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.

KEYWORDS
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 interspecific 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 [Colour figure can be viewed at wileyonlinelibrary.com]
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, Luissell, & 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):

\[
\text{Niche Breadth} = \frac{1}{\sum_{i=1}^{n} p_i^2}
\]

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 breadth (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 scolecodphilians; 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 & Burbrik, 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 \( \lambda \) (Pagel, 1997) implemented in the R package Caper (Orme et al., 2014). We report the results of the phylogenetic models only when the \( \lambda \) value was significantly different from zero. All statistical analyses were done in R (R Core Team, 2016). The full \( \kappa \) 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 \( \text{km}^2 \) 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: \(-0.377 \pm 0.094, t = -3.98, p < .002 \)), and study area (slope: \(-0.409 \pm 0.079, t = -5.16, p < .002 \)). The \( \lambda \) of the phylogenetic model was not significantly different from zero. Lizard richness and predator species richness were lower on
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 = .85, p = .40; non-phylogenetic model: islands: 4.59 ± 0.43, mainland: 4.99 ± 0.54; t = .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, R² = 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, R² = 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, R² = 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, R² = 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, R² = 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, 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, R² < .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

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

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

**FIGURE 4** Relationship between dietary niche breadth and \( \log_{10} \) competitor species richness on islands (black) and the mainland (grey). N = 35 and 59 species respectively
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 interspecific 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, Papilis, & Valakos, 2015). Alternatively, marine subsidies (Barrett et al., 2005; Brooke & Houston, 1983; Papilis, 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


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Shai Meiri http://orcid.org/0000-0003-3839-6330
REFERENCES


DATA SOURCES


### Appendix 1a

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{APPENDIX 1b}

binomial sources for population density

Acanthodactylus boskianus  Shai Meiri pers. Comm.
Anolis humilis  Heinen, L.T. (1992). Comparisons of the leaf litter herpetofauna in abandoned cacao plantation and primary rain forest in Costa Rica:

Anolis lineatopus


Anolis oculatus


Brachylophus vitiensis


Ctenocephalus punctatus


Anolis punctatus


Aspidoscelis sexlineata


Aspidoscelis tigris


Brachylophus vitiensis


Cercosaura ocellata


Chlamydosaurus kingii


Cnemidophorus lemniscatus


Cnemidophorus lemniscatus


Cnemidophorus lemniscatus


Ctenosaura ocellata


binomial sources for population density

Leioplosima telfairii


Lepidoblepharis xanthostigma

Lygodactylus capensis

Mabuya mabouya

Menetia greyii

Morethia boulengeeri

Oligosoma grande

Oligosoma macmanni

Oligosoma nigriplantare

Phrynosoma cornutum

Phrynosoma douglassii

Phrynosoma modestum

Phylokepsus pollicaris

Pelloyscincus jagori

Pleistiodon reynoldsi

Plica plica

Plica umbra
binomial sources for population density

Podarcis gaigeae

Podarcis raffoneae

Salvator merianae

Sceloporus grammicus

Sceloporus poinsettii

Sceloporus grammicus

Scincella lateralis

Sphaerodactylus vincenti

Stellagama stellio

Tenuidactylus caspius

Trachylepis quinquetaeniata

Tropidurus itambere

Tropidurus torquatus

Tupinambis teguixin

Uma exsul

Uta stansburiana

Varanus brevicauda

Varanus tristis
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### Appendix 1d

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Aspidoscelis sexlineata  same locality
Brachylophus vitiensis  same locality
Cercosaura ocellata  same locality
Chlamydosaurus kingii  same locality
Cnemidophorus lenniscatus  same locality
Coleodactylus natalensis  same locality
Ctenosaura pectinata  same locality
Ctenotus leonhardii  same locality
Ctenotus pantherinus  same locality
Ctenotus piankai  same locality
Ctenotus quatuourdecimlineatus  same locality
Ctenotus taeniolatus  same locality
Cyclura carinata  same locality
Cyclura pinguis  same locality
Draco volans  same locality
Egernia kingii  same locality
Emoia atrocostata  different localities
Eremiasiscuncus richardsonii  same locality
Eutropis multifasciata  same locality
Gallotia galloti  same locality
Gonatodes humeralis  same locality


Medica, P. A. (1967). Food Habits, Habitat Preference, Reproduction, And Diurnal Activity In Four Sympatric Species Of Whiptail Lizards (Cnemidophorus) In South Central Ne.


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### Appendix 1e: competitors and predators sources

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### Appendix 1f: List of diet categories

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<tr>
<td>Ants Pooled</td>
<td>Non identified Pooled</td>
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<tr>
<td>Aranae and Acari Pooled</td>
<td>Vertebrate Pooled (includes lizard shed skin and vertebrate egg)</td>
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<tr>
<td>Opiliones Pooled</td>
<td>Plant material Pooled</td>
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<tr>
<td>Chilopoda and Myriapoda Pooled</td>
<td>Flowers</td>
</tr>
<tr>
<td>Cockroaches Pooled</td>
<td>Fruits/seeds</td>
</tr>
<tr>
<td>Coleoptera Pooled</td>
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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 mainland.

