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Incorporating regional-scale ecological knowledge to improve the effectiveness of large-scale conservation programs

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ABSTRACT

Land-stewardship programs are a major focus of investment by governments for conserving biodiversity in agricultural landscapes. These programs are generally large-scale (e.g. >1000 km) spanning multiple biogeographic regions but developed using spatially limited (e.g. landscape-scale; <100 km) ecological data interpolated across broad areas for one, or a few, well-studied taxonomic groups. Information about how less-studied taxa respond to regional differences in management and environmental effects has potential to further inform land-stewardship conservation programs, but suitable datasets are rarely available. In this study, we sought to enhance planning of large-scale conservation programs by quantifying relationships between reptile assemblages and key environmental attributes at regional scales within a large-scale (>172,000 km^2) Australian land-stewardship program. Using 234 remnant woodland monitoring sites spanning four distinct biogeographic regions, we asked: Do reptile assemblages show different environmental associations across biogeographically distinct regions? We found that environmental features important to reptile diversity differed over each region. Abundance and rare species richness of reptiles responded at regional-scales to elevation, native groundcover and aspect. We identified four implications from our study: 1) large-scale conservation schemes can achieve better outcomes for reptiles using regional-scale knowledge of environmental associations, 2) regional-scale knowledge is particularly valuable for conservation of rare reptile taxa, 3) consideration of abiotic environmental features which cannot be directly managed (e.g. aspect, elevation) is important, 4) programs can be tailored to better support reptile groups at higher conservation risk. Our study shows that reptile-environment associations differ among biogeographic regions, and this presents opportunity for tailoring stronger policy and management strategies for conserving large-scale agricultural landscapes globally.

KEY WORDS: Agri-environment schemes, agro-ecology, agricultural landscapes, ecosystem services, Environmental Stewardship Programme, herpetofauna, South-eastern Australia.

INTRODUCTION

Agricultural expansion and intensification are major causes of biodiversity loss (Barnosky *et al.*, 2011). To address this, billions of dollars are committed by governments to large-scale land-stewardship conservation programs targeting private-tenure agricultural landscapes (European Commission, 2014; USDA, 2014). While increasing the scope of these programs is a global priority (e.g. UN Millennium Development Goals; IUCN, 2010), they remain founded on spatially limited ecological data interpolated across broad areas (Whittingham *et al.*, 2007; Gonthier *et al.*, 2014) and largely focus on one, or a few, well-studied taxonomic groups (Lüscher *et al.*, 2014). An emerging challenge for conservation practitioners is to find ways to refine large-scale land-stewardship programs, by incorporating high-resolution ecological information for an increasing range of taxa.

Species respond to environmental drivers and ecological processes at multiple spatial scales (Cushman & McGarigal, 2002), so an understanding of these issues is likely to improve effectiveness of large-scale conservation programs. However, it can be difficult to implement large-scale programs (i.e. across >1000 km) while accommodating complexity in fine-scale (i.e. 1-10 km) biological patterns. Subsequently, land-stewardship programs have generally focused only on a few management objectives across coarse scales. Exploring regional-scale (i.e. 10-100 km) habitat relationships using regions defined by shared environmental condition (e.g. biogeographic regions) is likely to capture important patterns of response to habitats and management (Batáry *et al.*, 2011; Concepción *et al.*, 2012; Báldi, Batáry & Kleijn, 2013) and provides a possible balance between generality and finer resolution. The benefits of incorporating regional-scale criteria into conservation planning have recently been acknowledged for some beetles (Liu *et al.*, 2014) and birds (Whittingham *et al.*, 2007) but there are only a few studies, limited to European landscapes. Broadening our understanding of biodiversity responses in larger multi-regional contexts, and in other parts of the world, is therefore important.

Another challenge facing conservation managers is to develop conservation programs based on a wide variety of taxa. Data for large-scale land-stewardship programs are generally limited to a few well-studied groups like plants, birds and some invertebrates (for review see Whittingham, 2011; Batáry *et al.*, 2015). Ground-dependent reptiles have received considerably less attention (but see Michael *et al.*, 2014) despite representing one of the most diverse and rapidly declining vertebrate groups in agricultural landscapes globally (Böhm *et al.*, 2013). Further, reptiles have ecological requirements that are distinct from other vertebrate taxa, such as limited dispersal capacity and temperature-dependent activity (Guisan & Hofer, 2003; Schutz & Driscoll, 2008). Consequently, building on known ecological requirements of reptiles by incorporating regional-scale knowledge of environmental associations can enhance effectiveness of large-scale conservation programs.

