S2), but we doubt whether such small sample sizes adequately characterize population-level niches. We found no correlation between sample size (the number of individuals analysed) and niche breath (Appendix S2).

Population density is strongly and negatively correlated with the area over which density is estimated (Blackburn & Gaston, 1996; Novosolov et al., 2016). Thus, for each species, we recorded the size of the study area (hectare) for which the population density was estimated. For species for which we had density data for more than one population, we chose the population that was sampled over the largest area. To account for a potential effect of body size on population density (Damuth, 1981), we used estimated body mass (g) for each species from Feldman, Sabath, Pyron, Mayrose, and Meiri (2016).

Lizard richness was used as a proxy for competitor richness. The combined richness of birds, mammals and snakes (excluding species not eating lizards; i.e. vertebrate-eating carnivores such as members of the Falconiformes, Carnivora and Viperidae but not, e.g. herbivorous and insectivorous taxa such as Columbiformes, artiodactyls and scolecophidians; see Novosolov et al., 2016) was used as a proxy for predator richness. Richness at the area where diet data were collected was calculated using ArcGIS 10.0 (distributed by ESRI) and distribution maps were generated by the GARD project (for lizards and snakes; <http://www.gardinitiative.org/>), IUCN (for mammals; <http://www.iucnredlist.org/>) and BirdLife (for bird; Only breeding ranges; BirdLife International & NatureServe, 2013). This was achieved by first

identifying the equal area Behrmann projection $1 \times 1^\circ$ grid cells that represent the localities, and then spatially joining the lizard, snake, mammal and bird species distribution maps with a Behrmann grid to assess species richness of each group in each cell. GIS distribution maps for lizards, snakes and mammals overestimate richness on small islands. Thus, for small islands in our dataset, we collected richness data of lizards, snakes and mammals from the literature.

2.2 | Statistical analyses

All variables (except niche breadth) were \log_{10} transformed to normalize the model's residual distribution and reduce heteroscedasticity. All the analyses were repeated on both the "full" and the "clumped" datasets. We first used ANOVA to determine how dietary niche breadth and lizard species richness varied between islands and the mainland. We then used dietary niche breadth as a response variable in an ANCOVA to determine its relationship with competitor richness (i.e. lizard richness) and predator richness (see above) as a continuous predictor, and on islands vs. the mainland as a categorical predictor. Finally, we examined the relationship between population density (individual/ha) and dietary niche breadth accounting for insularity, study area (ha) and body mass (g), in an ANCOVA. For 15 species, out of the total 94, the dietary and population density data were from different localities. To make sure this does not introduce bias to our results, we ran sensitivity analyses by running all the models while excluding these species from the data. The sensitivity analyses showed no qualitative difference from the main analyses; thus, we used the complete species data in our models to increase the power of our results. The R code and results for the sensitivity analyses can be found in Appendix S2.

Because species traits are phylogenetically conserved, we accounted for phylogenetic non-independence by using a comprehensive phylogeny of squamates (Pyron & Burbrink, 2014), pruned to the species in our dataset. We repeated all analyses using phylogenetic generalized least square regression (Freckleton, Harvey, & Pagel, 2002). We corrected the branch lengths of the phylogenetic tree using the maximum likelihood value of the scaling parameter λ (Pagel, 1997) implemented in the R package *Caper* (Orme et al., 2014). We report the results of the phylogenetic models only when the λ value was significantly different from zero. All statistical analyses were done in R (R Core Team, 2016). The full R code used in this study and the raw analytical output are reported in Appendix S2.

3 | RESULTS

Island area in our data ranges between 0.04 km^2 and $151,215 \text{ km}^2$. Population density was higher on islands than on the mainland (islands: 2.78 ± 0.22 , mainland: 1.68 ± 0.17 , $t = -6.64$, $p < .002$), corrected for body mass (slope: -0.377 ± 0.094 , $t = -3.98$, $p < .002$), and study area (slope: -0.409 ± 0.079 , $t = -5.16$, $p < .002$). The λ of the phylogenetic model was not significantly different from zero. Lizard richness and predator species richness were lower on

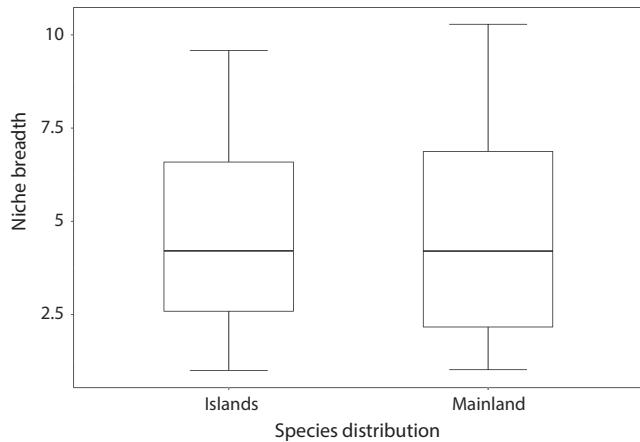


FIGURE 2 Comparison of dietary niche breadth in lizard species on islands and on the mainland ($N = 94$)

islands than on the mainland (back transformed from logarithm estimates: lizard richness—Islands: 16 ± 1.15 , mainland: 35 ± 1.21 ; $t = 3.94$; $p < .002$; predator richness—Islands: 67 ± 1.31 , mainland: 257 ± 1.17 , $t = 8.61$, $p < .002$).

Dietary niche breadths were similar on islands and the mainland in the “full” dataset (phylogenetic model: islands: 4.26 ± 1.10 , mainland: 4.76 ± 0.59 ; $t = 0.85$; $p = .40$; non-phylogenetic model: islands: 4.59 ± 0.43 , mainland: 4.99 ± 0.54 , $t = 0.74$, $p = .46$; Figure 2). In the “clumped” dataset island niche breadth was wider on islands than on the mainland (islands: 1.52 ± 0.08 , mainland: 1.30 ± 0.11 , $t = -2.07$, $p = .04$; λ was not significantly different from zero). Using the “full” and the “clumped” datasets, however, both models explained only ca 4% of the variation.

We found no significant relationship between dietary niche breadth and lizard species richness on either islands or the mainland, using either the “full” (intercept islands: 3.33 ± 0.92 , mainland: 3.40 ± 0.58 , $t = 0.12$, $p = .91$; slope = 1.04 ± 0.67 , $t = 1.56$, $p = .12$, $R^2 = 0.03$; no interaction between species richness and insularity, $p = .35$); or the “clumped” dataset (intercept islands: 1.37 ± 0.18 , mainland: 1.11 ± 0.11 , $t = -2.27$, $p = .03$; slope = 0.12 ± 0.13 , $t = 0.91$, $p = .37$, $R^2 = 0.05$; no interaction between species richness and insularity, $p = .30$; Figure 3). Moreover, we found no relationship between niche breadth and potential predator richness, using either the “full” (intercept islands: 2.59 ± 1.56 , mainland: 2.35 ± 0.73 , $t = -0.33$, $p = .74$; slope: 1.10 ± 0.82 , $t = 1.34$, $p = .18$, $R^2 = 0.02$; no interaction between species richness and insularity, $p = .78$) or the “clumped” datasets (intercept islands: 1.66 ± 0.31 , mainland: 1.48 ± 0.14 , $t = -1.23$, $p = .22$; slope = -0.07 ± 0.16 , $t = -0.46$, $p = .64$, $R^2 = 0.04$; no interaction between species richness and insularity, $p = .16$; Figure 4). λ was not significantly different from zero in any model.

Population density increases with the increase in dietary niche breadth in the “full” dataset (controlling for study area, mass intercept: islands: 1.84 ± 0.21 , mainland: 0.81 ± 0.17 , slope: 0.07 ± 0.03 , $t = 2.33$, $p = .02$, $R^2 = 0.56$). There was no interaction between niche breadth and insularity. However, in the “clumped” dataset, population density and dietary niche breadth were uncorrelated (intercept: islands: 2.52 ± 0.31 ,

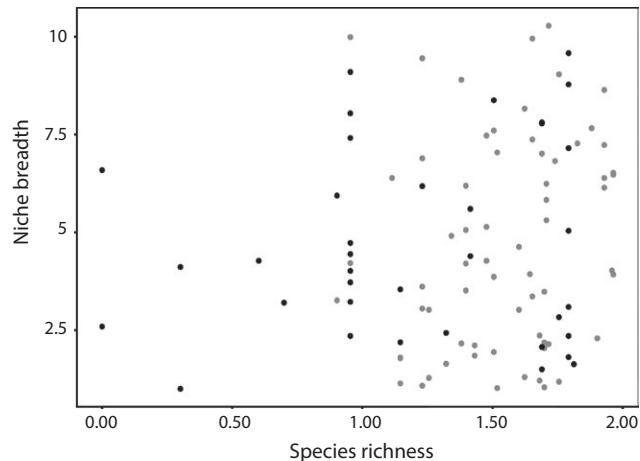


FIGURE 3 Relationship between dietary niche breadth and \log_{10} competitor species richness on islands (black) and the mainland (grey). $N = 35$ and 59 species respectively

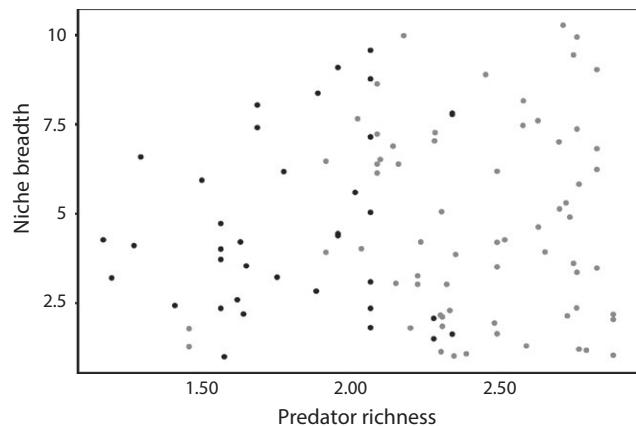


FIGURE 4 Relationship between dietary niche breadth and \log_{10} predator species richness on islands (black) and the mainland (grey). $N = 35$ and 59 species respectively

mainland: 1.49 ± 0.18 , slope -0.24 ± 0.18 , $t = -1.34$, $p = .18$; Figure 5). There was no interaction between niche breadth and insularity after correcting for the effects of study area (full dataset: -0.43 ± 0.08 , $t = 5.30$, $p < .002$; clumped dataset: -0.44 ± 0.08 , $t = -5.43$, $p < .002$) and body mass (full dataset: -0.64 ± 0.27 , $t = -2.36$, $p = .02$; clumped dataset: -0.57 ± 0.30 , $t = -1.93$, $p = .06$). Pagel’s λ was not significantly different from zero in any model. Using either the “full” or the “clumped” datasets, however, niche breadth explained no more than ca 4% of the variation.

4 | DISCUSSION

Our results show that insular lizard species have wider dietary niches than mainland ones only when accounting for their tendency to shift to herbivorous diet on islands. However, this pattern was statistically weak, explaining only c. 4% of the variation in niche breadth. In terms of animal prey taken, mainland and insular lizards have similar dietary niche breadths. Moreover, we did not find any relationship between

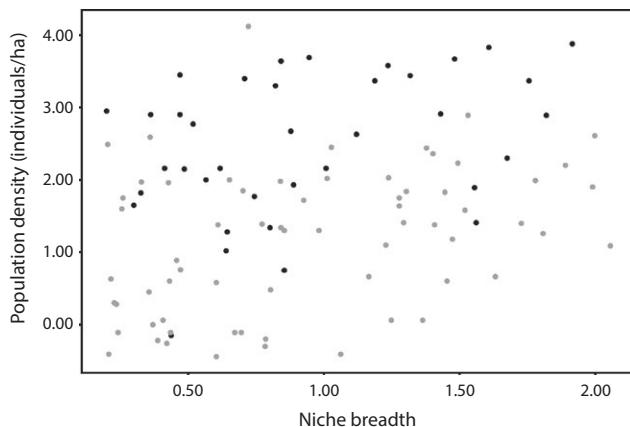


FIGURE 5 The relationship between \log_{10} population density (individuals/ha) and dietary niche breadth in lizards on islands (black) and the mainland (grey) ($N = 94$)

lizard species richness and predator richness and niche breadth either on islands or on the mainland. Contrary to our expectations, population density and niche breadth were not correlated either in insular or among mainland species.

Species are thought to increase their niche breadth where inter-specific competition is weak, as it is presumed to be on islands (Soule & Stewart, 1970; Van Valen, 1965). Niche breadth in our dataset was wider on islands than on the mainland but was unrelated to species richness. Moreover, the result explained only *ca* 4% of the variation in the data, making the result significant but weak. It is possible that insular species do not have the wider spectrum of resources that could enable them to expand their dietary niche. This hypothesis is reinforced by previous studies showing that islands may have lower resource availability (Ashmole, 1963) or that the available food sources on islands are often more restricted (Meiri et al., 2005).

Insular lizards are thought to often expand or shift their diets to include plant matter, perhaps to accommodate narrower invertebrate diversity or to substitute for invertebrates due to seasonal shortages (Janzen, 1973; Olesen & Valido, 2003; Pérez-Cembranos, León, & Pérez-Mellado, 2016). This expansion to include plant matter in the diet is supported by our results showing niche breadth to be wider on islands only when using the clumped dataset, which increases the weight given to plant matter when calculating dietary niche breadth. In other cases, insular species may increase their foraging time in order to compensate for scarce resources, utilize foods with low energetic values (Pérez-Cembranos et al., 2016) or digest more efficiently (Sagonas, Pafilis, & Valakos, 2015). Alternatively, marine subsidies (Barrett et al., 2005; Brooke & Houston, 1983; Pafilis, Meiri, Foufopoulos, & Valakos, 2009) may allow insular lizards to use otherwise unobtainable resources—but whether this will result in niche expansion, contraction or simply in niche shift, is unclear.

Population density is hypothesized to increase with increasing niche breadth (Van Valen, 1965). A population is hypothesized to be able to expand its niche by dividing it among individuals (i.e. with different individuals specializing in different dietary items) or by having each individual consume a wider range of food. Either will result in

decreased intraspecific competition (Bolnick et al., 2007, 2010). This, in turn, can facilitate an increase in population density (Van Valen, 1965) which suggests that the higher population density on islands may be partially due to dietary niche expansion (MacArthur et al., 1972). The lack of relationship between niche breadth and insularity may indicate that adopting broader niches does not directly cause population density to increase on islands (MacArthur et al., 1972; Van Valen, 1965).

Despite their prominence in the ecological literature, our results do not support any of the three hypotheses we tested we found that dietary niches are not wider on islands. Likewise, we identify no relationship between dietary niche breadth and population density, and between niche breadth and predator or competitor richness. Finally, niche breadth did not correlate with population density, species richness or predator richness and did not differ between islands and the mainland. Our results suggest that niche expansion does not stimulate decrease in intraspecific competition. Decreased intraspecific competition does not result in niche expansion. Although insular species often shift their dietary niches when adapting to insular environments, the depauperate nature of the islands does not in itself allow them to expand their dietary niches. We hypothesize that islands not only harbour fewer competitors but also fewer prey species, and thus dietary niches remain narrow on islands despite the lack of competitors.

ACKNOWLEDGEMENTS

Members of the Global Assessment of Reptile Distribution (GARD) group were instrumental in obtaining data on lizard distributions. Maria Novosolov is funded by the Clore Israel Foundation for the years 2015–2017. This study is funded by ISF grant number 1005/12 to S.M. A.G. is grateful to the Azrieli Foundation for the award of an Azrieli Fellowship.

AUTHORS' CONTRIBUTIONS

M.N. collected data and performed statistical analyses, G.H.R. collected data, A.G. collected data and S.M. collected data. M.N. wrote the first draft of the manuscript, and all authors contributed substantially to revisions.

DATA ACCESSIBILITY

Lizard natural history data: available in Supporting information. Phylogenetic data: Originated from Pyron and Burbrink (2014) study <https://doi.org/10.1111/ele.12168>. Data on lizards, snakes and mammals collected from the literature, data and source list in Appendix S1 and Dryad Digital Repository <https://doi.org/10.5061/dryad.5gc43> (Novosolov, Rodda, Gainsbury, & Meiri, 2017).

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SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

How to cite this article: Novosolov M, Rodda GH, Gainsbury AM, Meiri S. Dietary niche variation and its relationship to lizard population density. *J Anim Ecol*. 2017;00:1–8.
<https://doi.org/10.1111/1365-2656.12762>

Appendix 1a

binomial	what	distribution	island area (sq km)	population density (individuals/ha)	collection area	Latitude	Longitude	study area (ha)
<i>Acanthodactylus boskianus</i>	dif	Mainland	NA	2.83	Israel	30.788	35.24	6.00
<i>Acanthodactylus scutellatus</i>	dif	Mainland	NA	39.67	Tunisia	33.29	10.8	0.50
<i>Agama agama</i>	dif	Mainland	NA	93.90	Kanya	2.03333	36.066667	0.14
<i>Algyroides fitzingeri</i>	same	Island	24090.00	86.00	Sardinia	40.12	9.01	0.25
<i>Amblyrhynchus cristatus</i>	dif	Island	97	889.00	Fernandina island	-0.27	-91.44	0.01
<i>Ameiva ameiva</i>	same	Mainland	NA	4.62	Brazil	-12.55	-69.05	2.60
<i>Ameiva chrysolaema</i>	same	Island	76192.00	144.00	Hispaniola	18.2	-71.08	0.14
<i>Ameiva exsul</i>	same	Island	9104.00	400.00	Puerto Rico	18.13	-67.14	0.01
<i>Anolis acutus</i>	same	Island	348.50	460.00	Grenada	12.01	-61.78	0.05
<i>Anolis aeneus</i>	same	Island	348.50	4726.20	Grenada	11.99	-61.75	0.01
<i>Anolis bahorucoensis</i>	same	Island	76192.00	2323.75	Hispaniola	18.16	-71.41	0.04
<i>Anolis barkeri</i>	same	Mainland	NA	169.50	Mexico	18.44	-95	4.70
<i>Anolis brevirostris</i>	same	Island	76192.00	800.00	Hispaniola	18.2	-71.08	0.08
<i>Anolis coelestinus</i>	same	Island	76192.00	7600.00	Hispaniola	18.11	-71.41	0.01
<i>Anolis cybotes</i>	same	Island	76192.00	818.75	Hispaniola	18.16	-71.41	0.04
<i>Anolis distichus</i>	same	Island	76192.00	2795.00	Hispaniola	25.69	-79.27	0.01
<i>Anolis fuscoauratus</i>	dif	Mainland	NA	18.08	Brazil	-12.55	-69.05	2.60
<i>Anolis humilis</i>	same	Mainland	NA	13183.33	Costa Rica	10.43	-84	0.02
<i>Anolis limifrons</i>	same	Mainland	NA	160.00	Costa Rica	10.43	-84	0.06
<i>Anolis lineatopus</i>	same	Island	10911.00	470.58	Jamaica	18.02	-77.21	0.09
<i>Anolis oculatus</i>	same	Island	751.00	3832.33	Dominica	15.56	-61.3	0.06
<i>Anolis opalinus</i>	same	Island	10911.00	429.41	Jamaica	18.02	-77.21	0.09
<i>Anolis polylepis</i>	same	Mainland	NA	230.00	Costa Rica	9.325	-83.86	0.08
<i>Anolis punctatus</i>	dif	Mainland	NA	1.15	Brazil	-12.55	-69.05	2.60
<i>Anolis richardii</i>	same	Island	348.50	6790.00	Grenada	11.99	-61.75	0.01