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   12.43  <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)
Test if using only species with stomach number larger than 8 give different results than if using all the data

Subset the data

```r
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 = binomial, 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, vcv.dim = 3, vcv = TRUE, na.omit = FALSE, warn.dropped = TRUE)

```r
# Warning in comparative.data(phy = diet.tree, data = sub.diet.data, names.col = binomial, vcv.dim = 3, vcv = TRUE, na.omit = FALSE, warn.dropped = TRUE)
```
**Discriptive statistics**

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

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

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

**Sensitivity analysis - exclude different locations**

```r
# 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)
```

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

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

**Run the models on this data**

**full dataset**

**non-phylogenetic**

```r
model.sub1 <- lm(niche_breadth_full ~ distribution, sub.local.data)
summary(model.sub1)
```

```r
# 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
#```

```r
# 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

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

```r
## Call:
## pglsl(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

```r
model.sub1.1 <- lm(niche_breadth_clumped ~ distribution, sub.local.data)
summary(model.sub1.1)
```

```r
## 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

```r
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

```r
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(formula = 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 0.005241 **
## 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,  

```r
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,  

#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<- pgl(...
summary(model.sub2phy)
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
#
# Residual. 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,sub.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 1.52e-08 ***
# 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
# ---
model.sub3.1a<- lm(niche_breadth_clumped~log10(lizard_richness)+distribution, sub.local.data)
summary(model.sub3.1a)

model.sub3.1phy<- pglss(niche_breadth_clumped~log10(lizard_richness)*distribution,comp.sub.local.data, lambda = "ML")
summary(model.sub3.1phy)
## 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)            2.0461     2.783   0.735   0.465
## log10(predator_richness) 1.5717     1.511   1.041   0.302
## distributionMainland      4.0074     4.331   0.925   0.358
## log10(predator_richness):distributionMainland -1.8275     2.032  -0.899   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:
## Model Summary

|                | 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

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

## Model Call

```
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
```

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 ~ \texttt{log10}(\texttt{predator\_richness}) + \texttt{distribution}, data = \texttt{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 ~ \texttt{log10}(\texttt{predator\_richness})*\texttt{distribution}, data = \texttt{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 0.00021 **
## log10(predator_richness)  1.1009     0.5507  2.000 0.04969 *
## distributionMainland     -0.0416     0.9434 -0.044 0.96490

#delta
```
## 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
```

```r
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:  0.03431
## F-statistic: 2.334 on 2 and 73 DF,  p-value: 0.1041
```

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

```
## Call:
## pglsl(formula = niche_breadth_clumped ~ log10(predator_richness) * distribution, data = comp.sub.local.data, lambda = "ML")
#### Residuals:
```
## 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:
##
<table>
<thead>
<tr>
<th></th>
<th>Estimate</th>
<th>Std. Error</th>
<th>t value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>2.36941</td>
<td>0.60384</td>
<td>3.9239</td>
</tr>
<tr>
<td>log10(predator_richness)</td>
<td>-0.39424</td>
<td>0.31676</td>
<td>-1.2446</td>
</tr>
<tr>
<td>distributionMainland</td>
<td>-0.99877</td>
<td>1.00010</td>
<td>-0.9987</td>
</tr>
<tr>
<td>log10(predator_richness):distributionMainland</td>
<td>0.37653</td>
<td>0.45461</td>
<td>0.8283</td>
</tr>
</tbody>
</table>
##
| Pr(>|t|)                | 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~\texttt{log10}(predator_richness)+distribution,comp.sub.local.data,lambda = "ML")
summary(model.sub4.1aphy)
## 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

```r
#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  

```r
#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")
##
#### 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
## 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<- pglsl(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
#phylogenetic
model.sub1.phy<- pgl(s(niche_breadth_full~distribution,comp.diet2, lambda="ML")
summary(model.sub1.phy)

#clumped dataset
#non-phylogenetic
model.sub1.1<- lm(niche_breadth_clumped~distribution,diet.data)
summary(model.sub1.1)
## 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<- pglsl(niche_breadth_clumped~distribution,comp.diet2, lambda ="ML")
summary(model.sub1.1.phy)

##
## Call:
## pglsl(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*

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

```r
data.frame(
    call = "lm(formula = log_population_density ~ distribution + log_study_area + log_mass, data = sub.diet.data)",
    residuals = data.frame(
        Min = -1.68571, 1Q = -0.59632, Median = 0.04558, 3Q = 0.62029, Max = 1.89981),
    coefficients = data.frame(
        Estimate = c(2.16604, -0.98099, -0.45041, -0.72299),
        Std. Error = c(0.15634, 0.17429, 0.08192, 0.27634),
        t value = c(13.855, -5.629, -5.498, -2.616),
        Pr(>|t|) = c(< 2e-16, 2.04e-07, 3.55e-07, 0.0104)
    )
)
```

```r
## Call:
## lm(formula = log_population_density ~ distribution + log_study_area +
##     log_mass, data = sub.diet.data)
##
## Residuals:
##    Min     1Q  Median     3Q    Max
## -1.6857 -0.5963  0.0456  0.6203  1.8998
##
## 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:  
##  *** 0.001 *** 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*

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