In this study, we examined habitat requirements for reptiles by studying their associations with a set of biotic and abiotic environmental variables, across multiple biogeographic regions, within the Australian Environmental Stewardship Programme (Commonwealth of Australia, 2009, 2013; Lindenmayer *et al.*, 2012). This topic is of particular conservation interest given its relevance to the widely adopted and costly agri-environment schemes (sensu Kleijn & Sutherland, 2003). These schemes aim to promote biodiversity in farming landscapes, but despite billions of dollars of investment annually, their benefit remains undemonstrated for declining ground-dwelling vertebrates including reptiles (see Michael *et al.*, 2014). Our study is the first to examine spatial variation in habitat requirements for reptiles across a conservation program of this scale, covering >172,000 km^2 (approximately the size of Uruguay). Using 234 remnant woodland monitoring sites across four distinct biogeographic regions (sensu Thackway & Cresswell, 1995; Commonwealth of Australia, 2014), we asked: Do reptile assemblages show different environmental associations across biogeographically distinct region? To answer this question, we examined different aspects of the reptile assemblages, including total abundance and species richness, as well as richness of rare species and relative abundance (evenness) of the assemblage. Because reptiles exhibit strong associations with climate and geography (McCain, 2010; Kay *et al.*, 2013) we predicted that the relationships between environmental variables and measures of reptile diversity would vary across the regions observed, providing opportunity for improving design of land-stewardship programs. Our results identify four key conservation implications for decision makers, underscoring opportunities to advance conservation programs in the future.

MATERIALS AND METHODS

Study Area

Our study is set within the critically endangered Box Gum Grassy Woodland ecological community targeted under the Environmental Stewardship Programme in south-eastern Australia (Lindenmayer *et al.*, 2012). This woodland community is characterised by an understorey of native tussock grasses, herbs and scattered shrubs, and an open tree strata that was originally dominated by white box (*Eucalyptus albens*), yellow box (*E. melliodora*) and Blakely's red gum (*E. blakelyi*) (Commonwealth of Australia, 2013). Spanning >1000 km north-to-south, this community has been reduced to <4% of its original extent due to clearing over the past 150 years (Lindenmayer, Bennett & Hobbs, 2010). The southern extent is particularly threatened by intensive agriculture (Hoekstra *et al.*, 2005) and now occurs as small and isolated remnants of varying condition (Commonwealth of Australia, 2013). The community also supports a rich woodland-dependent reptile fauna (Kay *et al.*, 2013), with over 120 species of reptiles recorded across the extent of the study area (Wilson & Swan, 2013).

Experimental design

We established 234 monitoring sites in remnant woodland on 152 farms (≤ two sites per farm) involved in the Programme (Fig. 1). These sites represent the highest quality woodland remnants remaining (see Fig. S1 for typical site). An implicit assumption from the outset of the Programme was that its effectiveness for biodiversity would be homogenous across its spatial extent despite spanning a range of biogeographic and climatic boundaries known to influence ecological communities (Commonwealth of Australia, 2009). To test this, we grouped sites of similar climate, geology and landform by well-defined biogeographic regions (sensu Thackway & Cresswell, 1995) which have been used to define agro-climatic systems throughout our study area (Hutchinson *et al.*, 2005).

We first separated sites on the basis of broad agro-climatic system from Hutchinson *et al.* (2005): a winter-rainfall improved-pasture system and a low-rainfall native-pasture system. Within each agro-climatic system, we then grouped sites by clearly defined biogeographic regions (Commonwealth of Australia, 2014). Sites within the winter-rainfall system were thus separated into the elevated Southern Highlands region (61 sites) and the fertile Southern Slopes region (82 sites). Sites within the low-rainfall system were similarly separated into a Northern Slopes (53 sites) region and two smaller northern biogeographic regions that, due to limited sampling across both biogeographic regions, were combined to create a single Northern region (38 sites). Additional descriptions for the final set of four regions are provided as supporting information (Table S1).