binomial	what	distribution	island area (sq km)	population density (individuals/ha)	collection area	Latitude	Longitude	study area (ha)
<i>Aspidoscelis sexlineata</i>	same	Mainland	NA	22.00	Florida	28.083	-82.33	0.89
<i>Aspidoscelis tigris</i>	same	Mainland	NA	24.50	Arizona	33.34	-112.08	1.10
<i>Brachylophus vitiensis</i>	same	Island	0.70	142.86	Yadua Taba	-16.83	178.33	0.25
<i>Cercosaura ocellata</i>	same	Mainland	NA	0.38	Brazil	-12.55	-69.05	2.60
<i>Chlamydosaurus kingii</i>	same	Mainland	NA	7.74	Australia	-12.38	130.88	8.90
<i>Cnemidophorus lemniscatus</i>	same	Mainland	NA	80.00	Brazil	-21.51	-55	0.10
<i>Coleodactylus natalensis</i>	same	Mainland	NA	98.50	Brazil	-5.83	-35.18	0.01
<i>Ctenosaura pectinata</i>	same	Mainland	NA	0.60	Mexico	16.1	97.15	0.20
<i>Ctenotus leonhardii</i>	same	Mainland	NA	25.00	Australia	-23.971	133.89	0.30
<i>Ctenotus pantherinus</i>	same	Mainland	NA	56.00	Australia	-23.971	133.89	0.30
<i>Ctenotus piankai</i>	same	Mainland	NA	12.50	Australia	-23.98	133.94	0.10
<i>Ctenotus quattuordecimlineatus</i>	same	Mainland	NA	68.00	Australia	-23.971	133.89	0.30
<i>Ctenotus taeniolatus</i>	same	Mainland	NA	4.00	Australia	-16.5	145.2	1.00
<i>Cyclura carinata</i>	same	Island	417.00	19.18	Caicos	21.87	-72.08	0.90
<i>Cyclura pinguis</i>	same	Island	10911.00	0.36	Anegada	18.74	-64.37	12.50
<i>Draco volans</i>	same	Island	12706.00	66.35	Negros	9.3	123.28	25.00
<i>Egernia kingii</i>	same	Island	0.12	100.00	Penguin Island	-32.3	115.69	12.00
<i>Emoia atrocostata</i>	dif	Island	104688.00	144.98	Negros	9.481	123.181	3.59
<i>Eremiascincus richardsonii</i>	same	Mainland	NA	69.50	Australia	-32.46	142.33	0.50
<i>Eutropis multifasciata</i>	same	Island	12706.00	25.76	Negros	9.3	123.28	25.00
<i>Gallotia galloti</i>	same	Island	2034.00	2321.20	Tenerife	28.3	-16.42	0.15
<i>Gonatodes humeralis</i>	same	Mainland	NA	12.31	Brazil	-12.55	-69.05	2.60
<i>Gymnodactylus darwini</i>	same	Mainland	NA	20.00	Brazil	-22.55	-42.01	0.00
<i>Heliobolus spekii</i>	same	Mainland	NA	311.35	Kenya	2.03	36.06	0.14
<i>Hemidactylus mabouia</i>	same	Mainland	NA	20.00	Brazil	-22.55	-42.01	0.00
<i>Holbrookia propinqua</i>	same	Mainland	NA	104.34	Texas	26.110148	-97.168057	0.37
<i>Iberolacerta monticola</i>	same	Mainland	NA	274.00	Spain	40.81	-3.96	1.00
<i>Kentropyx pelviceps</i>	same	Mainland	NA	5.77	Brazil	-12.55	-69.05	2.60

binomial	what	distribution	island area (sq km)	population density (individuals/ha)	collection area	Latitude	Longitude	study area (ha)
<i>Kentropyx striata</i>	same	Mainland	NA	15.00	Brazil	-21.51	-55	0.10
<i>Lamprolepis smaragdina</i>	same	Island	12706.00	78.25	Negros	9.3	123.28	25.00
<i>Leiocephalus schreibersii</i>	same	Island	76192.00	143.00	Hispaniola	18.2	-71.08	0.14
<i>Leioploisma telfairii</i>	same	Island	1.53	5.64	Round Island	-19.85	57.78	6.75
<i>Lepidoblepharis xanthostigma</i>	same	Mainland	NA	91.67	Costa Rica	10.43	-84	0.06
<i>Lygodactylus capensis</i>	dif	Mainland	NA	56.25	South Africa	-24.48	28.7	1.00
<i>Mabuya mabouya</i>	dif	Mainland	NA	0.77	Brazil	-12.55	-69.05	2.60
<i>Menetia greyii</i>	same	Mainland	NA	3.00	Australia	-32.11	115.89	1.00
<i>Morethia boulengeri</i>	same	Mainland	NA	783.25	Australia	-32.46	142.33	0.01
<i>Oligosoma grande</i>	same	Island	151215.00	58.50	South Island	-45.45	170.41	0.72
<i>Oligosoma maccanni</i>	same	Island	151215.00	786.37	South Island	-45.85	169.77	0.04
<i>Oligosoma nigriplantare</i>	same	Island	145836.40	300.00	South Island	-43.83	172.68	0.02
<i>Oligosoma otagense</i>	same	Island	151215.00	22.00	South Island	-45.45	170.41	0.72
<i>Phrynosoma cornutum</i>	same	Mainland	NA	0.55	Mexico	26.66	-103.66	1.00
<i>Phrynosoma douglasii</i>	same	Mainland	NA	99.50	Idaho	43.63	-112.75	1.00
<i>Phrynosoma modestum</i>	same	Mainland	NA	1.00	Mexico	26.66	-103.66	1.00
<i>Phyllopezus pollicaris</i>	same	Mainland	NA	4.56	Brazil	-7.1027	-36.845	0.14
<i>Pinoyscincus jagori</i>	dif	Island	104688.00	44.44	Negros	9.26	123.25	0.09
<i>Plestiodon reynoldsi</i>	same	Mainland	NA	387.50	Florida	28.45	-81.8	0.04
<i>Plica plica</i>	dif	Mainland	NA	1.15	Brazil	-12.55	-69.05	2.60
<i>Plica umbra</i>	same	Mainland	NA	1.92	Brazil	-12.55	-69.05	2.60
<i>Podarcis filfolensis</i>	dif	Island	0.04	2000.00	Linosa	35.864709	12.86737	0.22
<i>Podarcis gaigeae</i>	same	Island	NA	584.00	Skyros	38.85	24.56	0.08
<i>Podarcis raffoneae</i>	same	Island	NA	2750.00	Scoglio Faraglione	38.58	14.8	0.00
<i>Salvator merianae</i>	same	Mainland	NA	0.63	Brazil	-19.16	-39.98	3.20
<i>Sceloporus grammicus</i>	same	Mainland	NA	107.25	Mexico	19.16	-98.6	2.50
<i>Sceloporus magister</i>	dif	Mainland	NA	0.37	Arizona	32.26	-111.12	3.14
<i>Sceloporus poinsettii</i>	dif	Mainland	NA	71.00	Texas	31.54	-100.88	1.00

binomial	what	distribution	island area (sq km)	population density (individuals/ha)	collection area	Latitude	Longitude	study area (ha)
<i>Scincella lateralis</i>	same	Mainland	NA	405.00	Florida	29.64	-82.35	0.10
<i>Sphaerodactylus vincenti</i>	same	Island	389.00	2500.00	St. Vincent	13.21	-61.22	0.00
<i>Stellagama stellio</i>	dif	Mainland	NA	24.00	Israel	30.69	34.78	4.50
<i>Tenuidactylus caspius</i>	dif	Mainland	NA	3.76	Uzbek SSR	39.61	64.65	1.00
<i>Trachylepis quinquetaeniata</i>	dif	Mainland	NA	2.00	Kenya	2.03	36.06	0.14
<i>Tropidurus itambere</i>	same	Mainland	NA	52.30	Brazil	-22.93	-46.55	1.72
<i>Tropidurus torquatus</i>	same	Mainland	NA	282.10	Brazil	-15.9	-47.93	0.31
<i>Tupinambis teguixin</i>	same	Mainland	NA	0.77	Brazil	-12.55	-69.05	2.60
<i>Uma exsul</i>	same	Mainland	NA	24.00	Mexico	26.66	-103.66	1.00
<i>Uta stansburiana</i>	dif	Mainland	NA	43.58	United States	36.66	-116.17	9.00
<i>Varanus brevicauda</i>	same	Mainland	NA	26.00	Australia	-23.971	133.89	0.30
<i>Varanus tristis</i>	same	Mainland	NA	0.50	Australia	-16.5	145.2	1.00
<i>Xenosaurus grandis</i>	same	Mainland	NA	37.60	Mexico	18.86	-97.01	5.00

Appendix 1b

binomial	sources for population density
<i>Acanthodactylus boskianus</i>	Shai Meiri pers. Comm. Busack, S.D. (1975). Biomass estimates and thermal environment of a population of the fringe-toed lizard, <i>Acanthodactylus pardalis</i> . Br. J. Herpetol., 5, 457–459.
<i>Acanthodactylus scutellatus</i>	Western, D. (1974). The distribution, density and biomass density of lizards in a semi-arid environment of northern Kenya. Afr. J. Ecol., 12, 49–62.
<i>Agama agama</i>	Capula, M., Luiselli, L., Filippi, E. & Ceccarelli, A. (2002). Habitat characteristics and demography of high-altitude populations of the lacertid lizard, <i>Algyrodes fitzingeri</i> . Ital. J. Zool., 69, 33–36.
<i>Algyrodes fitzingeri</i>	Carpenter, C.C. (1966). the marine iguana of the Galapagos Islands, its behavior and ecology. Calif. Acad. Sci., 34, 329–376.
<i>Amblyrhynchus cristatus</i>	Duellman, W.E. (1987). Lizards in an Amazonian Rain Forest Community Resouce Utilization and Abundance. Natl. Geogr. Res., 3, 489–500.
<i>Ameiva ameiva</i>	Schell, P.T., Powell, R., Parmerlee Jr., J.S., Lathrop, A. & Smith, D.D. (1993). Notes on the natural history of <i>Ameiva chrysolaema</i> (Sauria: Teiidae) from Barahona, Dominican Republic. Copeia, 1993, 859–862.
<i>Ameiva chrysolaema</i>	Lewis, A.R. 1989 Diet Selection And Depression Of Prey Abundance By An Intensively Foraging Lizard. Journal Of Herpetology, 23, 164-170.
<i>Ameiva exsul</i>	Simmons, P.M., Greene, B.T., Williamson, K.E., Powell, R. And Parmerlee, J.S. 2005 Ecological Interactions Within A Lizard Community On Grenada. Herperologica, 61, 124-134.
<i>Anolis acutus</i>	Harris, B.R., Yorks, D.T., Bohnert, C. a., Parmerlee, J.S. & Powell, R. (2004). Population densities and structural habitats in lowland populations of <i>Anolis</i> lizards on Grenada. Caribb. J. Sci., 40, 31–40.
<i>Anolis aeneus</i>	Cast, E.E., Gifford, M.E., Schneider, K.R., Hardwick, A.J., Parmerlee, J.S. & Powell, R. (2000). Natural history of an anoline lizard community in the Sierrade Baoruco, Dominican Republic. Caribb. J. Sci., 36, 258–266.
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<i>Anolis brevirostris</i>	Sifers, S.M., Yeska, M.L., Ramos, Y.M., Powell, R. & Parmerlee, J.S. (2001). <i>Anolis</i> lizards restricted to altered edge habitats in a Hispaniolan cloud forest. Caribb. J. Sci., 37, 55–62.
<i>Anolis coelestinus</i>	Fobes, T.M., Powell, R., Parmerlee, J.S., Lathrop, a. & Smith, D.D. (1992). Natural history of <i>Anolis cybotes</i> (Sauria: Polychridae) from an altered habitat in Barahona, Dominican Republic. Caribb. J. Sci., 28, 200–207.
<i>Anolis cybotes</i>	Cast, E.E., Gifford, M.E., Schneider, K.R., Hardwick, A.J., Parmerlee, J.S. & Powell, R. (2000). Natural history of an anoline lizard community in the Sierrade Baoruco, Dominican Republic. Caribb. J. Sci., 36, 258–266.
<i>Anolis distichus</i>	Duellman, W.E. (1987). Lizards in an Amazonian Rain Forest Community Resouce Utilization and Abundance. Natl. Geogr. Res., 3, 489–500.
<i>Anolis fuscoauratus</i>	Guyer, C. (1988). Food Supplementation in a Tropical Mainland Anole, <i>Norops Humilis</i> : Effects on Individuals. Ecology, 69, 362–369.
<i>Anolis humilis</i>	Heinen, L.T. (1992). Comparisons of the leaf litter herpetofauna in abandoned cacao plantation and primary rain forest in Costa Rica:
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Appendix 1c

binomial	lizard richness	predator richness	maximum body mass (g)	diet data origin	diet data type	number of stomachs	niche breadth from clumped dataset	niche breadth from full dataset	diet data collection area	Diet Latitude	Diet Longitude
<i>Acanthodactylus boskianus</i>	14	29	1.293262359	Stomach contents	Numeric proportion	33	1.00	1.78	Libya	23.32	20.60
<i>Acanthodactylus scutellatus</i>	18	29	1.15071525	Stomach contents	Numeric proportion	89	1.01	1.28	Libya	23.68	16.81
<i>Agama agama</i>	21	309	2.070763359	Stomach contents	Numeric proportion	21	1.10	1.64	Nigeria	9.44	12.54
<i>Algyroides fitzingeri</i>	9	91	0.335630128	Faecal pellet	Numeric proportion	40	1.39	4.44	Sardinia	40.12	9.01
<i>Amblyrhynchus cristatus</i>	2	38	3.869614816	Stomach contents	Volumetric proportion	48	1.00	1.00	Santa Fe	-0.83	-90.04
<i>Ameiva ameiva</i>	51	580	2.475102007	Stomach contents	Volumetric proportion	35	1.00	5.83	Brazil	-10.80	-65.37
<i>Ameiva chrysolaema</i>	62	117	2.107813146	Stomach contents	Volumetric proportion	26	1.11	5.04	Hispaniola	17.83	-71.44
<i>Ameiva exsul</i>	32	78	2.415939739	Stomach contents	Numeric proportion	32	3.13	8.38	Puerto Rico	18.13	-67.14
<i>Anolis acutus</i>	9	43	0.797840336	Stomach contents	Volumetric proportion	27	1.43	4.21	Grenada	12.01	-61.78
<i>Anolis aeneus</i>	9	49	1.024384351	Stomach contents	Volumetric proportion	167	1.17	7.41	Grenada	12.09	-61.74
<i>Anolis bahorucoensis</i>	62	117	0.449253052	Stomach contents	Volumetric proportion	20	1.08	8.78	Hispaniola	18.16	-71.41
<i>Anolis barkeri</i>	30	377	1.322161537	Stomach contents	Numeric proportion	33	1.13	7.47	Mexico	18.57	-95.07
<i>Anolis brevirostris</i>	62	117	0.500801788	Stomach contents	Numeric proportion	19	1.00	1.81	Hispaniola	18.20	-71.08
<i>Anolis coelestinus</i>	62	117	1.086713734	Stomach contents	Numeric proportion	24	1.92	9.58	Hispaniola	18.11	-71.41
<i>Anolis cybotes</i>	62	117	1.041830294	Stomach contents	Volumetric proportion	17	1.03	7.15	Hispaniola	18.16	-71.41
<i>Anolis distichus</i>	62	117	0.62234171	Stomach contents	Volumetric proportion	29	1.06	2.35	Hispaniola	18.16	-71.41
<i>Anolis fuscoauratus</i>	57	665	0.474059635	Stomach contents	Numeric proportion	217	1.03	9.04	Ecuador	0.05	-76.98
<i>Anolis humilis</i>	17	556	0.423955216	Stomach contents	Volumetric proportion	19	1.00	3.61	Costa Rica	9.97	-83.43
<i>Anolis limifrons</i>	17	556	0.449253052	Stomach contents	Numeric proportion	65	1.07	9.45	Costa Rica	9.97	-83.43
<i>Anolis lineatopus</i>	26	91	0.907407359	Stomach contents	Numeric proportion	45	1.06	4.39	Jamaica	18.00	-76.76
<i>Anolis oculatus</i>	17	60	1.283641063	Stomach contents	Volumetric proportion	32	1.36	6.18	Dominica	15.56	-61.30
<i>Anolis opalinus</i>	26	104	0.568732491	Stomach contents	Volumetric proportion	340	1.04	5.60	Jamaica	18.03	-77.50
<i>Anolis polylepis</i>	49	497	0.644031517	Stomach contents	Numeric proportion	22	1.08	7.01	Costa Rica	8.48	-83.60

binomial	lizard richness	predator richness	maximum body mass (g)	diet data origin	diet data type	number of stomachs	niche breadth from clumped dataset	niche breadth from full dataset	diet data collection area	Diet Latitude	Diet Longitude
<i>Anolis punctatus</i>	55	665	1.202930084	Stomach contents	Volumetric proportion	63	1.09	6.82	Ecuador	0.05	-76.98
<i>Anolis richardii</i>	9	49	1.739292923	Stomach contents	Volumetric proportion	129	2.32	8.04	Grenada United States	12.09	-61.74
<i>Aspidoscelis sexlineata</i>	9	172	1.34561873	Stomach contents	Volumetric proportion	100	1.18	4.21	United States	35.36	-92.94
<i>Aspidoscelis tigris</i>	32	225	1.898200964	Stomach contents	Volumetric proportion	138	1.39	3.86	United States	34.41	-111.93
<i>Brachylophus vitiensis</i>	21	26	2.748813687	Faecal pellet	Numeric proportion	233	2.43	2.43	Yadua Taba	-16.82	178.30
<i>Cercosaura ocellata</i>	51	525	0.808239904	Stomach contents	Numeric proportion	56	1.18	5.31	Brazil	-12.50	-60.82
<i>Chlamydosaurus kingii</i>	80	215	2.959745783	Stomach contents	Volumetric proportion	24	1.00	2.29	Australia	-12.72	132.43
<i>Cnemidophorus lemniscatus</i>	45	571	1.638073959	Stomach contents	Volumetric proportion	90	1.31	9.95	Brazil	2.83	-60.67
<i>Coleodactylus natalensis</i>	24	283	#REF!	Stomach contents	Numeric proportion	49	1.14	8.90	Brazil	-5.80	-35.15
<i>Ctenosaura pectinata</i>	32	303	3.425605386	Stomach contents	Volumetric proportion	19	1.94	1.94	Mexico	18.60	-98.72
<i>Ctenotus leonhardii</i>	85	123	1.002437878	Stomach contents	Volumetric proportion	87	1.18	8.64	Australia	-23.00	134.88
<i>Ctenotus pantherinus</i>	85	123	1.65709649	Stomach contents	Volumetric proportion	86	1.40	6.39	Australia	-23.00	134.88
<i>Ctenotus piankai</i>	85	123	0.616650387	Stomach contents	Volumetric proportion	50	1.31	6.14	Australia	-23.00	134.88
<i>Ctenotus quattuordecimlineatus</i>	85	123	0.852713208	Stomach contents	Volumetric proportion	212	1.19	7.23	Australia	-23.00	134.88
<i>Ctenotus taeniolatus</i>	67	192	1.169580331	Stomach contents	Numeric proportion	261	1.28	7.27	Australia	-26.42	149.03
<i>Cyclura carinata</i>	9	57	3.748898563	Stomach contents	Volumetric proportion	126	2.00	3.22	Caicos	21.88	-72.09
<i>Cyclura pinguis</i>	8	47	3.869614816	Faecal pellet	Volumetric proportion	27	2.19	2.19	Anegada	18.74	-64.37
<i>Draco volans</i>	65	219	0.927160598	Stomach contents	Volumetric proportion	181	1.32	1.63	Negros Penguin Island	9.31	123.31
<i>Egernia kingii</i>	57	77	2.617948288	Stomach contents	Numeric proportion	167	2.60	2.83	Luzon	-32.34	117.85
<i>Emoia atrocostata</i>	49	190	1.333	Stomach contents	Numeric proportion	318	1.03	2.07	Luzon	13.92	123.85
<i>Eremiascincus richardsonii</i>	92	126	1.668182215	Stomach contents	Volumetric proportion	22	1.16	6.52	Australia	-24.00	133.90
<i>Eutropis multifasciata</i>	49	219	1.804847427	Stomach contents	Volumetric proportion	133	1.76	7.81	Negros	9.31	123.31
<i>Gallotia galloti</i>	8	32	1.835196975	Faecal pellet	Volumetric proportion	20	1.51	5.94	Tenerife	28.35	-16.89
<i>Gonatodes humeralis</i>	52	513	0.407129009	Stomach contents	Numeric proportion	42	1.10	10.28	Brazil	2.00	-62.83
<i>Gymnodactylus darwini</i>	22	540	0.735325131	Stomach contents	Numeric proportion	19	1.00	4.91	Brazil	-22.40	-42.73