```r
data.frame(
    call = "pgls(formula = log_population_density ~ distribution + log_study_area + log_mass, data = comp.sub.diet, lambda = "ML")",
    residuals = data.frame(
        Min = -0.10264, 1Q = -0.04730, Median = -0.01489, 3Q = 0.03004, Max = 0.14908),
    branch_length_transforms = data.frame()
)
```

```r
## Call:
## pgls(formula = log_population_density ~ distribution + log_study_area +
##     log_mass, data = comp.sub.diet, lambda = "ML")
##
## Residuals:
##    Min     1Q  Median     3Q    Max
## -0.1026 -0.0473 -0.0149  0.0300  0.1491
##
## 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  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)
```r
## 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```
model.sub2phy <- pgls(log_population_density~niche_breadth_full+distribution+log_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       -0.428539   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+log_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 <- pgl(s(log_population_density ~ niche_breadth_clumped + distribution + log_study_area + log_mass, comp.sub.diet, lambda = "ML")  
summary(model.sub2.1phy)  

## Call:  
## pgl(s(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)
## 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,comp.sub.diet,lambda = "ML")
summary(model.sub3phy)

## Coefficients:

|                        | Estimate | Std. Error | t value | Pr(>|t|) |
|------------------------|----------|------------|---------|----------|
| (Intercept)            | 4.2558043| 1.5210968  | 2.7979  | 0.006292 ** |
| 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 |          |

---

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

```r
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, sub.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
##  -0.64264  -0.16475  -0.01051  0.13693  0.64264
```

```r
```
## Model 1

### Min 1Q Median 3Q Max
-0.5217 -0.2968 -0.1308 0.1012 2.3735

### Coefficients:

<table>
<thead>
<tr>
<th>Estimate Std. Error t value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
</tr>
<tr>
<td>log10(lizard_richness)</td>
</tr>
<tr>
<td>distributionMainland</td>
</tr>
<tr>
<td>log10(lizard_richness):distributionMainland</td>
</tr>
</tbody>
</table>

### Pr(>|t|)

- 1.49e-10 ***
- 0.9852
- 0.0639 .
- 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 2

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

### Call:
```r
lm(formula = niche_breadth_clumped ~ log10(lizard_richness) + distribution, data = sub.diet.data)
```

### Residuals:

# 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
```r
model.sub3.1phy <- pgls(niche_breadth_clumped ~ log10(lizard_richness) * distribution, data = 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)
## 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)               1.4485   0.2225  6.5101 4.029e-09 ***
## log10(lizard_richness)    0.0907   0.1402  0.6472   0.51915
## distributionMainland    -0.2875   0.1189 -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    0.220
## log10(predator_richness)  0.7996   1.3722  0.583    0.562
## distributionMainland    -1.1943   3.5739 -0.334    0.739
## log10(predator_richness):distributionMainland 0.4696  1.7186  0.273
##
## 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|)
# log10(predator_richness)               1.0998     0.8233   1.337    0.185
# distributionMainland                  -0.2380     0.7261  -0.327    0.744
# log10(predator_richness):distributionMainland
#    lower bound : 0.000, p = 0.051972
#    upper bound : 1.000, p = 0.049407
#    95.0% CI    : (NA, 1.000)
model.sub4aphy <- pgls(niche_breadth_full ~ log10(predator_richness) + distribution, data = comp.sub.diet, lambda = "ML")
summary(model.sub4aphy)
model.sub4.1 <- lm(niche_breadth_clumped ~ log10(predator_richness) * distribution, data = 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  2.29e-05 ***
## log10(predator_richness)     -0.3781     0.2673  -1.415   0.161
## distributionMainland       -1.1425     0.6963  -1.641   0.104
## log10(predator_richness):distributionMainland 0.4745     0.3348   1.417  0.160
##                              Pr(>|t|)
## (Intercept)                                   2.29e-05 ***
## log10(predator_richness)                         0.161
## distributionMainland                             0.104
## log10(predator_richness):distributionMainland    0.160
## ---
## Signif. codes:  < 0.001 '***' 0.001 '*' 0.01 '.' 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, data = 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)                    1.6579     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
##                              Pr(>|t|)
## (Intercept)                                    5.23e-07 ***
## log10(predator_richness)                         0.641
## distributionMainland                  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

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

```r
## Call:
## pgls(formula = niche_breadth_clumped ~ log10(predator_richness) *
##     distribution, data = comp.sub.diet, lambda = "ML")
##
## Residuals:
##        Min       1Q    Median       3Q      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
```

```r
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:

<table>
<thead>
<tr>
<th></th>
<th>Min</th>
<th>1Q</th>
<th>Median</th>
<th>3Q</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>Residuals</td>
<td>-0.118788</td>
<td>-0.018805</td>
<td>0.002205</td>
<td>0.025526</td>
<td>0.092838</td>
</tr>
</tbody>
</table>

## 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 |

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## 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