**README**

**Title: Variable vulnerability to climate change in New Zealand lizards**

**Abstract**

**Aim:** The primary drivers of species and population extirpations have been habitat loss, overexploitation, and invasive species, but human-mediated climate change is expected to be a major driver in future. To minimise biodiversity loss, conservation managers should identify species vulnerable to climate change and prioritise their protection. Here, we estimate climatic suitability for two speciose taxonomic groups, then use phylogenetic analyses to assess vulnerability to climate change. **Location:** Aotearoa New Zealand (NZ) **Taxa:** NZ lizards: diplodactylid geckos and eugongylinae skinks **Methods:** We built correlative species distribution models (SDMs) for NZ geckos and skinks to estimate climatic suitability under current climate and 2070 future-climate scenarios. We then used Bayesian phylogenetic mixed models (BPMMs) to assess vulnerability for both groups with predictor variables for life history traits (body size and activity phase) and current distribution (elevation and latitude). We explored two scenarios: an unlimited dispersal scenario, where projections track climate, and a no-dispersal scenario, where projections are restricted to areas currently identified as suitable. **Results:** SDMs projected vulnerability to climate change for most modelled lizards. For species’ ranges projected to decline in climatically suitable areas, average decreases were between 42–45% for geckos and 33–91% for skinks, although area did increase or remain stable for a minority of species. For the no-dispersal scenario, the average decrease for geckos was 37–52% and for skinks was 33–52%. Our BPMMs showed phylogenetic signal in climate change vulnerability for both groups, with elevation increasing vulnerability for geckos, and body size reducing vulnerability for skinks. **Main conclusions:** NZ lizards showed variable vulnerability to climate change, with most species’ ranges predicted to decrease. For species whose suitable climatic space is projected to disappear from within their current range, managed relocation could be considered to establish populations in regions that will be suitable under future climates.

**Data Description**

*Climate variables*

Although GPS coordinates for current populations are not included due to the potential threat of poaching, the climate variables for each species are provided in the zipped folder for modelled species. The records for extant gecko and skinks mainly came from the New Zealand's Department of Conervation Herpetofauna Database. After updating the taxonomy and cleaning the data to reflect the taxonomy as at 2019 of 43 geckos speceis recognised across seven genera and 61 species in genus, we then thinned the occurrence records at a 1 km resolution for all species then predicted distributions for those with > 15 records using species distribution models. The climate variables for each species were selected among annual mean temperature (bio1), maximum temperature of the warmest month (bio5), minimum temperature of the coldest month (bio6), mean temperature of driest quarter (bio9), mean temperature of wettest quarter (bio10), and precipitation of the driest quarter (bio17). To reduce multicollinearity in species distribution models for each species, we only retained climate variables with a variable inflation factor < 10. The climate variables were from the CHELSA database (<https://chelsa-climate.org/>), which can be freely downloaded for current and future scenarios. More information is provided in the main text and Supporting Information of the paper.

*MCC tree files*

We also provide MCC tree files for the geckos and skinks. The phylogenetic trees have been constructed for NZ geckos by (Nielsen et al., 2011) and for NZ skinks by (Chapple et al., 2009). For geckos we used a subset of the sequences used by Nielsen et al. (2011) for four genes, two nuclear (RAG 1, PDC) and two mitochondrial (16S, ND2 along with flanking tRNA sequences). For skinks, we used sequences from Chapple et al. (2009) for one nuclear (RAG 1) and five mitochondrial (ND2, ND4, Cyt *b*, 12S and 16S) genes, and additional ND2 sequences for taxa not included in the original phylogeny (Chapple et al., 2011, p. 201). In total we used sequences for all recognised extant taxa (Hitchmough et al., 2016) as at 2019 except for three species of skink (*O.* aff. *inconspicuum* “Okuru”, *O.* *robinsoni*, and *O*. aff. *inconspicuum* “North Otago”) and two species of gecko (*M*. “Cupola” and *W.* “Kaikouras”) for which genetic data were not available. More information is provided in the main text and Supporting Information of the paper.

Scripts

Scripts to run examples of species distribution models and Bayesian phylogenetic mixed in the programming language R are provided. More information is provided in the main text and Supporting Information of the paper.