binomial	lizard richness	predator richness	maximum body mass (g)	diet data origin	diet data type	number of stomachs	niche breadth from clumped dataset	niche breadth from full dataset	diet data collection area	Diet Latitude	Diet Longitude
<i>Heliobolus spekii</i>	33	222	0.70432434	Stomach contents	Numeric proportion	17	1.02	1.02	Kenya	2.90	39.70
<i>Hemidactylus mabouia</i>	30	328	1.154045266	Stomach contents	Volumetric proportion	53	1.08	4.27	Brazil United States	-8.61	-34.53
<i>Holbrookia propinqua</i>	25	202	0.943232553	Stomach contents	Volumetric proportion	28	1.20	5.06	United States	27.94	-98.20
<i>Iberolacerta monticola</i>	17	139	1.144669941	Stomach contents	Numeric proportion	172	1.09	6.89	Spain	42.55	-7.04
<i>Kentropyx pelviceps</i>	48	569	1.827363826	Stomach contents	Numeric proportion	15	1.05	2.36	Brazil	-8.33	-65.72
<i>Kentropyx striata</i>	45	571	1.795829572	Stomach contents	Numeric proportion	433	1.41	7.37	Brazil	2.83	-60.67
<i>Lamprolepis smaragdina</i>	49	219	1.541134847	Stomach contents	Volumetric proportion	176	1.68	7.78	Negros	9.31	123.31
<i>Leiocephalus schreibersii</i>	62	117	1.548291591	Stomach contents	Volumetric proportion	17	1.11	3.09	Hispaniola Round Island	18.20	-71.09
<i>Leioploisma telfairii</i>	4	15	2.08534444	Faecal pellet	Numeric proportion	59	1.97	4.27	Island	-19.90	57.78
<i>Lepidoblepharis xanthostigma</i>	52	530	0.351045202	Stomach contents	Volumetric proportion	9	1.81	2.14	Costa Rica	11.05	-85.67
<i>Lygodactylus capensis</i>	42	387	0.268259793	Stomach contents	Numeric proportion	22	1.02	1.30	Zimbabwe	-17.71	31.13
<i>Mabuya mabouya</i>	50	754	1.541134847	Stomach contents	Volumetric proportion	29	1.56	2.18	Ecuador	0.05	-76.98
<i>Menetia greyii</i>	91	109	0.048051712	Stomach contents	Numeric proportion	44	1.18	4.02	Australia	-25.30	133.16
<i>Morethia boulengeri</i>	76	106	0.544719909	Stomach contents	Numeric proportion	80	1.32	7.66	Australia South Island	-25.21	136.95
<i>Oligosoma grande</i>	9	37	1.565107002	Faecal pellet	Numeric proportion	167	2.09	3.72	South Island	-45.43	170.43
<i>Oligosoma maccanni</i>	9	37	0.929572819	Faecal pellet	Numeric proportion	29	1.00	2.35	South Island	-43.83	172.68
<i>Oligosoma nigriplantare</i>	9	37	1.304668998	Faecal pellet	Numeric proportion	10	1.55	4.73	South Island	-43.83	172.68
<i>Oligosoma otagense</i>	9	37	1.732916949	Faecal pellet	Numeric proportion	78	2.20	4.01	South Island	-45.43	170.43
<i>Phrynosoma cornutum</i>	27	203	1.804026354	Stomach contents	Volumetric proportion	10	1.07	2.11	Mexico United States	31.17	-106.22
<i>Phrynosoma douglasii</i>	8	168	1.758428105	Stomach contents	Volumetric proportion	42	1.01	3.26	United States	44.11	-118.38
<i>Phrynosoma modestum</i>	27	203	1.1008186	Stomach contents	Volumetric proportion	12	1.36	1.85	Mexico	31.17	-106.22
<i>Phyllopezus pollicaris</i>	42	378	1.342396018	Stomach contents	Numeric proportion	24	1.40	8.16	Brazil	-10.67	-46.15
<i>Pinoyscincus jagori</i>	49	190	1.47047633	Stomach contents	Numeric proportion	363	1.05	1.50	Luzon United States	13.92	123.85
<i>Plestiodon reynoldsi</i>	14	159	0.728897229	Stomach contents	Numeric proportion	14	1.00	1.80	United States	28.17	-81.92

binomial	lizard richness	predator richness	maximum body mass (g)	diet data origin	diet data type	number of stomachs	niche breadth from clumped dataset	niche breadth from full dataset	diet data collection area	Diet Latitude	Diet Longitude
Plica plica	51	665	2.227489717	Stomach contents	Volumetric proportion	22	1.26	6.24	Ecuador	0.05	-76.98
Plica umbra	57	613	1.5533	Stomach contents	Volumetric proportion	12	1.00	1.18	Brazil	-2.88	-59.97
Podarcis filfolensis	2	19	1.16570493	Faecal pellet	Numeric proportion	23	1.22	4.11	Lampione Skyros	35.55	12.31
Podarcis gaigeae	1	42	1.359	Stomach contents	Numeric proportion	50	1.10	2.59	Archipelago Scoglio Faraglione islet	36.69	24.39
Podarcis raffoneae	1	20	1.15071525	Faecal pellet	Numeric proportion	34	1.21	6.59		35.55	12.31
Salvator merianae	44	447	3.646796713	Stomach contents	Volumetric proportion	15	3.71	3.93	Brazil	-15.63	-53.99
Sceloporus grammicus	25	309	1.254014396	Stomach contents	Volumetric proportion	25	1.30	6.19	Mexico	22.83	-104.08
Sceloporus magister	18	168	1.906675898	Stomach contents	Volumetric proportion	123	1.17	3.02	Mexico	28.37	-111.43
Sceloporus poinsettii	25	309	1.865000958	Stomach contents	Volumetric proportion	12	1.92	3.51	Mexico United States Saint Vincent	22.83	-104.08
Scincella lateralis	9	151	0.593081146	Stomach contents	Volumetric proportion	142	1.09	9.99		33.93	-89.09
Sphaerodactylus vincenti	14	45	0.199137556	Stomach contents	Volumetric proportion	40	1.08	3.54		13.21	-61.22
Stellagama stellio	17	142	2.52449091	Stomach contents	Numeric proportion	91	1.01	3.05	Turkey	35.81	32.93
Tenuidactylus caspius	40	210	1.01279269	Stomach contents	Numeric proportion	20	1.00	3.02	Iran	36.53	54.12
Trachylepis quinquesquamata	14	201	1.910916563	Stomach contents	Numeric proportion	10	1.06	1.14	Chad	12.95	17.15
Tropidurus itambere	40	424	1.492734938	Stomach contents	Volumetric proportion	244	1.11	4.63	Brazil	-15.85	-48.95
Tropidurus torquatus	30	499	1.898872526	Stomach contents	Volumetric proportion	29	2.45	5.14	Brazil	-22.95	-43.01
Tupinambis teguixin	45	571	3.646796713	Stomach contents	Numeric proportion	51	1.66	3.36	Brazil	2.83	-60.67
Uma exsul	33	191	1.499	Stomach contents	Volumetric proportion	23	1.15	7.04	Mexico	25.38	-103.50
Uta stansburiana	13	145	1.195135671	Stomach contents	Volumetric proportion	556	1.33	6.39	Spain	40.80	0.00
Varanus brevicauda	92	83	1.493698713	Stomach contents	Numeric proportion	26	1.88	6.47	Australia	-28.20	123.58
Varanus tristis	92	83	2.73570998	Stomach contents	Numeric proportion	75	2.52	3.92	Australia	-28.20	123.58
Xenosaurus grandis	32	423	1.752423751	Stomach contents	Numeric proportion	25	1.17	7.60	Mexico	18.87	æ-97.03

Appendix 1d

binomial	locality for density and diet	sources for dietary data
<i>Acanthodactylus boskianus</i>	different localities	Pérez-Mellado, V. (1992). Ecology Of Lacertid Lizards In A Desert Area Of Eastern Morocco. <i>Journal Of Zoology</i> , 226(3), 369-386. Svl: Meiri, S. 2008 Evolution And Ecology Of Lizard Body Sizes
<i>Acanthodactylus scutellatus</i>	different localities	Pérez-Mellado, V. (1992). Ecology Of Lacertid Lizards In A Desert Area Of Eastern Morocco. <i>Journal Of Zoology</i> , 226(3), 369-386. Svl: Meiri, S. 2008 Evolution And Ecology Of Lizard Body Sizes
<i>Agama agama</i>	different localities	Hardy, L. M., & Crnkovic, A. C. (2006). Diet Of Amphibians And Reptiles From The Engare Ondare River Region Of Central Kenya, During The Dry Season. <i>African Journal Of Herpetology</i> , 55(2), 143-159.
<i>Algyroides fitzingeri</i>	same locality	Capula, M. And Luiselli, L. 1994 Resource Partitioning In A Mediterranean Lizard Community. <i>Bulletino Di Zoologia</i> , 61, 173-177.
<i>Amblyrhynchus cristatus</i>	different localities	Wikelski, M., Gall, B. And Trillmich, F. 1993 Ontogenetic Changes In Food Intake And Digestion Rate Of The Herbivorous Marine Iguana (<i>Amblyrhynchus Criscatus</i> , Bell). <i>Oecologia</i> , 94, 373-379.
<i>Ameiva ameiva</i>	same locality	Gainsbury, A. M. And Colli, G. 2003 Lizard Assemblages From Natural Cerrado Enclaves In Southwestern Amazonia: The Role Of Stochastic Extinctions And Isolation. <i>Biotropica</i> , 35, 503-519.
<i>Ameiva chrysoloma</i>	same locality	Sproston, A.L., Glor, R.E., Hartley, L.M., Censky, E.J., Powell, R. And Parmerlee, J.S. 1999 Niche Differences Among Three Sympatric Species Of <i>Ameiva</i> (Reptilia: Teiidae) On Hispaniola. <i>Journal Of Herpetology</i> , 33, 131-136.
<i>Ameiva exsul</i>	same locality	Lewis, A.R. 1989 Diet Selection And Depression Of Prey Abundance By An Intensively Foraging Lizard. <i>Journal Of Herpetology</i> , 23, 164-170.
<i>Anolis acutus</i>	same locality	Simmons, P.M., Greene, B.T., Williamson, K.E., Powell, R. And Parmerlee, J.S. 2005 Ecological Interactions Within A Lizard Community On Grenada. <i>Herperologica</i> , 61, 124-134.
<i>Anolis aeneus</i>	same locality	Schoener, T.W. & Gorman, G.C. 1968 Some Niche Differences In Three Lesser Antillean Lizards Of The Genus <i>Anolis</i> . <i>Ecology</i> , 49, 819-830.
<i>Anolis bahorucoensis</i>	same locality	Cast, E.E., Gifford, M.E., Schneider, K.R., Hardwick, A.J. And Parmerlee, J.S. 2000 Natural History Of The Aniliane Lizard Community In The Sierra De Baoruco, Republica Dominicana. <i>Caribbean Journal Of Science</i> , 36, 258-266.
<i>Anolis barkeri</i>	same locality	Birt, R. A., Powell, R. And Greene, B. D. 2001. Natural History Of <i>Anolis Barkeri</i> : A Semiaquatic Lizard From Southern Mexico. <i>Journal Of Herpetology</i> , 35: 161-166.
<i>Anolis brevirostris</i>	same locality	Moster, J.A., Powell, R., Parmerlee, J.S., Smith, D.D. And Lathrop, A. 1992 Natural History Notes On A Small Population Of <i>Anolis Brevirostris</i> (Sauria: Polychrididae) From Altered Habitat In The Dominican Republic. <i>Bulletin Of The Maryland Herpetological Society</i> , 28, 150-161.
<i>Anolis coelestinus</i>	same locality	Cast, E.E., Gifford, M.E., Schneider, K.R., Hardwick, A.J. And Parmerlee, J.S. 2000 Natural History Of The Aniliane Lizard Community In The Sierra De Baoruco, Republica Dominicana. <i>Caribbean Journal Of Science</i> , 36, 258-266.
<i>Anolis cybotes</i>	same locality	Cast, E.E., Gifford, M.E., Schneider, K.R., Hardwick, A.J. And Parmerlee, J.S. 2000 Natural History Of The Aniliane Lizard Community In The Sierra De Baoruco, Republica Dominicana. <i>Caribbean Journal Of Science</i> , 36, 258-266.
<i>Anolis distichus</i>	same locality	Sifers, S.M., Yeska, M.L., Ramos, Y.M., Powell, R. And Parmerlee, J.S. 2001 <i>Anolis</i> Lizards Restricted To Altered Edge Habitats In A Hispaniolan Cloud Forest. <i>Caribbean Journal Of Science</i> , 37, 55-62.
<i>Anolis fuscoauratus</i>	different localities	Vitt, L. J., Avila-Pires, T. C. S., Zani, P. A., Sartorius, S. S. And Esposito, M. C. 2003. Life Above Ground: Ecology Of <i>Anolis Fuscoauratus</i> In The Amazon Rain Forest, And Comparisons With Its Nearest Relatives. <i>Canadian Journal Of Zoology</i> 81: 142-156.
<i>Anolis humilis</i>	same locality	Andrews, R. M. 1979. Evolution Of Life Histories: A Comparison Of <i>Anolis</i> Lizards From Matched Island And Mainland Habitats. <i>Breviora</i> 454: 1-51.
<i>Anolis limifrons</i>	same locality	Andrews, R. M. 1979. Evolution Of Life Histories: A Comparison Of <i>Anolis</i> Lizards From Matched Island And Mainland Habitats. <i>Breviora</i> 454: 1-51.
<i>Anolis lineatopus</i>	same locality	Rand,S. 1967 Ecology And Social Organization In The Iguanid Lizard <i>Anolis Lineatopus</i> . <i>Proceedings Of The United States National Museum</i> , 122, 1-79.
<i>Anolis oculatus</i>	same locality	Andrews, R. M. 1979. Evolution Of Life Histories: A Comparison Of <i>Anolis</i> Lizards From Matched Island And Mainland Habitats. <i>Breviora</i> 454: 1-51.
<i>Anolis opalinus</i>	same locality	Floys, H.B. And Jenssen, A. 1983 Food Habits Of The Jamaican Lizard <i>Anolis Opalinus</i> : Resource Partitioning And Seasonal Effects Examined. <i>Copeia</i> , 1983, 319-331.

Anolis polylepis	same locality	Perry, G. (1996). The Evolution Of Sexual Dimorphism In The Lizard <i>Anolis Polylepis</i> (Iguania): Evidence From Intraspecific Variation In Foraging Behavior And Diet. Canadian Journal Of Zoology, 74(7), 1238-1245. Max Svl: Koehler, G., Dehling, D. M., & Koehler, J. (2010). Cryptic Species And Hybridization In The <i>Anolis Polylepis</i> Complex, With The Description Of A New Species From The Osa Peninsula, Costa Rica (Squamata: Polychrotidae). Zootaxa, 2718, 23-38.
Anolis punctatus	different localities	Vitt, L. J., Avila-Pires, T. C. S., Esposito, M. C., Sartorius, S. S. And Zani, P. A. 2003. Sharing Amazonian Rain-Forest Trees: Ecology Of <i>Anolis Punctatus</i> And <i>Anolis Transversalis</i> (Squamata: Polychrotidae). Journal Of Herpetology, 37: 276-285.
Anolis richardii	same locality	Schoener, T.W. & Gorman, G.C. 1968 Some Niche Differences In Three Lesser Antillean Lizards Of The Genus <i>Anolis</i> . Ecology, 49, 819-830.
Aspidoscelis sexlineata	same locality	Hamilton, W. J., & Pollack, J. A. (1961). The Food Of Some Lizards From Fort Benning, Georgia. Herpetologica, 99-106.
Aspidoscelis tigris	same locality	Medica, P. A. (1967). Food Habits, Habitat Preference, Reproduction, And Diurnal Activity In Four Sympatric Species Of Whiptail Lizards (<i>Cnemidophorus</i>) In South Central Ne
Brachylophus vitiensis	same locality	Morrison, C., Osborne, T., Harlow, P.S., Thomas, N., Biciloa, P. And Niukula, J. 2007 Diet And Habitat Preferences Of The Fijian Crested Iguana (<i>Brachylophus Vitiensis</i>) On Yadua Taba, Fiji: Implications For Conservation. Australian Journal Of Zoology, 55, 341-350.
Cercosaura ocellata	same locality	Gainsbury,A. M. And Colli, G. 2003 Lizard Assemblages From Natural Cerrado Enclaves In Southwestern Amazonia: The Role Of Stochastic Extinctions And Isolation. Biotrophica, 35, 503-519.
Chlamydosaurus kingii	same locality	Griffiths, A. D., & Christian, K. A. (1996). The Effects Of Fire On The Frillneck Lizard (<i>Chlamydosaurus Kingii</i>) In Northern Australia. Australian Journal Of Ecology, 21(4), 386-398.
Cnemidophorus lemniscatus	same locality	Vitt, L. J., Zani, P. A., Caldwell, J. P., De Araujo, M. C., & Magnusson, W. E. (1997). Ecology Of Whiptail Lizards (<i>Cnemidophorus</i>) In The Amazon Region Of Brazil. Copeia, 745-757.
Coleodactylus natalensis	same locality	Lisboa, C. M., Sales, R. F., & Freire, E. M. (2012). Feeding Ecology Of The Pygmy Gecko <i>Coleodactylus Natalensis</i> (Squamata: Sphaerodactylidae) In The Brazilian Atlantic Forest. Zoologia (Curitiba), 29(4), 293-299.
Ctenosaura pectinata	same locality	Durtsche, R. D. (2000). Ontogenetic Plasticity Of Food Habits In The Mexican Spiny-Tailed Iguana, <i>Ctenosaura Pectinata</i> . Oecologia, 124(2), 185-195.
Ctenotus leonhardii	same locality	James, C. D. (1991). Temporal Variation In Diets And Trophic Partitioning By Coexisting Lizards (<i>Ctenotus</i> : Scincidae) In Central Australia. Oecologia, 85(4), 553-561.
Ctenotus pantherinus	same locality	James, C. D. (1991). Temporal Variation In Diets And Trophic Partitioning By Coexisting Lizards (<i>Ctenotus</i> : Scincidae) In Central Australia. Oecologia, 85(4), 553-561.
Ctenotus piankai	same locality	James, C. D. (1991). Temporal variation in diets and trophic partitioning by coexisting lizards (<i>Ctenotus</i> : Scincidae) in central Australia. Oecologia, 85(4), 553-561.
Ctenotus quattuordecimlineatus	same locality	James, C. D. (1991). Temporal variation in diets and trophic partitioning by coexisting lizards (<i>Ctenotus</i> : Scincidae) in central Australia. Oecologia, 85(4), 553-561.
Ctenotus taeniatus	same locality	Taylor, J. A. (1986). Food And Foraging Behaviour Of The Lizard, <i>Ctenotus Taeniatus</i> . Australian Journal Of Ecology, 11(1), 49-54.
Cyclura carinata	same locality	Auffenberg, W. 1982. Feeding Strategy Of The Caicos Ground Iguana <i>Cyclura Carinata</i> . Pp. 84-116. In C. M. Burghardat Nd A. S. Rand (Eds.), Iguanas Of The World: Behavior, Ecology, And Conservation.
Cyclura pinguis	same locality	Mitchell, N.C. 1999 Effect Of Introduced Ungulates On Density, Dietary Preferences, Home Range, And Physicalcondition Of The Iguana (<i>Cyclura Pinguis</i>) On Anegada. Herpetologica, 55, 7-17.
Draco volans	same locality	Reyes, A.Y. 1968 Food Habits Of <i>Draco Volans Linnaeus</i> . The Silliman Journal, 15, 353-356.
Egernia kingii	same locality	Arena And Wooler 2003 The Reproduction And Diet Of <i>Egernia Kingii</i> (Reptilia: Scincidae) On Penguin Island, Western Australia. Australian Journal Of Zoology, 51: 495-504.
Emoia atrocostata	different localities	Auffenberg, W. And Auffenberg, T. 1988 Resource Partitioning In A Community Of Philippine Skinks (Sauria: Scincidae). Bulletin Of The Florida State Museum. Biological Sciences (Usa).
Eremiascincus richardsonii	same locality	Pianka, E. R. (2011). Notes On The Ecology Of Some Uncommon Skinks In The Great Victoria Desert. West. Aust. Nat, 28, 50-60.
Eutropis multifasciata	same locality	Auffenberg, W. And Auffenberg, T. 1988 Resource Partitioning In A Community Of Philippine Skinks (Sauria: Scincidae). Bulletin Of The Florida State Museum. Biological Sciences (Usa).
Gallotia galloti	same locality	Valido, A. And Nogales, M. 2003 Digestive Ecology Of Two Omnivorous Canarian Lizard Species (<i>Gallotia</i> , Lacertidae). Amphibia-Reptilia, 24, 331-344.
Gonatodes humeralis	same locality	Vitt, L. J., Souza, R. A., Sartorius, S. S., Avila-Pires, T. C. S. And Esposito, M. C. 2000. Comparative Ecology Of Sympatric Gonatodes (Squamata: Gekkonidae) In The Western Amazon Of Brazil. Copeia, 2000: 83-95.

<i>Gymnodactylus darwini</i>	same locality	Teixeira, R. L. (2002). Aspectos Ecológicos De <i>Gymnodactylus Darwinii</i> (Sauria: Gekkonidae) Em Pontal Do Ipiranga, Linhares, Espírito Santo, Sudeste Do Brasil. Boletim Do Museu De Biologia Mello Leitão, 14, 21-31.
<i>Heliobolus spekii</i>	same locality	Hardy, L. M., & Crnkovic, A. C. (2006). Diet Of Amphibians And Reptiles From The Engare Ondare River Region Of Central Kenya, During The Dry Season. African Journal Of Herpetology, 55(2), 143-159.
<i>Hemidactylus mabouia</i>	same locality	Vitt, L. J. 1995. The Ecology Of Tropical Lizards In The Caatinga Of Northeast Brazil. Occasional Papers Of The Oklahoma Museum Of Natural History 1: 1-29.
<i>Holbrookia propinqua</i>	same locality	Judd, F. W. (1976). Food And Feeding Behavior Of The Keeled Earless Lizard, <i>Holbrookia Propinqua</i> . The Southwestern Naturalist, 17-25.
<i>Iberolacerta monticola</i>	same locality	Pérez-Mellado, V., Bauwens, D., Gil, M., Guerrero, F., Lizana, M., & Ciudad, M. J. (1991). Diet Composition And Prey Selection In The Lizard <i>Lacerta Monticola</i> . Canadian Journal Of Zoology, 69(7), 1728-1735.
<i>Kentropyx pelviceps</i>	same locality	Vitt, L. J., Sartorius, S. S., Avila-Pires, T. C. S., Esposito, M. C. And Miles, D. B. 2000. Niche Segregation Among Sympatric Amazonian Teiid Lizards. Oecologia 122: 410-420.
<i>Kentropyx striata</i>	same locality	Vitt, L. J. And De Carvalho, C. M. 1995. Niche Partitioning In A Tropical Wet Season: Lizards In The Lavrado Area Of Northern Brazil. Copeia 1995: 305-329.
<i>Lamprolepis smaragdina</i>	same locality	Auffenberg, W. And Auffenberg, T. 1988 Resource Partitioning In A Community Of Philippine Skinks (Sauria: Scincidae). Bulletin Of The Florida State Museum. Biological Sciences (Usa).
<i>Leiocephalus schreibersii</i>	same locality	Schreiber, M.C., Powell, R., Parmerlee, J.S., Lathrop, A. And Smith, D.D. 1993 Natural History Of A Small Population Of <i>Leiocephalus Schreibersii</i> (Sauria: Tropiduridae) From Altered Habitat In The Dominican Republic. Biological Sciences, 56, 82-
<i>Leiolopisma telfairii</i>	same locality	Pernetta,A.P., Bell, D.J. And Jones, C.G. 2005 Macro- And Microhabitat Use Of Telfair'S Skink (<i>Leiolopisma Telfairii</i>) On Round Island, Mauritius: Implications For Their Translocation. Acta Oecologica, 28, 313-323.
<i>Lepidoblepharis xanthostigma</i>	same locality	Vitt, L. J., Sartorius, S. S., Avila-Pires, T. C. S., Zani, P. A., & Espósito, M. C. (2005). Small In A Big World: Ecology Of Leaf-Litter Geckos In New World Tropical Forests. Herpetological Monographs, 19(1), 137-152.
<i>Lygodactylus capensis</i>	different localities	Simbotwe, M. P. (1983). Comparative Ecology Of Diurnal Geckos (<i>Lygodactylus</i>) In Kafue Flats, Zambia*. African Journal Of Ecology, 21(3), 143-153.
<i>Mabuya mabouya</i>	different localities	Duellman, W. E. 1978. The biology of an equatorial herpetofauna in Amazonian Ecuador. University of Kansas Museum of Natural History Miscellaneous publications 65: 1-352.
<i>Menetia greyii</i>	same locality	Pianka 1986. Ecology and Natural History of Desert Lizards. Analyses of the Ecological Niche and Community Structure.
<i>Morethia boulengeri</i>	same locality	Smyth, M., & Smith, M. J. (1974). Aspects of the natural history of three Australian skinks, <i>Morethia boulengeri</i> , <i>Menetia greyii</i> and <i>Lerista bougainvillii</i> .Journal of herpetology, 329-335.
<i>Oligosoma grande</i>	same locality	Tocher, M.D. 2003 The Diet Of Grand Skinks (<i>Oligosoma Grande</i>) And Otago Skinks (<i>O. Otagense</i>) In Otago Seral Tussock Grasslands. New Zealand Journal Of Zoology, 30, 243-257.
<i>Oligosoma maccanni</i>	same locality	Freeman, A.B. 1997 Comparative Ecology Of Two <i>Oligosoma</i> Skinks In Coastal Canterbury: A Contrast With Central Otago. New Zealand Journal Of Ecology, 21, 153-160.
<i>Oligosoma nigriplantare</i>	same locality	Freeman, A.B. 1997 Comparative Ecology Of Two <i>Oligosoma</i> Skinks In Coastal Canterbury: A Contrast With Central Otago. New Zealand Journal Of Ecology, 21, 153-160.
<i>Oligosoma otagense</i>	same locality	Tocher, M.D. 2003 The Diet Of Grand Skinks (<i>Oligosoma Grande</i>) And Otago Skinks (<i>O. Otagense</i>) In Otago Seral Tussock Grasslands. New Zealand Journal Of Zoology, 30, 243-257.
<i>Phrynosoma cornutum</i>	same locality	Lemos-Espinal, J. A., Smith, G. R., & Ballinger, R. E. (2004). Diets Of Four Species Of Horned Lizards (Genus <i>Phrynosoma</i>) From Mexico. Herpetological Review, 35(2), 131-134.
<i>Phrynosoma douglasii</i>	same locality	Montanucci, R. R. (1981). Habitat Separation Between <i>Phrynosoma Douglassi</i> And <i>P. Orbiculare</i> (Lacertilia: Iguanidae) In Mexico. Copeia, 147-153.
<i>Phrynosoma modestum</i>	same locality	Lemos-Espinal, J. A., Smith, G. R., & Ballinger, R. E. (2004). Diets Of Four Species Of Horned Lizards (Genus <i>Phrynosoma</i>) From Mexico. Herpetological Review, 35(2), 131-134.
<i>Phyllopezus pollicaris</i>	same locality	Recoder, R., Teixeira Junior, M., Camacho, A., & Rodrigues, M. T. (2012). Natural History Of The Tropical Gecko <i>Phyllopezus Pollicaris</i> (Squamata, Phyllodactylidae) From A Sandstone Outcrop In Central Brazil. Herpetology Notes, 5, 49-58.
<i>Pinoyscincus jagori</i>	different localities	Auffenberg, W. And Auffenberg, T. 1988 Resource Partitioning In A Community Of Philippine Skinks (Sauria: Scincidae). Bulletin Of The Florida State Museum. Biological Sciences (Usa).
<i>Plestiodon reynoldsi</i>	same locality	Mccoy, E. D., Ihász, N., Britt, E. J., & Mushinsky, H. R. (2010). Is The Florida Sand Skink (<i>Plestiodon Reynoldsi</i>) A Dietary Specialist? Herpetologica, 66(4), 432-442.
<i>Plica plica</i>	different localities	Duellman, W. E. 1978. The biology of an equatorial herpetofauna in Amazonian Ecuador. University of Kansas Museum of Natural History Miscellaneous publications 65: 1-352.

<i>Plica umbra</i>	same locality	Gasnier, T. R., Magnusson, W. E. And Lima, A. P. 1994. Foraging Activity And Diet Of Four Sympatric Lizard Species In A Tropical Rainforest. <i>Journal Of Herpetology</i> , 28: 187-192.
<i>Podarcis filfolensis</i>	different localities	Lo Cascio, P., Luiselli, L. And Corti, C. 2006 Preliminary Data On The Ecology Of <i>Podarcis Filfolensis</i> Of Lampione Islet (Pelagian Islands, Channel Of Sicily, Italy). In: Mainland And Insular Lacertid Lizards: A Mediterranean Perspective (Eds: Corti, C., Lo Cascio, P., Baggini, M.). Firenze University Press. Adamopoulou, C., Valakos, E.D. And Pafilis, P. 1999 Summer Diet Of <i>Podarcis Milensis</i> , <i>P. Gaigeae</i> And <i>P. Erhardii</i> (Sauria: Lacertidae). Bonner Zoologische Beitrage, 48, 275-282.
<i>Podarcis gaigeae</i>	same locality	Lo Casio 2006 Aspetti Ecologici E Problemi Di Conservazione Di Una Popolazione Di <i>Podarcis Raffonei</i> (Mertens, 1952) (Reptilia Lacertidae). Naturalista Sicily, 30, 495-521.
<i>Podarcis raffoneae</i>	same locality	Colli, G. R., Peres Jr, A. K., & Da Cunha, H. J. (1998). A New Species Of <i>Tupinambis</i> (Squamata: Teiidae) From Central Brazil, With An Analysis Of Morphological And Genetic Variation In The Genus. <i>Herpetologica</i> , 477-492.
<i>Salvator merianae</i>	same locality	Barbault, R., Ortega, A., & Maury, M. E. (1985). Food Partitioning And Community Organization In A Mountain Lizard Guild Of Northern Mexico. <i>Oecologia</i> , 65(4), 550-554.
<i>Sceloporus grammicus</i>	same locality	Parker, W. S., & Pianka, E. R. (1973). Notes On The Ecology Of The Iguanid Lizard, <i>Sceloporus Magister</i> . <i>Herpetologica</i> , 143-152.
<i>Sceloporus magister</i>	different localities	Barbault, R., Ortega, A., & Maury, M. E. (1985). Food Partitioning And Community Organization In A Mountain Lizard Guild Of Northern Mexico. <i>Oecologia</i> , 65(4), 550-554.
<i>Sceloporus poinsettii</i>	different localities	Hamilton, W. J., & Pollack, J. A. (1961). The Food Of Some Lizards From Fort Benning, Georgia. <i>Herpetologica</i> , 99-106.
<i>Scincella lateralis</i>	same locality	Steinberg,D., Powell, S.D., Powell, R., Parmerlee, J.S. And Henderson, R.W. 2007 Population Densities, Water-Loss Rates, And Diets Of <i>Sphaerodactylus vincenti</i> On St. Vincent, West Indies. <i>Journal Of Herpetology</i> , 41, 330-336.
<i>Sphaerodactylus vincenti</i>	same locality	Düzen, S., & Öz, M. (2001). A Study On The Feeding Biology Of <i>Laudakia</i> (= <i>Agama</i>) <i>Stellio</i> (L. 1758)(Lacertilia: Agamidae) Populations In The Antalya Region. <i>Turkish Journal Of Zoology</i> , 25(3), 177-181.
<i>Stellagama stellio</i>	different localities	Hojati, V., & Babaei Savasari, R. (2014). The Diet And Sexual Differences Of The Caspian Bent-Toed Gecko, <i>Tenuidactylus Caspius</i> (Squamata: Gekkonidae), In Northern Iran. <i>International Journal Of Zoology</i> , 2014.
<i>Tenuidactylus caspius</i>	different localities	Hardy, L. M., & Crnkovic, A. C. (2006). Diet Of Amphibians And Reptiles From The Engare Ondare River Region Of Central Kenya, During The Dry Season. <i>African Journal Of Herpetology</i> , 55(2), 143-159.
<i>Trachylepis quinquetaeniata</i>	different localities	Faria, R. G., & Araújo, A. F. B. (2004). Sintopy Of Two <i>Tropidurus</i> Lizard Species (Squamata: Tropiduridae) In A Rocky Cerrado Habitat In Central Brazil. <i>Brazilian Journal Of Biology</i> , 64(4), 775-786.
<i>Tropidurus itambere</i>	same locality	Fialho, R. F., Rocha, C. F. D., & Vrcibradic, D. (2000). Feeding Ecology Of <i>Tropidurus Torquatus</i> : Ontogenetic Shift In Plant Consumption And Seasonal Trends In Diet. <i>Journal Of Herpetology</i> , 325-330.
<i>Tropidurus torquatus</i>	same locality	Vitt, L. J. And De Carvalho, C. M. 1995. Niche Partitioning In A Tropical Wet Season: Lizards In The Lavrado Area Of Northern Brazil. <i>Copeia</i> 1995: 305-329.
<i>Tupinambis teguixin</i>	same locality	Gadsden, H., Palacios-Orona, L. E., & Cruz-Soto, G. A. (2001). Diet Of The Mexican Fringe-Toed Lizard (<i>Uma Exsul</i>). <i>Journal Of Herpetology</i> , 493-496.
<i>Uma exsul</i>	same locality	Parker, W. S., & Pianka, E. R. (1975). Comparative Ecology Of Populations Of The Lizard <i>Uta Stansburiana</i> . <i>Copeia</i> , 615-632.
<i>Uta stansburiana</i>	different localities	Pianka, E. R. (1994). Comparative Ecology Of <i>Varanus</i> In The Great Victoria Desert. <i>Australian Journal Of Ecology</i> , 19(4), 395-408.
<i>Varanus brevicauda</i>	same locality	Pianka, E. R. (1994). Comparative Ecology Of <i>Varanus</i> In The Great Victoria Desert. <i>Australian Journal Of Ecology</i> , 19(4), 395-408.
<i>Varanus tristis</i>	same locality	Lemos-Espinal, J. A., Smith, G. R., & Ballinger, R. E. (2003). Diets Of Three Species Of Knob-Scaled Lizards (Genus <i>Xenosaurus</i>) From México. <i>The Southwestern Naturalist</i> , 48(1), 119-122.
<i>Xenosaurus grandis</i>	same locality	

Appendix 1e: competitors and predators sources

Binomial	WorldID	Where	Island	Birds	Bird richness source	Snakes	Snake richness source	Mammals	Mammals richness source	Sum
<i>Ailuronyx seychellensis</i>	25436	Island	Aride	13	http://www.birdlife.org/	1	Henkel, F. W., & Schmidt, W. (2000). Amphibians and reptiles of Madagascar and the Mascarene, Seychelles, and Comoro Islands. Krieger Publishing Company.	0	potential invasive species	14
<i>Ailuronyx trachygaster</i>	25436	Island	Praslin	13	http://www.birdlife.org/	1	Henkel, F. W., & Schmidt, W. (2000). Amphibians and reptiles of Madagascar and the Mascarene, Seychelles, and Comoro Islands. Krieger Publishing Company. Kadison, A.E. (2014). Disassembling the assemblage: delving into the story of insular faunal body size. MSc Thesis. Tel Aviv University.	0	potential invasive species	14
<i>Algyrodes fitzingeri</i>	44829	Island	Sardinia	83	http://www.birdlife.org/	4	Kadison, A.E. (2014). Disassembling the assemblage: delving into the story of insular faunal body size. MSc Thesis. Tel Aviv University.	4	http://www.stintino.net/en/Animali.php	91
<i>Amblyrhynchus cristatus</i>	26731	Island	Santa Fe	33	http://www.birdlife.org/	2	Kadison, A.E. (2014). Disassembling the assemblage: delving into the story of insular faunal body size. MSc Thesis. Tel Aviv University.	3	http://www.galapagos.org/about_galapagos/mammals/	38
<i>Ameiva chrysolaema</i>	35749	Island	Hispaniola	71	http://www.birdlife.org/	26	http://www.gardinitiative.org/	20	http://www.iucnredlist.org/	117
<i>Ameiva exsul</i>	35753	Island	Puerto Rico	53	http://www.birdlife.org/	12	http://www.gardinitiative.org/	13	http://www.iucnredlist.org/	78
<i>Anolis acutus</i>	32879	Island	Grenada	39	http://www.birdlife.org/	2	Kadison, A.E. (2014). Disassembling the assemblage: delving into the story of insular faunal body size. MSc Thesis. Tel Aviv University.	0	No known source for mammal numbers	41
<i>Anolis aeneus</i>	32879	Island	Grenada	39	http://www.birdlife.org/	4	Kadison, A.E. (2014). Disassembling the assemblage: delving into the story of insular faunal body size. MSc Thesis. Tel Aviv University.	6	http://culture.gd/index.php/oc/wild-life	49
<i>Anolis bahorucoensis</i>	35749	Island	Hispaniola	71	http://www.birdlife.org/	26	http://www.gardinitiative.org/	20	http://www.iucnredlist.org/	117
<i>Anolis brevirostris</i>	35749	Island	Hispaniola	71	http://www.birdlife.org/	26	http://www.gardinitiative.org/	20	http://www.iucnredlist.org/	117
<i>Anolis coelestinus</i>	35749	Island	Hispaniola	71	http://www.birdlife.org/	26	http://www.gardinitiative.org/	20	http://www.iucnredlist.org/	117
<i>Anolis cybotes</i>	35749	Island	Hispaniola	71	http://www.birdlife.org/	26	http://www.gardinitiative.org/	20	http://www.iucnredlist.org/	117
<i>Anolis distichus</i>	35749	Island	Hispaniola	71	http://www.birdlife.org/	26	http://www.gardinitiative.org/	20	http://www.iucnredlist.org/	117
<i>Anolis lineatopus</i>	35744	Island	Jamaica	57	http://www.birdlife.org/	12	http://www.gardinitiative.org/	22	http://www.avirtualdominica.com/nature.com	91
<i>Anolis oculatus</i>	34679	Island	Dominica	52	http://www.birdlife.org/	4	Kadison, A.E. (2014). Disassembling the assemblage: delving into the story of insular faunal body size. MSc Thesis. Tel Aviv University.	4	http://culture.gd/index.php/oc/wild-life	60
<i>Anolis opalinus</i>	35743	Island	Jamaica	70	http://www.birdlife.org/	12	http://www.gardinitiative.org/	22	http://www.iucnredlist.org/	104
<i>Anolis richardii</i>	32879	Island	Grenada	39	http://www.birdlife.org/	4	Kadison, A.E. (2014). Disassembling the assemblage: delving into the story of insular faunal body size. MSc Thesis. Tel Aviv University.	6	http://culture.gd/index.php/oc/wild-life	49

<i>Brachylophus vitiensis</i>	19799	Island	Yadua Taba	24	http://www.birdlife.org/	0	Paine, J.R. (1991) IUCN Directory of Protected Areas in Oceania. IUCN. 447p	0	No know sourcefor mammal numbers http://en.wikipedia.org/wiki/List_of_mammals_of_the_Turks_and_Caicos_Islands	24
<i>Cyclura carinata</i>	37548	Island	Caicos	52	http://www.birdlife.org/	0	Kadison, A.E. (2014). Disassembling the assemblage: delving into the story of insular faunal body size. MSc Thesis. Tel Aviv University.	5	http://www.iucnredlist.org/	57
<i>Cyclura pinguis</i>	36116	Island	Anegada	37	http://www.birdlife.org/	3	Kadison, A.E. (2014). Disassembling the assemblage: delving into the story of insular faunal body size. MSc Thesis. Tel Aviv University.	7	http://www.iucnredlist.org/	47
<i>Draco volans</i>	31984	Island	Negros Pinguin Island	121	http://www.birdlife.org/	38	http://www.gardinitiative.org/	60	http://www.iucnredlist.org/	219
<i>Egernia kingii</i>	12898	Island	Luzon	75	http://www.birdlife.org/	0	Penguin Island Information brochure	2	No know sourcefor mammal numbers http://www.iucnredlist.org/	77
<i>Emoia atrocostata</i>	34144	Island	Negros	117	http://www.birdlife.org/	28	http://www.gardinitiative.org/	45	http://www.iucnredlist.org/	190
<i>Eutropis multifasciata</i>	31984	Island	Tenerife	121	http://www.birdlife.org/	38	http://www.gardinitiative.org/	60	http://www.tenerife-information-centre.com/tenerife-mammals.html	219
<i>Gallotia galloti</i>	40484	Island	Hispaniola	26	http://www.birdlife.org/	0	http://www.focusonnature.com/CanaryIslandsAmphibia nsAndReptiles.htm	6	http://www.iucnredlist.org/	32
<i>Lamprolepis smaragdina</i>	31984	Island	Negros	121	http://www.birdlife.org/	38	http://www.gardinitiative.org/	60	http://www.iucnredlist.org/	219
<i>Leiocephalus schreibersii</i>	35749	Island	Round Island South	71	http://www.birdlife.org/	26	http://www.gardinitiative.org/	20	North, S.G. & Bullock, D.J. (1986). Changes in the vegetation and populations of introduced mammals of Round Island and Gunner's Quoin, Mauritius. Biol. Conserv., 37, 99–117	117
<i>Leiopisma telfairii</i>	18238	Island	Round Island South	11	http://www.birdlife.org/	2	Bullock, D.J. (1986) The ecology and conservation of reptiles on Round Island and Gunner's Quoin, Mauritius. Biological Conservation, 37, 135–156.	2	http://www.iucnredlist.org/	15
<i>Oligosoma grande</i>	7911	Island	Island South	37	http://www.birdlife.org/	0	http://www.gardinitiative.org/	0	http://www.iucnredlist.org/	37
<i>Oligosoma maccanni</i>	8633	Island	Island South	37	http://www.birdlife.org/	0	http://www.gardinitiative.org/	0	http://www.iucnredlist.org/	37
<i>Oligosoma nigriplantare</i>	8633	Island	Island South	37	http://www.birdlife.org/	0	http://www.gardinitiative.org/	0	http://www.iucnredlist.org/	37
<i>Oligosoma otagense</i>	7911	Island	Island	37	http://www.birdlife.org/	0	http://www.gardinitiative.org/	0	http://www.iucnredlist.org/	37
<i>Pinoyscincus jagori</i>	34144	Island	Luzon	117	http://www.birdlife.org/	28	http://www.gardinitiative.org/	45	http://www.iucnredlist.org/	190

Podarcis filfolensis	43393	Island	Lampione	19	http://www.birdlife.org/	0	Cascio and Pasta (2012) Lampione, a paradigmatic case of Mediterranean island biodiversity. <i>Biodiversity Journal</i> , 3, 311-330	0	Cascio and Pasta (2012) Lampione, a paradigmatic case of Mediterranean island biodiversity. <i>Biodiversity Journal</i> , 3, 311-330	19	
Podarcis gaigeae	43765	Island	Skyros Archipelago Scoglio Faraglione islet	37	http://www.birdlife.org/	0	Kadison, A.E. (2014). Disassembling the assemblage: delving into the story of insular faunal body size. MSc Thesis. Tel Aviv University.	5	Masetti, M. (2012). <i>Atlas of terrestrial mammals of the Ionian and Aegean islands</i> . Walter de Gruyter.	42	
Podarcis raffoneae	43393	Island		19	http://www.birdlife.org/	1	http://www.hylawerkgroep.be/jeroen/index.php?id=51	0	http://www.iucnredlist.org/	20	
Podarcis tiliguerta	44829	Island	Sardinia	83	http://www.birdlife.org/	4	http://www.gardinitiative.org/	4	http://www.iucnredlist.org/	91	
Sphaerodactylus vincenti	33599	Island	Saint Vincent	37	http://www.birdlife.org/	2	Kadison, A.E. (2014). Disassembling the assemblage: delving into the story of insular faunal body size. MSc Thesis. Tel Aviv University.	8	http://en.wikipedia.org/wiki/List_of_mammals_of_Saint_Vincent_and_the_Grenadines	45	
Acanthodactylus boskianus	38361	Mainland	NA	10	http://www.birdlife.org/	7	http://www.gardinitiative.org/	12	http://www.iucnredlist.org/	29	
Acanthodactylus scutellatus	38357	Mainland	NA	8	http://www.birdlife.org/	11	http://www.gardinitiative.org/	10	http://www.iucnredlist.org/	29	
Agama agama	31873	Mainland	NA	154	http://www.birdlife.org/	57	http://www.gardinitiative.org/	98	http://www.iucnredlist.org/	309	
Agama rueppelli	29743	Mainland	NA	116	http://www.birdlife.org/	22	http://www.gardinitiative.org/	62	http://www.iucnredlist.org/	200	
Ameiva ameiva	22075	Mainland	NA	296	http://www.birdlife.org/	112	http://www.gardinitiative.org/	172	http://www.iucnredlist.org/	580	
Anolis barkeri	36085	Mainland	NA	195	http://www.birdlife.org/	63	http://www.gardinitiative.org/	119	http://www.iucnredlist.org/	377	
Anolis fuscoauratus	27464	Mainland	NA	359	http://www.birdlife.org/	100	http://www.gardinitiative.org/	206	http://www.iucnredlist.org/	665	
Anolis humilis	32137	Mainland	NA	264	http://www.birdlife.org/	113	http://www.gardinitiative.org/	179	http://www.iucnredlist.org/	556	
Anolis limifrons	32137	Mainland	NA	264	http://www.birdlife.org/	113	http://www.gardinitiative.org/	179	http://www.iucnredlist.org/	556	
Anolis ortonii	27464	Mainland	NA	359	http://www.birdlife.org/	100	http://www.gardinitiative.org/	206	http://www.iucnredlist.org/	665	
Anolis polylepis	31417	Mainland	NA	240	http://www.birdlife.org/	88	http://www.gardinitiative.org/	169	http://www.iucnredlist.org/	497	
Anolis punctatus	27464	Mainland	NA	359	http://www.birdlife.org/	100	http://www.gardinitiative.org/	206	http://www.iucnredlist.org/	665	
Aspidoscelis sexlineata	42928	Mainland	NA	84	http://www.birdlife.org/	32	http://www.gardinitiative.org/	56	http://www.iucnredlist.org/	172	
Aspidoscelis tigris	42549	Mainland	NA	103	http://www.birdlife.org/	33	http://www.gardinitiative.org/	89	http://www.iucnredlist.org/	225	

<i>Cercosaura eigenmanni</i>	21360	Mainland	NA	271	http://www.birdlife.org/	105	http://www.gardinitiative.org/	149	http://www.iucnredlist.org/	525
<i>Cercosaura ocellata</i>	21360	Mainland	NA	271	http://www.birdlife.org/	105	http://www.gardinitiative.org/	149	http://www.iucnredlist.org/	525
<i>Chlamydosaurus kingii</i>	21553	Mainland	NA	119	http://www.birdlife.org/	37	http://www.gardinitiative.org/	59	http://www.iucnredlist.org/	215
<i>Cnemidophorus lemniscatus</i>	28560	Mainland	NA	267	http://www.birdlife.org/	108	http://www.gardinitiative.org/	196	http://www.iucnredlist.org/	571
<i>Coleodactylus natalensis</i>	24625	Mainland	NA	122	http://www.birdlife.org/	43	http://www.gardinitiative.org/	118	http://www.iucnredlist.org/	283
<i>Ctenosaura pectinata</i>	36082	Mainland	NA	134	http://www.birdlife.org/	47	http://www.gardinitiative.org/	122	http://www.iucnredlist.org/	303
<i>Ctenotus leonhardii</i>	16875	Mainland	NA	73	http://www.birdlife.org/	21	http://www.gardinitiative.org/	29	http://www.iucnredlist.org/	123
<i>Ctenotus pantherinus</i>	16875	Mainland	NA	73	http://www.birdlife.org/	21	http://www.gardinitiative.org/	29	http://www.iucnredlist.org/	123
<i>Ctenotus piankai</i>	16875	Mainland	NA	73	http://www.birdlife.org/	21	http://www.gardinitiative.org/	29	http://www.iucnredlist.org/	123
<i>Ctenotus quattuordecimlineatus</i>	16875	Mainland	NA	73	http://www.birdlife.org/	21	http://www.gardinitiative.org/	29	http://www.iucnredlist.org/	123
<i>Ctenotus taeniolatus</i>	15450	Mainland	NA	111	http://www.birdlife.org/	36	http://www.gardinitiative.org/	45	http://www.iucnredlist.org/	192
<i>Eremiascincus richardsonii</i>	16514	Mainland	NA	73	http://www.birdlife.org/	22	http://www.gardinitiative.org/	31	http://www.iucnredlist.org/	126
<i>Gonatodes humeralis</i>	28198	Mainland	NA	222	http://www.birdlife.org/	110	http://www.gardinitiative.org/	181	http://www.iucnredlist.org/	513
<i>Gymnodactylus darwini</i>	17058	Mainland	NA	279	http://www.birdlife.org/	91	http://www.gardinitiative.org/	170	http://www.iucnredlist.org/	540
<i>Heliobolus spekii</i>	28660	Mainland	NA	123	http://www.birdlife.org/	28	http://www.gardinitiative.org/	71	http://www.iucnredlist.org/	222
<i>Hemidactylus mabouia</i>	23186	Mainland	NA	162	http://www.birdlife.org/	42	http://www.gardinitiative.org/	124	http://www.iucnredlist.org/	328
<i>Holbrookia propinqua</i>	40042	Mainland	NA	108	http://www.birdlife.org/	39	http://www.gardinitiative.org/	55	http://www.iucnredlist.org/	202
<i>Iberolacerta monticola</i>	45894	Mainland	NA	68	http://www.birdlife.org/	8	http://www.gardinitiative.org/	63	http://www.iucnredlist.org/	139
<i>Iphisa elegans</i>	27463	Mainland	NA	418	http://www.birdlife.org/	91	http://www.gardinitiative.org/	245	http://www.iucnredlist.org/	754
<i>Kentropyx pelviceps</i>	23155	Mainland	NA	293	http://www.birdlife.org/	110	http://www.gardinitiative.org/	166	http://www.iucnredlist.org/	569
<i>Kentropyx striata</i>	28560	Mainland	NA	267	http://www.birdlife.org/	108	http://www.gardinitiative.org/	196	http://www.iucnredlist.org/	571
<i>Latastia longicaudata</i>	32602	Mainland	NA	139	http://www.birdlife.org/	33	http://www.gardinitiative.org/	72	http://www.iucnredlist.org/	244
<i>Lepidoblepharis xanthostigma</i>	32495	Mainland	NA	293	http://www.birdlife.org/	85	http://www.gardinitiative.org/	152	http://www.iucnredlist.org/	530
<i>Lygodactylus capensis</i>	19292	Mainland	NA	198	http://www.birdlife.org/	50	http://www.gardinitiative.org/	139	http://www.iucnredlist.org/	387
<i>Mabuya mabouya</i>	27463	Mainland	NA	418	http://www.birdlife.org/	91	http://www.gardinitiative.org/	245	http://www.iucnredlist.org/	754

<i>Menetia greyii</i>	15794	Mainland	NA	62	http://www.birdlife.org/	19	http://www.gardinitiative.org/	28	http://www.iucnredlist.org/	109
<i>Mochlus sundevalli</i>	21811	Mainland	NA	202	http://www.birdlife.org/	41	http://www.gardinitiative.org/	146	http://www.iucnredlist.org/	389
<i>Morethia boulengeri</i>	15798	Mainland	NA	66	http://www.birdlife.org/	15	http://www.gardinitiative.org/	25	http://www.iucnredlist.org/	106
<i>Phrynosoma cornutum</i>	41474	Mainland	NA	92	http://www.birdlife.org/	32	http://www.gardinitiative.org/	79	http://www.iucnredlist.org/	203
<i>Phrynosoma douglasii</i>	46142	Mainland	NA	81	http://www.birdlife.org/	9	http://www.gardinitiative.org/	78	http://www.iucnredlist.org/	168
<i>Phrynosoma modestum</i>	41474	Mainland	NA	92	http://www.birdlife.org/	32	http://www.gardinitiative.org/	79	http://www.iucnredlist.org/	203
<i>Phyllopezus pollicaris</i>	22094	Mainland	NA	163	http://www.birdlife.org/	83	http://www.gardinitiative.org/	132	http://www.iucnredlist.org/	378
<i>Plestiodon reynoldsi</i>	40059	Mainland	NA	85	http://www.birdlife.org/	32	http://www.gardinitiative.org/	42	http://www.iucnredlist.org/	159
<i>Plica plica</i>	27464	Mainland	NA	359	http://www.birdlife.org/	100	http://www.gardinitiative.org/	206	http://www.iucnredlist.org/	665
<i>Plica umbra</i>	26040	Mainland	NA	308	http://www.birdlife.org/	114	http://www.gardinitiative.org/	191	http://www.iucnredlist.org/	613
<i>Polychrus marmoratus</i>	27463	Mainland	NA	418	http://www.birdlife.org/	91	http://www.gardinitiative.org/	245	http://www.iucnredlist.org/	754
<i>Salvator merianae</i>	19926	Mainland	NA	215	http://www.birdlife.org/	99	http://www.gardinitiative.org/	133	http://www.iucnredlist.org/	447
<i>Sceloporus grammicus</i>	37876	Mainland	NA	150	http://www.birdlife.org/	36	http://www.gardinitiative.org/	123	http://www.iucnredlist.org/	309
<i>Sceloporus jarrovii</i>	37876	Mainland	NA	150	http://www.birdlife.org/	36	http://www.gardinitiative.org/	123	http://www.iucnredlist.org/	309
<i>Sceloporus magister</i>	40029	Mainland	NA	89	http://www.birdlife.org/	25	http://www.gardinitiative.org/	54	http://www.iucnredlist.org/	168
<i>Sceloporus poinsettii</i>	37876	Mainland	NA	150	http://www.birdlife.org/	36	http://www.gardinitiative.org/	123	http://www.iucnredlist.org/	309
<i>Sceloporus scalaris</i>	37876	Mainland	NA	150	http://www.birdlife.org/	36	http://www.gardinitiative.org/	123	http://www.iucnredlist.org/	309
<i>Scincella lateralis</i>	42571	Mainland	NA	72	http://www.birdlife.org/	32	http://www.gardinitiative.org/	47	http://www.iucnredlist.org/	151
<i>Stellagama stellio</i>	43413	Mainland	NA	74	http://www.birdlife.org/	15	http://www.gardinitiative.org/	53	http://www.iucnredlist.org/	142
<i>Tenuidactylus caspius</i>	43795	Mainland	NA	102	http://www.birdlife.org/	36	http://www.gardinitiative.org/	72	http://www.iucnredlist.org/	210
<i>Thecadactylus rapicauda</i>	27463	Mainland	NA	418	http://www.birdlife.org/	91	http://www.gardinitiative.org/	245	http://www.iucnredlist.org/	754
<i>Trachylepis quinquestaeniata</i>	33678	Mainland	NA	126	http://www.birdlife.org/	25	http://www.gardinitiative.org/	50	http://www.iucnredlist.org/	201
<i>Tropidurus itambere</i>	19931	Mainland	NA	195	http://www.birdlife.org/	95	http://www.gardinitiative.org/	134	http://www.iucnredlist.org/	424
<i>Tropidurus torquatus</i>	16698	Mainland	NA	258	http://www.birdlife.org/	81	http://www.gardinitiative.org/	160	http://www.iucnredlist.org/	499
<i>Tupinambis teguixin</i>	28560	Mainland	NA	267	http://www.birdlife.org/	108	http://www.gardinitiative.org/	196	http://www.iucnredlist.org/	571

<i>Uma exsul</i>	38957	Mainland	NA	81	http://www.birdlife.org/	30	http://www.gardinitiative.org/	80	http://www.iucnredlist.org/	191
<i>Uracentron azureum</i>	28915	Mainland	NA	280	http://www.birdlife.org/	104	http://www.gardinitiative.org/	196	http://www.iucnredlist.org/	580
<i>Uta stansburiana</i>	45181	Mainland	NA	93	http://www.birdlife.org/	7	http://www.gardinitiative.org/	45	http://www.iucnredlist.org/	145
<i>Varanus brevicauda</i>	14704	Mainland	NA	42	http://www.birdlife.org/	18	http://www.gardinitiative.org/	23	http://www.iucnredlist.org/	83
<i>Varanus tristis</i>	14704	Mainland	NA	42	http://www.birdlife.org/	18	http://www.gardinitiative.org/	23	http://www.iucnredlist.org/	83
<i>Xenosaurus grandis</i>	36083	Mainland	NA	203	http://www.birdlife.org/	58	http://www.gardinitiative.org/	162	http://www.iucnredlist.org/	423

Appendix 1f: List of diet categories

Full dataset	clumped dataset
Amblypygi Pooled	Annelida
Amphipoda	Arthropoda
Annelida Pooled	Mollusca
Ants Pooled	Non identified Pooled
Aranae and Acari Pooled	Vertebrate Pooled (includes lizard shed skin and vertebrate egg)
Opiliones Pooled	Plant material Pooled
Chilopoda and Myriapoda Pooled	Flowers
Cockroaches Pooled	Fruits/seeds
Coleoptera Pooled	
Collembola Pooled	
Crustaceans Pooled	
Dermaptera Pooled	
Diplopoda Pooled	
Diptera Pooled	
Embioptera	
Ephemeroptera Pooled	
Gastropoda Pooled	
Hemiptera/Homoptera Pooled	
Hirudinea Pooled	
Hymenoptera (non ants) Pooled	
Insect larvae and pupae Pooled	
Insect egg Pooled	
Isoptera Pooled	
Isopoda Pooled	
Lepidoptera Pooled	
Mantodea Pooled	

Mollusca Pooled
Microcoryphia Individual
Neuroptera Pooled
Non identified Pooled
Odonata Pooled
Oligochaeta Pooled
Orthoptera Pooled
Phasmida Pooled
Plant material Pooled
Flowers
Fruits/seeds
Plecoptera Pooled
Pseudoscorpionidae Pooled
Scorpionida Pooled
Solifuga Pooled
Thysanura Pooled
Tricoptera Pooled
Vertebrate Pooled (includes lizard shed skin and vertebrate egg)

Niche variation hypothesis and its relationship to lizard population density

This is the R code used to test the niche variation hypothesis in lizards using dietary niche data and looking at its relationship to population density and lizard and predator richness on both island and the mainalnd

Sensitivity analysis

In these analyses we are testing a few things to make sure our data does not give a bias based on skewed collection of the data. We include diet data type, diet data origin and number of stomach used in the analysis

Stomach number

```
#preanalysis tests
# dietary data type
model.type<- lm(niche_breadth_full~diet_data_type, diet.data)
summary(model.type)

##
## Call:
## lm(formula = niche_breadth_full ~ diet_data_type, data = diet.data)
##
## Residuals:
##     Min      1Q      Median      3Q      Max 
## -3.9494 -2.2696 -0.4096  2.1355  5.5404 
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)                 4.7396    0.3813 12.430 <2e-16 ***
## diet_data_typeVolumetric_proportion_   0.2098    0.5281  0.397   0.692  
## 
## (Intercept)                 ***
## diet_data_typeVolumetric_proportion_  
## ---                        
## Signif. codes:  0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.558 on 92 degrees of freedom
## Multiple R-squared:  0.001713,  Adjusted R-squared:  -0.009138 
## F-statistic: 0.1579 on 1 and 92 DF,  p-value: 0.6921

model.origin<- lm(niche_breadth_full~diet_data_origin,diet.data)
summary(model.origin)

##
## Call:
## lm(formula = niche_breadth_full ~ diet_data_origin, data = diet.data)
```

```

## 
## Residuals:
##   Min     1Q Median     3Q    Max
## -3.9520 -1.9320 -0.0515  2.0805  5.3280
## 
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             4.0709    0.7670   5.307 7.66e-07 ***
## diet_data_originStomach_contant 0.8811    0.8163   1.079   0.283  
## ---                        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.544 on 92 degrees of freedom
## Multiple R-squared:  0.01251, Adjusted R-squared:  0.001773 
## F-statistic: 1.165 on 1 and 92 DF,  p-value: 0.2832

model.stomach.nu<- lm(niche_breadth_full~number_of_stomachs,diet.data)
summary(model.stomach.nu)

## 
## Call:
## lm(formula = niche_breadth_full ~ number_of_stomachs, data = diet.data)
## 
## Residuals:
##   Min     1Q Median     3Q    Max
## -4.3556 -2.2988 -0.4631  1.9016  5.5698
## 
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             4.560338   0.337844 13.498 <2e-16 ***
## number_of_stomachs 0.003568   0.002645   1.349   0.181  
## ---                        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.535 on 92 degrees of freedom
## Multiple R-squared:  0.0194, Adjusted R-squared:  0.008738 
## F-statistic:  1.82 on 1 and 92 DF,  p-value: 0.1807

```

Test if using only species with stomach number larger than 8 give different results than if using all the data

Subset the data

```

sub.diet.data<- diet.data
sub.diet.data<- subset(diet.data,number_of_stomachs>8)
comp.sub.diet<- comparative.data(phy=diet.tree,data=sub.diet.data,names.col=b
inomial,vcv.dim=3,vcv=TRUE,na.omit=FALSE,Warn.dropped=TRUE)

## Warning in comparative.data(phy = diet.tree, data = sub.diet.data,
## names.col = binomial, : Data dropped in compiling comparative data object

```

```

Descriptive statistics
min(sub.diet.data$island_area,na.rm = T)
## [1] 0.04

max(sub.diet.data$island_area,na.rm = T)
## [1] 151215

ddply(sub.diet.data,.(distribution),summarize,count_species=length(binomial))
##   distribution count_species
## 1      Island            35
## 2    Mainland            59

```

Sensitivity analysis - exclude different locations

```

#create the dataset without the species for which data was from different Locations
sub.local.data<- subset(sub.diet.data,what=="same")
comp.sub.local.data<- comparative.data(phy=diet.tree,data=sub.local.data,
                                         names.col=binomial,vcv.dim=3,vcv=TRUE,na.omit=FALSE, warn.dropped=TRUE)

## Warning in comparative.data(phy = diet.tree, data = sub.local.data,
## names.col = binomial, : Data dropped in compiling comparative data object

length(sub.local.data$binomial)
## [1] 76

#run the models on this data

#full dataset
#non-phylogenetic
model.sub1<- lm(niche_breadth_full~distribution,sub.local.data)
summary(model.sub1)

##
## Call:
## lm(formula = niche_breadth_full ~ distribution, data = sub.local.data)
##
## Residuals:
##       Min     1Q     Median      3Q     Max 
## -4.4162 -1.8886 -0.3362  1.8588  4.8438 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 4.9058     0.4427 11.081   <2e-16 ***
## distributionMainland 0.5304     0.5753  0.922     0.36  
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.465 on 74 degrees of freedom

```

```

## Multiple R-squared:  0.01135,     Adjusted R-squared:  -0.002005
## F-statistic: 0.8499 on 1 and 74 DF,  p-value: 0.3596

#phylogenetic
model.sub1.phy<- pgls(niche_breadth_full~distribution,comp.sub.local.data, lambda="ML")
summary(model.sub1.phy)

##
## Call:
## pgls(formula = niche_breadth_full ~ distribution, data = comp.sub.local.data,
##       lambda = "ML")
##
## Residuals:
##      Min      1Q  Median      3Q      Max
## -0.71868 -0.12833 -0.02248  0.15383  0.57687
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.556
## lower bound : 0.000, p = 0.34353
## upper bound : 1.000, p = 0.030488
## 95.0% CI : (NA, 0.992)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             4.82318   0.91670  5.2615 1.342e-06 ***
## distributionMainland    0.44285   0.63291  0.6997  0.4863    
## ---                        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.218 on 74 degrees of freedom
## Multiple R-squared: 0.006573,   Adjusted R-squared: -0.006852
## F-statistic: 0.4896 on 1 and 74 DF,  p-value: 0.4863

#clumped dataset
#non-phylogenetic
model.sub1.1<- lm(niche_breadth_clumped~distribution,sub.local.data)
summary(model.sub1.1)

##
## Call:
## lm(formula = niche_breadth_clumped ~ distribution, data = sub.local.data)
##
## Residuals:
##      Min      1Q  Median      3Q      Max
## -0.57742 -0.32761 -0.16011  0.08181  2.37489
##

```

```

## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.57742   0.09511  16.59 <2e-16 ***
## distributionMainland -0.24231   0.12360  -1.96  0.0537 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5295 on 74 degrees of freedom
## Multiple R-squared:  0.04937, Adjusted R-squared:  0.03653
## F-statistic: 3.843 on 1 and 74 DF, p-value: 0.05371

#phylogenetic
model.sub1.phy<- pgls(niche_breadth_clumped~distribution,comp.sub.local.data,
lambda="ML")
summary(model.sub1.phy)

##
## Call:
## pgls(formula = niche_breadth_clumped ~ distribution, data = comp.sub.local.
## .data,
##       lambda = "ML")
##
## Residuals:
##      Min       1Q     Median       3Q      Max
## -0.117932 -0.028514 -0.002409  0.028606  0.094319
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 0.431
## lower bound : 0.000, p = 0.072442
## upper bound : 1.000, p = 1.5943e-08
## 95.0% CI : (NA, 0.764)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.64956   0.17260  9.5573 1.488e-14 ***
## distributionMainland -0.32248   0.13143 -2.4537  0.01649 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04375 on 74 degrees of freedom
## Multiple R-squared: 0.07524, Adjusted R-squared: 0.06274
## F-statistic: 6.021 on 1 and 74 DF, p-value: 0.01649

#non-phylogenetic
model.d<- lm(log_population_density~distribution+log_study_area+log_mass,sub.
local.data)
summary(model.d)

```

```

## 
## Call:
## lm(formula = log_population_density ~ distribution + log_study_area +
##      log_mass, data = sub.local.data)
## 
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -1.68549 -0.51239  0.05699  0.58107  1.87155 
## 
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             2.14534   0.16884 12.707 < 2e-16 ***
## distributionMainland -0.91555   0.18987 -4.822 7.69e-06 ***
## log_study_area        -0.44693   0.09005 -4.963 4.49e-06 *** 
## log_mass               -0.69467   0.30844 -2.252  0.0274 *  
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.7902 on 72 degrees of freedom
## Multiple R-squared:  0.5235, Adjusted R-squared:  0.5037 
## F-statistic: 26.37 on 3 and 72 DF,  p-value: 1.286e-11

#phylogenetic
model.d.phy<- pgls(log_population_density~distribution+log_study_area+log_mass,data=comp.sub.local.data, lambda="ML")
summary(model.d.phy)

## 
## Call:
## pgls(formula = log_population_density ~ distribution + log_study_area +
##      log_mass, data = comp.sub.local.data, lambda = "ML")
## 
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -0.13764 -0.02938  0.02141  0.04839  0.17731 
## 
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.441
## lower bound : 0.000, p = 0.067711
## upper bound : 1.000, p = 7.4082e-06
## 95.0% CI : (NA, 0.819)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             1.899129   0.275844  6.8848 1.802e-09 *** 
## distributionMainland -0.706889   0.203526 -3.4732 0.0008742 *** 
## log_study_area        -0.450699   0.088326 -5.1027 2.621e-06 *** 

```

```

## log_mass           -0.416280   0.319047 -1.3048 0.1961301
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06548 on 72 degrees of freedom
## Multiple R-squared:  0.4174, Adjusted R-squared:  0.3931
## F-statistic: 17.19 on 3 and 72 DF, p-value: 1.609e-08

#full dataset
#non-phylogenetic
model.sub3<- lm(niche_breadth_full~log10(lizard_richness)*distribution,sub.local.data)
summary(model.sub3)

##
## Call:
## lm(formula = niche_breadth_full ~ log10(lizard_richness) * distribution,
##      data = sub.local.data)
##
## Residuals:
##       Min     1Q Median     3Q    Max
## -4.3790 -1.7535 -0.2369  1.8910  4.9463
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                  4.13974   1.19823   3.455
## log10(lizard_richness)        0.61641   0.89466   0.689
## distributionMainland         0.30313   2.43508   0.124
## log10(lizard_richness):distributionMainland 0.01322   1.59708   0.008
##                                     Pr(>|t|)
## (Intercept)                  0.000927 ***
## log10(lizard_richness)        0.493045
## distributionMainland          0.901277
## log10(lizard_richness):distributionMainland 0.993419
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.487 on 72 degrees of freedom
## Multiple R-squared:  0.02089, Adjusted R-squared:  -0.01991
## F-statistic: 0.5121 on 3 and 72 DF, p-value: 0.6752

model.sub3a<- lm(niche_breadth_full~log10(lizard_richness)+distribution,sub.local.data)
summary(model.sub3a)

##
## Call:
## lm(formula = niche_breadth_full ~ log10(lizard_richness) + distribution,
##      data = sub.local.data)
##
## Residuals:

```

```

##      Min     1Q Median     3Q    Max
## -4.380 -1.756 -0.236  1.891  4.941
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             4.1346    1.0166   4.067 0.000119 ***
## log10(lizard_richness)  0.6206    0.7360   0.843 0.401908
## distributionMainland    0.3226    0.6270   0.515 0.608424
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.47 on 73 degrees of freedom
## Multiple R-squared:  0.02089, Adjusted R-squared:  -0.005936
## F-statistic: 0.7787 on 2 and 73 DF, p-value: 0.4628

#phylogenetic
model.sub3phy<- pgls(niche_breadth_full~log10(lizard_richness)*distribution,
comp.sub.local.data,lambda = "ML")
summary(model.sub3phy)

##
## Call:
## pgls(formula = niche_breadth_full ~ log10(lizard_richness) *
##       distribution, data = comp.sub.local.data, lambda = "ML")
##
## Residuals:
##      Min     1Q Median     3Q    Max
## -0.65559 -0.17282 -0.02628  0.12058  0.34436
##
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.527
##   lower bound : 0.000, p = 0.57267
##   upper bound : 1.000, p = 0.030078
## 95.0% CI : (NA, 0.991)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             4.35433   1.51215   2.8796
## log10(lizard_richness)  0.38024   0.97474   0.3901
## distributionMainland    0.85064   2.52627   0.3367
## log10(lizard_richness):distributionMainland -0.33285   1.66977  -0.1993
##                                         Pr(>|t|)
## (Intercept)                 0.005241 ***
## log10(lizard_richness)      0.697619
## distributionMainland        0.737310
## log10(lizard_richness):distributionMainland 0.842560
## ---

```

```

## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2178 on 72 degrees of freedom
## Multiple R-squared:  0.008806,   Adjusted R-squared: -0.03249
## F-statistic: 0.2132 on 3 and 72 DF,  p-value: 0.8869

model.sub3aphy<- pgls(niche_breadth_full~log10(lizard_richness)+distribution,
comp.sub.local.data,lambda = "ML")
summary(model.sub3aphy)

##
## Call:
## pgls(formula = niche_breadth_full ~ log10(lizard_richness) +
##       distribution, data = comp.sub.local.data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.65805 -0.16889 -0.06265  0.07011  0.36621
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.520
## lower bound : 0.000, p = 0.59895
## upper bound : 1.000, p = 0.028508
## 95.0% CI   : (NA, 0.990)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             4.48616   1.34177  3.3435 0.001308 **
## log10(lizard_richness) 0.27002   0.78813  0.3426 0.732878
## distributionMainland    0.36546   0.67517  0.5413 0.589966
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2157 on 73 degrees of freedom
## Multiple R-squared:  0.008322,   Adjusted R-squared: -0.01885
## F-statistic: 0.3063 on 2 and 73 DF,  p-value: 0.7371

#full dataset
#non-phylogenetic
model.sub3<- lm(log_population_density~niche_breadth_full+distribution+log_study_area+log_mass,sub.local.data)
summary(model.sub3)

##
## Call:
## lm(formula = log_population_density ~ niche_breadth_full + distribution +
##       log_study_area + log_mass, data = sub.local.data)
##

```

```

## Residuals:
##      Min      1Q   Median      3Q     Max
## -1.53777 -0.64105  0.02481  0.50102  2.09982
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             1.73447   0.23591   7.352 2.64e-10 ***
## niche_breadth_full     0.08924   0.03695   2.415  0.0183 *
## distributionMainland -0.97639   0.18552  -5.263 1.44e-06 ***
## log_study_area        -0.41126   0.08841  -4.652 1.48e-05 ***
## log_mass                -0.64618   0.29925  -2.159  0.0342 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7649 on 71 degrees of freedom
## Multiple R-squared:  0.5597, Adjusted R-squared:  0.5349
## F-statistic: 22.56 on 4 and 71 DF,  p-value: 4.705e-12

#phylogenetic
model.sub2phy<- pgls(log_population_density~niche_breadth_full+distribution+
log_study_area+log_mass,comp.sub.local.data,lambda = "ML")
summary(model.sub2phy)

##
## Call:
## pgls(formula = log_population_density ~ niche_breadth_full +
##       distribution + log_study_area + log_mass, data = comp.sub.local.data,
##       lambda = "ML")
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -0.161037 -0.044547 -0.009403  0.032162  0.130246
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 0.343
##   lower bound : 0.000, p = 0.071081
##   upper bound : 1.000, p = 7.7756e-07
## 95.0% CI : (NA, 0.768)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             1.530058   0.295419   5.1793 1.995e-06 ***
## niche_breadth_full     0.087183   0.035955   2.4248 0.0178632 *
## distributionMainland -0.789639   0.195168  -4.0459 0.0001309 ***
## log_study_area        -0.416974   0.086787  -4.8046 8.376e-06 ***
## log_mass                -0.481469   0.307240  -1.5671 0.1215422
## ---

```

```

## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06127 on 71 degrees of freedom
## Multiple R-squared:  0.4785, Adjusted R-squared:  0.4492
## F-statistic: 16.29 on 4 and 71 DF,  p-value: 1.646e-09

#clumped dataset
#non-phylogenetic)
model.sub3.1<- lm(log_population_density~niche_breadth_clumped+distribution+
log_study_area+log_mass,sub.local.data)
summary(model.sub3.1)

##
## Call:
## lm(formula = log_population_density ~ niche_breadth_clumped +
##      distribution + log_study_area + log_mass, data = sub.local.data)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -1.62388 -0.43015  0.06232  0.53376  1.87466
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.65411   0.34274   7.744 4.99e-11 ***
## niche_breadth_clumped -0.33121   0.19497  -1.699  0.0937 .  
## distributionMainland -0.98956   0.19243  -5.142 2.30e-06 ***
## log_study_area      -0.43855   0.08903  -4.926 5.29e-06 ***
## log_mass            -0.44665   0.33767  -1.323  0.1902  
## ---                
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.78 on 71 degrees of freedom
## Multiple R-squared:  0.5421, Adjusted R-squared:  0.5163
## F-statistic: 21.02 on 4 and 71 DF,  p-value: 1.83e-11

#phylogenetic
model.sub2.1phy<- pgls(log_population_density~niche_breadth_clumped+distribution+
log_study_area+log_mass,comp.sub.local.data,lambda = "ML")
summary(model.sub2.1phy)

##
## Call:
## pgls(formula = log_population_density ~ niche_breadth_clumped +
##      distribution + log_study_area + log_mass, data = comp.sub.local.data,
##      lambda = "ML") 
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -0.156014 -0.039934 -0.004197  0.036897  0.130192
##
## Branch length transformations:
```

```

## 
## kappa [Fix] : 1.000
## lambda [ML] : 0.328
##   lower bound : 0.000, p = 0.25924
##   upper bound : 1.000, p = 1.0996e-05
## 95.0% CI : (NA, 0.803)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            2.237861  0.389174  5.7503 2.075e-07 ***
## niche_breadth_clumped -0.196489  0.190579 -1.0310 0.3060335
## distributionMainland   -0.789916  0.205128 -3.8508 0.0002551 ***
## log_study_area        -0.448341  0.088605 -5.0600 3.165e-06 ***
## log_mass               -0.352011  0.345560 -1.0187 0.3118194
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.063 on 71 degrees of freedom
## Multiple R-squared: 0.4466, Adjusted R-squared: 0.4154
## F-statistic: 14.33 on 4 and 71 DF, p-value: 1.271e-08

#lizard richness
#clumped dataset
#non-phylogenetic
model.sub3.1<- lm(niche_breadth_clumped~log10(lizard_richness)*distribution,s
ub.local.data)
summary(model.sub3.1)

##
## Call:
## lm(formula = niche_breadth_clumped ~ log10(lizard_richness) *
##     distribution, data = sub.local.data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.58913 -0.29999 -0.15541  0.09562  2.34931
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            1.62786   0.25523   6.378
## log10(lizard_richness) -0.04059   0.19057  -0.213
## distributionMainland   -0.90607   0.51869  -1.747
## log10(lizard_richness):distributionMainland  0.42934   0.34019   1.262
##                               Pr(>|t|)
## (Intercept)            1.52e-08 ***
## log10(lizard_richness)  0.8319
## distributionMainland   0.0849 .
## log10(lizard_richness):distributionMainland  0.2110
## ---

```

```

## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5297 on 72 degrees of freedom
## Multiple R-squared:  0.07442,   Adjusted R-squared:  0.03585
## F-statistic:  1.93 on 3 and 72 DF,  p-value: 0.1324

model.sub3.1a<- lm(niche_breadth_clumped~log10(lizard_richness)+distribution,
sub.local.data)
summary(model.sub3.1a)

##
## Call:
## lm(formula = niche_breadth_clumped ~ log10(lizard_richness) +
##     distribution, data = sub.local.data)
##
## Residuals:
##       Min      1Q  Median      3Q     Max
## -0.62916 -0.29675 -0.17737  0.06323  2.36870
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             1.46042   0.21892   6.671 4.22e-09 ***
## log10(lizard_richness)  0.09414   0.15850   0.594  0.5544
## distributionMainland   -0.27383   0.13501  -2.028  0.0462 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5319 on 73 degrees of freedom
## Multiple R-squared:  0.05394,   Adjusted R-squared:  0.02802
## F-statistic: 2.081 on 2 and 73 DF,  p-value: 0.1321

#phylogenetic
model.sub3.1phy<- pgls(niche_breadth_clumped~log10(lizard_richness)*distribution,comp.sub.local.data,lambda = "ML")
summary(model.sub3.1phy)

##
## Call:
## pgls(formula = niche_breadth_clumped ~ log10(lizard_richness) *
##     distribution, data = comp.sub.local.data, lambda = "ML")
##
## Residuals:
##       Min      1Q  Median      3Q     Max
## -0.114689 -0.023162 -0.000738  0.025422  0.090022
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.388
##    lower bound : 0.000, p = 0.17084
##    upper bound : 1.000, p = 1.298e-08

```

```

##      95.0% CI    : (NA, 0.750)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                  1.702477  0.300982  5.6564
## log10(lizard_richness)       -0.051065  0.202317 -0.2524
## distributionMainland        -0.733769  0.530999 -1.3819
## log10(lizard_richness):distributionMainland  0.276698  0.350709  0.7890
##                               Pr(>|t|)
## (Intercept)                  2.93e-07 ***
## log10(lizard_richness)        0.8014
## distributionMainland          0.1713
## log10(lizard_richness):distributionMainland  0.4327
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04346 on 72 degrees of freedom
## Multiple R-squared: 0.08267, Adjusted R-squared: 0.04445
## F-statistic: 2.163 on 3 and 72 DF,  p-value: 0.09983

model.sub3.1aphy<- pgls(niche_breadth_clumped~log10(lizard_richness)+distribution,comp.sub.local.data,lambda = "ML")
summary(model.sub3.1aphy)

##
## Call:
## pgls(formula = niche_breadth_clumped ~ log10(lizard_richness) +
##       distribution, data = comp.sub.local.data, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.117768 -0.028916 -0.002979  0.030070  0.094204
##
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ML] : 0.424
##   lower bound : 0.000, p = 0.087964
##   upper bound : 1.000, p = 1.6754e-08
## 95.0% CI    : (NA, 0.762)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  1.602058  0.271338  5.9043 1.034e-07 ***
## log10(lizard_richness)       0.036974  0.165397  0.2235  0.82373
## distributionMainland        -0.332745  0.141131 -2.3577  0.02107 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

## 
## Residual standard error: 0.04391 on 73 degrees of freedom
## Multiple R-squared: 0.07567, Adjusted R-squared: 0.05034
## F-statistic: 2.988 on 2 and 73 DF, p-value: 0.05659

#predator richness
#full dataset
#non-phylogenetic
model.sub4<- lm(niche_breadth_full~log10(predator_richness)*distribution,sub.local.data)
summary(model.sub4)

## 
## Call:
## lm(formula = niche_breadth_full ~ log10(predator_richness) *
##     distribution, data = sub.local.data)
## 
## Residuals:
##      Min    1Q   Median    3Q   Max 
## -4.4367 -1.8789 -0.2427  1.8933  4.9158 
## 
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                  2.046     2.783   0.735
## log10(predator_richness)      1.572     1.511   1.041
## distributionMainland          4.007     4.331   0.925
## log10(predator_richness):distributionMainland -1.827     2.032  -0.899
##                                         Pr(>|t|) 
## (Intercept)                      0.465
## log10(predator_richness)          0.302
## distributionMainland              0.358
## log10(predator_richness):distributionMainland  0.372
## 
## Residual standard error: 2.48 on 72 degrees of freedom
## Multiple R-squared: 0.02647, Adjusted R-squared: -0.01409
## F-statistic: 0.6526 on 3 and 72 DF, p-value: 0.5839

model.sub4a<- lm(niche_breadth_full~log10(predator_richness)+distribution,sub.local.data)
summary(model.sub4a)

## 
## Call:
## lm(formula = niche_breadth_full ~ log10(predator_richness) +
##     distribution, data = sub.local.data)
## 
## Residuals:
##      Min    1Q   Median    3Q   Max 
## -4.4591 -2.0197 -0.2996  1.9561  4.6932 
## 
## Coefficients:

```

```

##                               Estimate Std. Error t value Pr(>|t|) *
## (Intercept)                  3.8827    1.8882   2.056   0.0433 *
## log10(predator_richness)    0.5626    1.0090   0.558   0.5789
## distributionMainland        0.1883    0.8430   0.223   0.8239
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.477 on 73 degrees of freedom
## Multiple R-squared:  0.01555,   Adjusted R-squared: -0.01142
## F-statistic: 0.5764 on 2 and 73 DF,  p-value: 0.5644

#phylogenetic
model.sub4phy<- pgls(niche_breadth_full~log10(predator_richness)*distribution
,comp.sub.local.data,lambda = "ML")
summary(model.sub4phy)

##
## Call:
## pgls(formula = niche_breadth_full ~ log10(predator_richness) *
##       distribution, data = comp.sub.local.data, lambda = "ML")
##
## Residuals:
##      Min      1Q      Median      3Q      Max
## -0.69508 -0.15122 -0.00788  0.09518  0.54953
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.489
##   lower bound : 0.000, p = 0.51158
##   upper bound : 1.000, p = 0.021578
## 95.0% CI : (NA, 0.983)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|) *
## (Intercept)                  2.56113   2.88835   0.8867
## log10(predator_richness)     1.24346   1.50657   0.8254
## distributionMainland         2.08422   4.79961   0.4342
## log10(predator_richness):distributionMainland -0.98246   2.17650 -0.4514
##                                         Pr(>|t|) 
## (Intercept)                      0.3782
## log10(predator_richness)          0.4119
## distributionMainland             0.6654
## log10(predator_richness):distributionMainland  0.6531
##
## Residual standard error: 0.2135 on 72 degrees of freedom
## Multiple R-squared:  0.0163,   Adjusted R-squared: -0.02468
## F-statistic: 0.3978 on 3 and 72 DF,  p-value: 0.755

```

```

model.sub4aphy<- pgls(niche_breadth_full~log10(predator_richness)+distribution,
comp.sub.local.data,lambda = "ML")
summary(model.sub4aphy)

##
## Call:
## pgls(formula = niche_breadth_full ~ log10(predator_richness) +
##       distribution, data = comp.sub.local.data, lambda = "ML")
##
## Residuals:
##      Min      1Q   Median      3Q     Max 
## -0.66110 -0.16576 -0.02108  0.11411  0.32757
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.530
## lower bound : 0.000, p = 0.30038
## upper bound : 1.000, p = 0.023627
## 95.0% CI : (NA, 0.986)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             3.349120  2.308709  1.4506  0.1512    
## log10(predator_richness) 0.806635  1.160249  0.6952  0.4891    
## distributionMainland    -0.041696  0.943420 -0.0442  0.9649    
## 
## Residual standard error: 0.2161 on 73 degrees of freedom
## Multiple R-squared: 0.01322, Adjusted R-squared: -0.01382
## F-statistic: 0.4889 on 2 and 73 DF,  p-value: 0.6153

#clumped dataset
#non-phylogenetic
model.sub4.1<- lm(niche_breadth_clumped~log10(predator_richness)*distribution,
sub.local.data)
summary(model.sub4.1)

##
## Call:
## lm(formula = niche_breadth_clumped ~ log10(predator_richness) *
##       distribution, data = sub.local.data)
##
## Residuals:
##      Min      1Q   Median      3Q     Max 
## -0.68479 -0.32820 -0.16103  0.08784  2.37705
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)              2.3571    0.5953   3.959

```

```

## log10(predator_richness) -0.4287 0.3231 -1.327
## distributionMainland -0.9984 0.9264 -1.078
## log10(predator_richness):distributionMainland 0.4190 0.4346 0.964
##
## (Intercept) Pr(>|t|)
## 0.000175 ***
## log10(predator_richness) 0.188813
## distributionMainland 0.284733
## log10(predator_richness):distributionMainland 0.338243
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5304 on 72 degrees of freedom
## Multiple R-squared: 0.07207, Adjusted R-squared: 0.03341
## F-statistic: 1.864 on 3 and 72 DF, p-value: 0.1434

model.sub4.1a<- lm(niche_breadth_clumped~log10(predator_richness)+distribution,sub.local.data)
summary(model.sub4.1a)

##
## Call:
## lm(formula = niche_breadth_clumped ~ log10(predator_richness) +
##     distribution, data = sub.local.data)
##
## Residuals:
##     Min      1Q      Median      3Q      Max
## -0.6268 -0.2899 -0.1816  0.1563  2.4189
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.9358    0.4042   4.789 8.53e-06 ***
## log10(predator_richness) -0.1971    0.2160  -0.912  0.365
## distributionMainland -0.1225    0.1805  -0.679  0.500
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5301 on 73 degrees of freedom
## Multiple R-squared: 0.06009, Adjusted R-squared: 0.03434
## F-statistic: 2.334 on 2 and 73 DF, p-value: 0.1041

#phylogenetic
model.sub4.1phy<- pgls(niche_breadth_clumped~log10(predator_richness)*distribution,comp.sub.local.data,lambda = "ML")
summary(model.sub4.1phy)

##
## Call:
## pgls(formula = niche_breadth_clumped ~ log10(predator_richness) *
##     distribution, data = comp.sub.local.data, lambda = "ML")
##
## Residuals:

```

```

##      Min      1Q   Median      3Q     Max
## -0.115854 -0.021941 -0.000855  0.028082  0.093873
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 0.429
##   lower bound : 0.000, p = 0.082812
##   upper bound : 1.000, p = 1.73e-08
## 95.0% CI : (NA, 0.767)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                  2.36941  0.60384  3.9239
## log10(predator_richness)    -0.39424  0.31676 -1.2446
## distributionMainland        -0.99877  1.00010 -0.9987
## log10(predator_richness):distributionMainland 0.37653  0.45461  0.8283
##                                         Pr(>|t|) 
## (Intercept)                      0.0001971 ***
## log10(predator_richness)         0.2173171
## distributionMainland            0.3212980
## log10(predator_richness):distributionMainland 0.4102656
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04384 on 72 degrees of freedom
## Multiple R-squared: 0.09465, Adjusted R-squared: 0.05693
## F-statistic: 2.509 on 3 and 72 DF, p-value: 0.06554

model.sub4.1aphy<- pgls(niche_breadth_clumped~log10(predator_richness)+distribution,comp.sub.local.data,lambda = "ML")
summary(model.sub4.1aphy)

##
## Call:
## pgls(formula = niche_breadth_clumped ~ log10(predator_richness) +
##       distribution, data = comp.sub.local.data, lambda = "ML")
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -0.118305 -0.023964 -0.001961  0.029051  0.092840
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 0.435
##   lower bound : 0.000, p = 0.07083
##   upper bound : 1.000, p = 1.5298e-08
## 95.0% CI : (NA, 0.767)

```

```

## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             2.06197   0.47494  4.3416 4.483e-05 ***
## log10(predator_richness) -0.22512   0.24155 -0.9320   0.3544
## distributionMainland     -0.18708   0.19631 -0.9529   0.3438
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04384 on 73 degrees of freedom
## Multiple R-squared: 0.0862, Adjusted R-squared: 0.06116
## F-statistic: 3.443 on 2 and 73 DF, p-value: 0.03725

```

Compare the niche breadth between islands and the mainland

```

#using sub data
#full dataset
#non-phylogenetic
model.sub1<- lm(niche_breadth_full~distribution,sub.diet.data)
summary(model.sub1)

##
## Call:
## lm(formula = niche_breadth_full ~ distribution, data = sub.diet.data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -3.9807 -2.1231 -0.3469  2.0062  5.2793 
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             4.5931    0.4314 10.647 <2e-16 ***
## distributionMainland    0.4075    0.5445  0.748   0.456
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.552 on 92 degrees of freedom
## Multiple R-squared: 0.006051, Adjusted R-squared: -0.004753
## F-statistic: 0.5601 on 1 and 92 DF, p-value: 0.4561

#phylogenetic
model.sub1.phy<- pgls(niche_breadth_full~distribution,comp.sub.diet, lambda="ML")
summary(model.sub1.phy)

##
## Call:
## pgls(formula = niche_breadth_full ~ distribution, data = comp.sub.diet,
##       lambda = "ML")
## 
```

```

## Residuals:
##      Min     1Q   Median     3Q    Max
## -0.62715 -0.11602  0.00569  0.17877  0.80524
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 0.746
##   lower bound : 0.000, p = 0.020806
##   upper bound : 1.000, p = 0.054859
## 95.0% CI : (0.133, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             4.25631   1.10253  3.8605 0.0002101 ***
## distributionMainland  0.50559   0.59109  0.8554 0.3945744
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2485 on 92 degrees of freedom
## Multiple R-squared: 0.00789, Adjusted R-squared: -0.002894
## F-statistic: 0.7316 on 1 and 92 DF,  p-value: 0.3946

#clumped dataset
#non-phylogenetic
model.sub1.1<- lm(niche_breadth_clumped~distribution,sub.diet.data)
summary(model.sub1.1)

##
## Call:
## lm(formula = niche_breadth_clumped ~ distribution, data = sub.diet.data)
##
## Residuals:
##      Min     1Q   Median     3Q    Max
## -0.52000 -0.29898 -0.15398  0.09852  2.41102
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             1.52000   0.08422 18.047 <2e-16 ***
## distributionMainland -0.22102   0.10631 -2.079  0.0404 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4983 on 92 degrees of freedom
## Multiple R-squared: 0.04487, Adjusted R-squared: 0.03449
## F-statistic: 4.322 on 1 and 92 DF,  p-value: 0.0404

#phylogenetic
model.sub1.1.phy<- pgls(niche_breadth_clumped~distribution,comp.sub.diet, lam

```

```

bda="ML")
summary(model.sub1.1.phy)

##
## Call:
## pgls(formula = niche_breadth_clumped ~ distribution, data = comp.sub.diet,
##       lambda = "ML")
##
## Residuals:
##      Min      1Q Median      3Q     Max
## -0.114676 -0.017458  0.001844  0.030235  0.093809
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 0.306
## lower bound : 0.000, p = 0.13356
## upper bound : 1.000, p = 1.9607e-11
## 95.0% CI : (NA, 0.654)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             1.56150   0.14054 11.111 < 2e-16 ***
## distributionMainland -0.26116   0.11104 -2.352  0.02081 *
## ---
## Signif. codes:  0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03998 on 92 degrees of freedom
## Multiple R-squared: 0.05672, Adjusted R-squared: 0.04646
## F-statistic: 5.532 on 1 and 92 DF,  p-value: 0.02081

#using all data
#full dataset
#non-phylogenetic
model.sub1<- lm(niche_breadth_full~distribution,diet.data)
summary(model.sub1)

##
## Call:
## lm(formula = niche_breadth_full ~ distribution, data = diet.data)
##
## Residuals:
##      Min      1Q Median      3Q     Max
## -3.9807 -2.1231 -0.3469  2.0062  5.2793
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             4.5931    0.4314 10.647 <2e-16 ***
## distributionMainland  0.4075    0.5445  0.748   0.456

```

```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.552 on 92 degrees of freedom
## Multiple R-squared:  0.006051,  Adjusted R-squared:  -0.004753
## F-statistic: 0.5601 on 1 and 92 DF,  p-value: 0.4561

#phylogenetic
model.sub1.phy<- pgls(niche_breadth_full~distribution,comp.diet2, lambda="ML")
summary(model.sub1.phy)

##
## Call:
## pgls(formula = niche_breadth_full ~ distribution, data = comp.diet2,
##       lambda = "ML")
##
## Residuals:
##      Min      1Q   Median      3Q     Max 
## -0.62715 -0.11602  0.00569  0.17877  0.80524
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.746
## lower bound : 0.000, p = 0.020806
## upper bound : 1.000, p = 0.054859
## 95.0% CI : (0.133, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 4.25631   1.10253  3.8605 0.0002101 ***
## distributionMainland 0.50559   0.59109  0.8554 0.3945744
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2485 on 92 degrees of freedom
## Multiple R-squared: 0.00789, Adjusted R-squared: -0.002894
## F-statistic: 0.7316 on 1 and 92 DF,  p-value: 0.3946

#clumped dataset
#non-phylogenetic
model.sub1.1<- lm(niche_breadth_clumped~distribution,diet.data)
summary(model.sub1.1)

##
## Call:
## lm(formula = niche_breadth_clumped ~ distribution, data = diet.data)
##
## Residuals:

```

```

##      Min      1Q   Median      3Q     Max
## -0.52000 -0.29898 -0.15398  0.09852  2.41102
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             1.52000   0.08422 18.047 <2e-16 ***
## distributionMainland -0.22102   0.10631 -2.079  0.0404 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4983 on 92 degrees of freedom
## Multiple R-squared:  0.04487,    Adjusted R-squared:  0.03449
## F-statistic: 4.322 on 1 and 92 DF,  p-value: 0.0404

#phylogenetic
model.sub1.1.phy<- pgls(niche_breadth_clumped~distribution,comp.diet2, lambda = "ML")
summary(model.sub1.1.phy)

##
## Call:
## pgls(formula = niche_breadth_clumped ~ distribution, data = comp.diet2,
##       lambda = "ML")
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -0.114676 -0.017458  0.001844  0.030235  0.093809
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 0.306
## lower bound : 0.000, p = 0.13356
## upper bound : 1.000, p = 1.9607e-11
## 95.0% CI : (NA, 0.654)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             1.56150   0.14054 11.111 < 2e-16 ***
## distributionMainland -0.26116   0.11104 -2.352  0.02081 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03998 on 92 degrees of freedom
## Multiple R-squared: 0.05672, Adjusted R-squared: 0.04646
## F-statistic: 5.532 on 1 and 92 DF,  p-value: 0.02081

```

Conclusion: The results are quantitatively different, thus we will use the sub data that has species with number of stomachs 9 or larger

Test the data for various patterns by comparing islands and the mainland

Compare population density

```
#non-phylogenetic
model.d<- lm(log_population_density~distribution+log_study_area+log_mass,sub.
diet.data)
summary(model.d)

##
## Call:
## lm(formula = log_population_density ~ distribution + log_study_area +
##      log_mass, data = sub.diet.data)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -1.68571 -0.59632  0.04558  0.62029  1.89981
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.16604   0.15634 13.855 < 2e-16 ***
## distributionMainland -0.98099   0.17429 -5.629 2.04e-07 ***
## log_study_area    -0.45041   0.08192 -5.498 3.55e-07 ***
## log_mass          -0.72299   0.27634 -2.616  0.0104 *  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7802 on 90 degrees of freedom
## Multiple R-squared:  0.5374, Adjusted R-squared:  0.522 
## F-statistic: 34.85 on 3 and 90 DF,  p-value: 4.843e-15

#phylogenetic
model.d.phy<- pgls(log_population_density~distribution+log_study_area+log_mas
s,data=comp.sub.diet, lambda="ML")
summary(model.d.phy)

##
## Call:
## pgls(formula = log_population_density ~ distribution + log_study_area +
##      log_mass, data = comp.sub.diet, lambda = "ML")
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -0.10264 -0.04730 -0.01489  0.03004  0.14908
##
## Branch length transformations:
```

```

## 
## kappa [Fix] : 1.000
## lambda [ML] : 0.102
##   lower bound : 0.000, p = 0.32987
##   upper bound : 1.000, p = 9.5837e-10
## 95.0% CI : (NA, 0.489)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            2.097491  0.189713 11.0561 < 2.2e-16 ***
## distributionMainland -0.942502  0.177814 -5.3005 8.163e-07 ***
## log_study_area        -0.451057  0.081304 -5.5478 2.878e-07 ***
## log_mass               -0.708543  0.284725 -2.4885  0.01467 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05989 on 90 degrees of freedom
## Multiple R-squared: 0.5166, Adjusted R-squared: 0.5004
## F-statistic: 32.06 on 3 and 90 DF, p-value: 3.458e-14

```

Compare predators richness

```

model.p<- lm(log10(predator_richness)~distribution,sub.diet.data)
summary(model.p)

##
## Call:
## lm(formula = log10(predator_richness) ~ distribution, data = sub.diet.data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.94790 -0.24003 -0.00154  0.24548  0.51773
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            1.82271   0.05449 33.452 < 2e-16 ***
## distributionMainland  0.58759   0.06878  8.544 2.64e-13 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3224 on 92 degrees of freedom
## Multiple R-squared: 0.4424, Adjusted R-squared: 0.4363
## F-statistic: 72.99 on 1 and 92 DF, p-value: 2.638e-13

```

Compare lizard richness

```

model.l<- lm(log10(lizard_richness)~distribution,sub.diet.data)
summary(model.l)

```

```

## 
## Call:
## lm(formula = log10(lizard_richness) ~ distribution, data = sub.diet.data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.21453 -0.26029  0.03788  0.28893  0.59838
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             1.21453   0.06696 18.138 < 2e-16 ***
## distributionMainland    0.32768   0.08452  3.877 0.000198 ***  
## ---                        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3962 on 92 degrees of freedom
## Multiple R-squared:  0.1404, Adjusted R-squared:  0.1311 
## F-statistic: 15.03 on 1 and 92 DF,  p-value: 0.0001983

```

Compare the relationship between population density and niche breadth

```

#full dataset
#non-phylogenetic
model.sub3<- lm(log_population_density~niche_breadth_full+distribution+log_study_area+log_mass,sub.diet.data)
summary(model.sub3)

## 
## Call:
## lm(formula = log_population_density ~ niche_breadth_full + distribution +
##     log_study_area + log_mass, data = sub.diet.data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.59377 -0.63756  0.03951  0.54098  2.07267
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             1.83647   0.20787  8.835 8.26e-14 ***
## niche_breadth_full     0.07443   0.03187  2.335  0.0218 *  
## distributionMainland   -1.02157   0.17102 -5.973 4.69e-08 ***  
## log_study_area          -0.42640   0.08062 -5.289 8.72e-07 ***  
## log_mass                 -0.64095   0.27203 -2.356  0.0207 *  
## ---                        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7616 on 89 degrees of freedom
## Multiple R-squared:  0.5641, Adjusted R-squared:  0.5445 
## F-statistic: 28.8 on 4 and 89 DF,  p-value: 2.335e-15

```

```

#phylogenetic
model.sub2phy<- pgls(log_population_density~niche_breadth_full+distribution+
og_study_area+log_mass,comp.sub.diet,lambda = "ML")
summary(model.sub2phy)

##
## Call:
## pgls(formula = log_population_density ~ niche_breadth_full +
##       distribution + log_study_area + log_mass, data = comp.sub.diet,
##       lambda = "ML")
##
## Residuals:
##      Min        1Q     Median        3Q       Max
## -0.097319 -0.050435 -0.007344  0.031500  0.143261
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.100
##   lower bound : 0.000, p = 0.31624
##   upper bound : 1.000, p = 1.3313e-10
##   95.0% CI    : (NA, 0.469)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             1.775628  0.230162  7.7147 1.666e-11 ***
## niche_breadth_full     0.074487  0.031739  2.3469  0.02115 *
## distributionMainland -0.983112  0.174285 -5.6408 1.977e-07 ***
## log_study_area         -0.428529  0.079923 -5.3617 6.440e-07 ***
## log_mass                -0.633213  0.279571 -2.2649  0.02594 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05843 on 89 degrees of freedom
## Multiple R-squared: 0.5451, Adjusted R-squared: 0.5247
## F-statistic: 26.67 on 4 and 89 DF,  p-value: 1.507e-14

#clumped dataset
#non-phylogenetic)
model.sub3.1<- lm(log_population_density~niche_breadth_clumped+distribution+
og_study_area+log_mass,sub.diet.data)
summary(model.sub3.1)

##
## Call:
## lm(formula = log_population_density ~ niche_breadth_clumped +
##       distribution + log_study_area + log_mass, data = sub.diet.data)
##
## Residuals:

```

```

##      Min      1Q   Median      3Q     Max
## -1.61081 -0.56983  0.09027  0.59670  1.90237
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)              2.52089   0.30659   8.222 1.52e-12 ***
## niche_breadth_clumped -0.23990   0.17857  -1.343  0.1826
## distributionMainland   -1.03138   0.17752  -5.810 9.56e-08 ***
## log_study_area         -0.44394   0.08169  -5.434 4.75e-07 ***
## log_mass                -0.57238   0.29708  -1.927  0.0572 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7768 on 89 degrees of freedom
## Multiple R-squared:  0.5466, Adjusted R-squared:  0.5262
## F-statistic: 26.83 on 4 and 89 DF,  p-value: 1.307e-14

#phylogenetic
model.sub2.1phy<- pgls(log_population_density~niche_breadth_clumped+distribution+log_study_area+log_mass,comp.sub.diet,lambda = "ML")
summary(model.sub2.1phy)

##
## Call:
## pgls(formula = log_population_density ~ niche_breadth_clumped +
##       distribution + log_study_area + log_mass, data = comp.sub.diet,
##       lambda = "ML")
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -0.128652 -0.038757 -0.008393  0.024265  0.145134
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 0.048
##   lower bound : 0.000, p = 0.5991
##   upper bound : 1.000, p = 1.5683e-09
## 95.0% CI : (NA, 0.435)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)              2.429473   0.316482   7.6765 1.993e-11 ***
## niche_breadth_clumped -0.204655   0.177759  -1.1513  0.25269
## distributionMainland   -1.003128   0.179687  -5.5826 2.535e-07 ***
## log_study_area          -0.444838   0.081499  -5.4582 4.294e-07 ***
## log_mass                 -0.595395   0.301074  -1.9776  0.05107 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

## 
## Residual standard error: 0.05936 on 89 degrees of freedom
## Multiple R-squared:  0.5344, Adjusted R-squared:  0.5135 
## F-statistic: 25.54 on 4 and 89 DF,  p-value: 4.18e-14

```

Compare lizard richness and niche breadth

```

#full dataset
#non-phylogenetic
model.sub3<- lm(niche_breadth_full~log10(lizard_richness)*distribution,sub.diet.data)
summary(model.sub3)

## 
## Call:
## lm(formula = niche_breadth_full ~ log10(lizard_richness) * distribution,
##      data = sub.diet.data)
## 
## Residuals:
##      Min      1Q  Median      3Q     Max 
## -4.2370 -2.0972 -0.0028  1.9299  6.1350 
## 
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                  3.8441    1.0693   3.595
## log10(lizard_richness)        0.6167    0.8067   0.765
## distributionMainland         -1.8485    2.1446  -0.862
## log10(lizard_richness):distributionMainland  1.3318    1.4346   0.928
## 
##                               Pr(>|t|)    
## (Intercept)                  0.000529 ***
## log10(lizard_richness)        0.446556  
## distributionMainland          0.391008  
## log10(lizard_richness):distributionMainland  0.355685  
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.535 on 90 degrees of freedom
## Multiple R-squared:  0.04103, Adjusted R-squared:  0.009062 
## F-statistic: 1.284 on 3 and 90 DF,  p-value: 0.2849

model.sub3a<- lm(niche_breadth_full~log10(lizard_richness)+distribution,sub.diet.data)
summary(model.sub3a)

## 
## Call:
## lm(formula = niche_breadth_full ~ log10(lizard_richness) + distribution,
##      data = sub.diet.data)
## 
## Residuals:
##      Min      1Q  Median      3Q     Max 
## -4.2370 -2.0972 -0.0028  1.9299  6.1350 
## 
```

```

## -4.0424 -2.0971 -0.1329  1.9318  5.5995
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            3.33264   0.91578  3.639 0.000454 ***
## log10(lizard_richness) 1.03785   0.66655  1.557 0.122933
## distributionMainland    0.06745   0.58285  0.116 0.908119
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.533 on 91 degrees of freedom
## Multiple R-squared:  0.03184,   Adjusted R-squared:  0.01057
## F-statistic: 1.497 on 2 and 91 DF,  p-value: 0.2294

#phylogenetic
model.sub3phy<- pgls(niche_breadth_full~log10(lizard_richness)*distribution,c
omp.sub.diet,lambda = "ML")
summary(model.sub3phy)

##
## Call:
## pgls(formula = niche_breadth_full ~ log10(lizard_richness) *
##       distribution, data = comp.sub.diet, lambda = "ML")
##
## Residuals:
##      Min      1Q      Median      3Q      Max
## -0.61987 -0.14385  0.02417  0.14547  0.56188
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.685
## lower bound : 0.000, p = 0.089921
## upper bound : 1.000, p = 0.040095
## 95.0% CI   : (NA, 0.997)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            4.2558043  1.5210968  2.7979
## log10(lizard_richness) 0.0076099  0.8838424  0.0086
## distributionMainland    -1.3056769  2.2288858 -0.5858
## log10(lizard_richness):distributionMainland  1.1608212  1.4759841  0.7865
##                                         Pr(>|t|)
## (Intercept)                      0.006292 ***
## log10(lizard_richness)           0.993149
## distributionMainland             0.559477
## log10(lizard_richness):distributionMainland 0.433657
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

## 
## Residual standard error: 0.24 on 90 degrees of freedom
## Multiple R-squared:  0.0175, Adjusted R-squared: -0.01525
## F-statistic: 0.5345 on 3 and 90 DF, p-value: 0.6598

model.sub3aphy<- pgls(niche_breadth_full~log10(lizard_richness)+distribution,
comp.sub.diet,lambda = "ML")
summary(model.sub3aphy)

## 
## Call:
## pgls(formula = niche_breadth_full ~ log10(lizard_richness) +
##       distribution, data = comp.sub.diet, lambda = "ML")
## 
## Residuals:
##      Min      1Q  Median      3Q     Max 
## -0.65055 -0.16475 -0.01051  0.13693  0.64264 
## 
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.728
##   lower bound : 0.000, p = 0.075885
##   upper bound : 1.000, p = 0.049361
##   95.0% CI   : (NA, 1.000)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)            3.77702   1.42652  2.6477 0.009552 **  
## log10(lizard_richness) 0.38351   0.73034  0.5251 0.600789    
## distributionMainland   0.39224   0.62664  0.6259 0.532919    
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 

## 
## Residual standard error: 0.2463 on 91 degrees of freedom
## Multiple R-squared: 0.01076, Adjusted R-squared: -0.01098
## F-statistic: 0.4948 on 2 and 91 DF, p-value: 0.6113

#clumped dataset
#non-phylogenetic
model.sub3.1<- lm(niche_breadth_clumped~log10(lizard_richness)*distribution,s
ub.diet.data)
summary(model.sub3.1)

## 
## Call:
## lm(formula = niche_breadth_clumped ~ log10(lizard_richness) *
##       distribution, data = sub.diet.data)
## 
## Residuals:

```

```

##      Min     1Q   Median     3Q    Max
## -0.5217 -0.2968 -0.1308  0.1012  2.3735
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                1.516419  0.209602  7.235
## log10(lizard_richness)      0.002948  0.158120  0.019
## distributionMainland       -0.788468  0.420375 -1.876
## log10(lizard_richness):distributionMainland  0.367320  0.281196  1.306
##                                         Pr(>|t|)
## (Intercept)                1.49e-10 ***
## log10(lizard_richness)      0.9852
## distributionMainland        0.0639 .
## log10(lizard_richness):distributionMainland  0.1948
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4968 on 90 degrees of freedom
## Multiple R-squared:  0.07105,   Adjusted R-squared:  0.04008
## F-statistic: 2.294 on 3 and 90 DF,  p-value: 0.08322

model.sub3.1a<- lm(niche_breadth_clumped~log10(lizard_richness)+distribution,
sub.diet.data)
summary(model.sub3.1a)

##
## Call:
## lm(formula = niche_breadth_clumped ~ log10(lizard_richness) +
##     distribution, data = sub.diet.data)
##
## Residuals:
##      Min     1Q   Median     3Q    Max
## -0.58882 -0.26983 -0.16156  0.08903  2.39896
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                1.3754     0.1803   7.627 2.26e-11 ***
## log10(lizard_richness)      0.1191     0.1313   0.907  0.3666
## distributionMainland       -0.2600     0.1148  -2.266  0.0258 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4988 on 91 degrees of freedom
## Multiple R-squared:  0.05343,   Adjusted R-squared:  0.03263
## F-statistic: 2.569 on 2 and 91 DF,  p-value: 0.0822

#phylogenetic
model.sub3.1phy<- pgls(niche_breadth_clumped~log10(lizard_richness)*distribution,
comp.sub.diet,lambda = "ML")
summary(model.sub3.1phy)

```

```

## 
## Call:
## pgls(formula = niche_breadth_clumped ~ log10(lizard_richness) *
##       distribution, data = comp.sub.diet, lambda = "ML")
##
## Residuals:
##      Min        1Q     Median        3Q       Max
## -0.118250 -0.008967  0.005928  0.034218  0.112781
##
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.252
##   lower bound : 0.000, p = 0.28845
##   upper bound : 1.000, p = 1.5175e-11
## 95.0% CI : (NA, 0.627)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                  1.5564388  0.2433950  6.3947
## log10(lizard_richness)      -0.0029274  0.1672017 -0.0175
## distributionMainland        -0.7103208  0.4290622 -1.6555
## log10(lizard_richness):distributionMainland  0.2951175  0.2859555  1.0320
## 
##                               Pr(>|t|)
## (Intercept)                  7.018e-09 ***
## log10(lizard_richness)        0.9861
## distributionMainland          0.1013
## log10(lizard_richness):distributionMainland  0.3048
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03946 on 90 degrees of freedom
## Multiple R-squared: 0.0712, Adjusted R-squared: 0.04024
## F-statistic:  2.3 on 3 and 90 DF,  p-value: 0.08266

model.sub3.1aphy<- pgls(niche_breadth_clumped~log10(lizard_richness)+distribution,comp.sub.diet,lambda = "ML")
summary(model.sub3.1aphy)

##
## Call:
## pgls(formula = niche_breadth_clumped ~ log10(lizard_richness) +
##       distribution, data = comp.sub.diet, lambda = "ML")
##
## Residuals:
##      Min        1Q     Median        3Q       Max
## -0.099977 -0.014330  0.003012  0.029092  0.110775
##
## Branch length transformations:

```

```

## 
## kappa [Fix] : 1.000
## lambda [ML] : 0.297
##   lower bound : 0.000, p = 0.1757
##   upper bound : 1.000, p = 2.5783e-11
## 95.0% CI : (NA, 0.652)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           1.448492  0.222500  6.5101 4.029e-09 ***
## log10(lizard_richness) 0.090709  0.140162  0.6472  0.51915
## distributionMainland -0.287501  0.118850 -2.4190  0.01755 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03999 on 91 degrees of freedom
## Multiple R-squared: 0.06088, Adjusted R-squared: 0.04024
## F-statistic:  2.95 on 2 and 91 DF,  p-value: 0.05739

```

Compare predator richness and niche breadth

```

#full dataset
#non-phylogenetic
model.sub4<- lm(niche_breadth_full~log10(predator_richness)*distribution,sub.diet.data)
summary(model.sub4)

##
## Call:
## lm(formula = niche_breadth_full ~ log10(predator_richness) *
##     distribution, data = sub.diet.data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.2994 -1.9804 -0.2872  2.1758  5.2829
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           3.1356    2.5380   1.235
## log10(predator_richness) 0.7996    1.3722   0.583
## distributionMainland -1.1943    3.5739  -0.334
## log10(predator_richness):distributionMainland  0.4696    1.7186   0.273
##                                         Pr(>|t|)
## (Intercept)                   0.220
## log10(predator_richness)      0.562
## distributionMainland          0.739
## log10(predator_richness):distributionMainland  0.785
##
## Residual standard error: 2.554 on 90 degrees of freedom

```

```

## Multiple R-squared:  0.02601,    Adjusted R-squared:  -0.006456
## F-statistic: 0.8011 on 3 and 90 DF,  p-value: 0.4964

model.sub4a<- lm(niche_breadth_full~log10(predator_richness)+distribution,sub
.diet.data)
summary(model.sub4a)

##
## Call:
## lm(formula = niche_breadth_full ~ log10(predator_richness) +
##     distribution, data = sub.diet.data)
##
## Residuals:
##      Min      1Q   Median      3Q      Max 
## -4.2352 -1.9435 -0.3032  2.1383  5.2436 
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)                2.5899    1.5586   1.662   0.100    
## log10(predator_richness)   1.0990    0.8220   1.337   0.185    
## distributionMainland      -0.2382    0.7261  -0.328   0.744    
## 
## Residual standard error: 2.541 on 91 degrees of freedom
## Multiple R-squared:  0.0252, Adjusted R-squared:  0.003778 
## F-statistic: 1.176 on 2 and 91 DF,  p-value: 0.3131

#phylogenetic
model.sub4phy<- pgls(niche_breadth_full~log10(predator_richness)*distribution
,comp.sub.diet,lambda = "ML")
summary(model.sub4phy)

##
## Call:
## pgls(formula = niche_breadth_full ~ log10(predator_richness) *
##     distribution, data = comp.sub.diet, lambda = "ML")
##
## Residuals:
##      Min      1Q   Median      3Q      Max 
## -0.72194 -0.13088 -0.00089  0.14421  0.64770 
##
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.698
## lower bound : 0.000, p = 0.051972
## upper bound : 1.000, p = 0.049407
## 95.0% CI : (NA, 1.000)
## delta [Fix] : 1.000
## 
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    

```

```

## (Intercept) 4.422646 2.706324 1.6342
## log10(predator_richness) -0.076015 1.341957 -0.0566
## distributionMainland -1.413714 3.826863 -0.3694
## log10(predator_richness):distributionMainland 0.807776 1.774237 0.4553
## Pr(>|t|)
## (Intercept) 0.1057
## log10(predator_richness) 0.9550
## distributionMainland 0.7127
## log10(predator_richness):distributionMainland 0.6500
##
## Residual standard error: 0.2427 on 90 degrees of freedom
## Multiple R-squared: 0.01151, Adjusted R-squared: -0.02144
## F-statistic: 0.3492 on 3 and 90 DF, p-value: 0.7898

model.sub4aphy<- pgls(niche_breadth_full~log10(predator_richness)+distribution,comp.sub.diet,lambda = "ML")
summary(model.sub4aphy)

##
## Call:
## pgls(formula = niche_breadth_full ~ log10(predator_richness) +
##       distribution, data = comp.sub.diet, lambda = "ML")
##
## Residuals:
##      Min      1Q      Median      3Q      Max
## -0.49174 -0.16935 -0.03484  0.10645  0.66761
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ML] : 0.713
## lower bound : 0.000, p = 0.056367
## upper bound : 1.000, p = 0.051731
## 95.0% CI : (NA, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)            3.62867   2.02542  1.7916  0.07653 .
## log10(predator_richness) 0.34630   0.93107  0.3719  0.71080
## distributionMainland    0.30473   0.78384  0.3888  0.69836
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2441 on 91 degrees of freedom
## Multiple R-squared: 0.009171, Adjusted R-squared: -0.01261
## F-statistic: 0.4211 on 2 and 91 DF, p-value: 0.6576

#clumped dataset
#non-phylogenetic

```

```

model.sub4.1<- lm(niche_breadth_clumped~log10(predator_richness)*distribution
,sub.diet.data)
summary(model.sub4.1)

##
## Call:
## lm(formula = niche_breadth_clumped ~ log10(predator_richness) *
##      distribution, data = sub.diet.data)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -0.61624 -0.29123 -0.15568  0.08309  2.38789
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)                  2.2092    0.4945   4.468  
## log10(predator_richness)    -0.3781    0.2673  -1.415  
## distributionMainland        -1.1425    0.6963  -1.641  
## log10(predator_richness):distributionMainland  0.4745    0.3348   1.417  
##                               Pr(>|t|)    
## (Intercept)                  2.29e-05 ***
## log10(predator_richness)    0.161      
## distributionMainland        0.104      
## log10(predator_richness):distributionMainland  0.160      
## ---                        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4977 on 90 degrees of freedom
## Multiple R-squared:  0.06796,    Adjusted R-squared:  0.03689 
## F-statistic: 2.187 on 3 and 90 DF,  p-value: 0.09498

model.sub4.1a<- lm(niche_breadth_clumped~log10(predator_richness)+distribution
,sub.diet.data)
summary(model.sub4.1a)

##
## Call:
## lm(formula = niche_breadth_clumped ~ log10(predator_richness) +
##      distribution, data = sub.diet.data)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -0.53925 -0.29819 -0.15759  0.08416  2.42917
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)                  1.65789    0.30688   5.402 5.23e-07 ***
## log10(predator_richness)    -0.07565    0.16185  -0.467   0.641  
## distributionMainland        -0.17657    0.14298  -1.235   0.220  
## ---                        

```

```

## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5004 on 91 degrees of freedom
## Multiple R-squared:  0.04716,   Adjusted R-squared:  0.02622
## F-statistic: 2.252 on 2 and 91 DF,  p-value: 0.111

#phylogenetic
model.sub4.1phy<- pgls(niche_breadth_clumped~log10(predator_richness)*distribution,comp.sub.diet,lambda = "ML")
summary(model.sub4.1phy)

##
## Call:
## pgls(formula = niche_breadth_clumped ~ log10(predator_richness) *
##       distribution, data = comp.sub.diet, lambda = "ML")
##
## Residuals:
##      Min        10      Median        30        Max
## -0.119663 -0.018772  0.003712  0.028319  0.096832
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.312
##   lower bound : 0.000, p = 0.11236
##   upper bound : 1.000, p = 1.1866e-11
##  95.0% CI    : (NA, 0.658)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value
## (Intercept)                  2.31657  0.50581  4.5799
## log10(predator_richness)     -0.41090  0.26467 -1.5525
## distributionMainland         -1.13185  0.71582 -1.5812
## log10(predator_richness):distributionMainland  0.45825  0.33754  1.3576
##                               Pr(>|t|)
## (Intercept)                  1.488e-05 ***
## log10(predator_richness)      0.1241
## distributionMainland          0.1173
## log10(predator_richness):distributionMainland  0.1780
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03994 on 90 degrees of freedom
## Multiple R-squared: 0.08226, Adjusted R-squared: 0.05167
## F-statistic: 2.689 on 3 and 90 DF,  p-value: 0.05106

model.sub4.1aphy<- pgls(niche_breadth_clumped~log10(predator_richness)+distribution,comp.sub.diet,lambda = "ML")
summary(model.sub4.1aphy)

```

```

## 
## Call:
## pgls(formula = niche_breadth_clumped ~ log10(predator_richness) +
##       distribution, data = comp.sub.diet, lambda = "ML")
##
## Residuals:
##      Min        1Q     Median        3Q       Max
## -0.118788 -0.018805  0.002205  0.025526  0.092838
##
## Branch length transformations:
## 
## kappa [Fix] : 1.000
## lambda [ ML] : 0.324
##   lower bound : 0.000, p = 0.10073
##   upper bound : 1.000, p = 1.6262e-11
## 95.0% CI : (NA, 0.663)
## delta [Fix] : 1.000
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             1.82458   0.35285  5.1709 1.374e-06 ***
## log10(predator_richness) -0.14293   0.17620 -0.8112   0.4194    
## distributionMainland    -0.18141   0.14980 -1.2110   0.2290    
## ---                        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.04029 on 91 degrees of freedom
## Multiple R-squared: 0.06378, Adjusted R-squared: 0.04321
## F-statistic: 3.1 on 2 and 91 DF,  p-value: 0.04985

```