Reptile surveys

We surveyed each site for reptiles three times (September 2010, February 2012 and September 2012) along a 200 x 40 m transect. We used a time- and area-constrained (20 min x 0.8 ha) survey protocol (following Michael *et al.*, 2012), involving active searches of natural habitat and inspections of two artificial refuge arrays. Both arrays were placed 100 m apart and consisted of four concrete roof tiles (32 x 42 cm), one double-layered stack of corrugated galvanized steel and four wooden railway sleepers (1.2 m long).

We conducted surveys on clear days between 0900 and 1600 hours with the same group of experienced field ecologists. We identified species using Wilson & Swan (2012). Our analyses focussed on whole assemblages at site level, so we pooled observations within sites and across survey times to define a reptile assemblage at every site.

Measurement of environmental features

We measured a suite of environmental features relevant to conservation managers. We included variables commonly considered for management (e.g. vegetation characteristics) plus those likely to be important for reptiles but not influenced by management (e.g. topographic position, climate).

We surveyed vegetation at each site during February 2010 and 2012 and averaged data at the site level. We measured native plant species richness in a 20 x 20 m plot midway along the transect and recorded length of logs in two 50 x 20 m plots at the extreme ends of a transect. We estimated percentage cover of bare ground, organic litter, rock, overstorey and midstorey by recording these attributes every metre along two 50 m transects (for details see Michael *et al.*, 2014).

We obtained elevation and aspect for each site using nine second resolution spatial data (Hutchinson, Stein & Stein, 2011). Large-scale geographic effects on species richness are known to occur for reptiles (Rodríguez, Belmontes & Hawkins, 2005; Brown, Dorrough & Ramsey, 2011) driven by latitudinal influences on ambient energy (temperature and solar radiation) and moisture-driven habitat gradients. Because our study area encompasses confounding latitudinal and rainfall gradients, we used a ‘growth index’ derived from ANUCLIM (Xu & Hutchinson, 2013) to combine the effect of temperature, moisture and daylight into one energy related variable (see Appendix S1 for details).

Statistical analysis

We used an information-theoretic approach (Burnham & Anderson, 2002) to test whether large-scale conservation programs could be made more effective by incorporating regional-scale ecological knowledge of reptiles. We fitted generalised linear mixed models (GLMMs) to examine the relationship between environmental variables and reptile diversity. Conservation programs generally measure biodiversity success through change in overall richness or abundance over time (Batáry *et al.*, 2011) despite these being relatively crude measures (Morris *et al.*, 2014). Additionally, biodiversity success may be measured through a positive response in species of conservation concern (Cunningham *et al.*, 2014), as well as the relative abundance (evenness) of species, where greater evenness implies more robust populations (Magurran & McGill, 2011). Therefore, we used four measures of reptile diversity as our response variables, with higher values indicating improved outcome: (i) richness of all reptile species, (ii) richness of rare reptile species (the number that occurred at < 5% of all sites), (iii) abundance of all reptile species, and (iv) assemblage evenness (Shannon Evenness; Magurran & McGill, 2011). We used a Poisson distribution with a log link to model richness, rare species richness and overall abundance. For evenness, we used a Gaussian distribution with an identity link. “Farm” was fitted as a random effect in all models.

We reduced the number of potential explanatory variables for use in models by: (i) using features identified in previous studies of reptile ecological requirements (e.g. Brown *et al.*, 2011 and references within), as well as expert knowledge of experienced wildlife scientists, from within Australian temperate woodlands, and (ii) eliminating highly correlated variables (examining pairwise scatterplots and correlation coefficients with $r > 0.5$ cutoff) (Zuur *et al.*, 2009). This gave a set of eight predictor variables useful for testing regional-scale habitat relationships for reptiles: growth index, aspect (scaled from +1 [northerly] to -1 [southerly]), elevation, richness of native groundcover, log cover (length), rock cover, bare ground cover and native overstorey cover.

To test whether regional-scale information could enhance conservation programs, we fitted region and the interaction of region with each of the eight predictor variables. To explore the correlative influence of region with environment, we repeated our analysis with the environmental variables standardised within region (i.e., the within-region mean subtracted from the values within that region). If region was important in models only with standardised environmental variables, we inferred that regional differences are otherwise accounted for by environmental gradients across the whole study area. Conversely, if environmental variables are important only in models without standardisation, it would imply that broad-scale regional differences drive changes in reptile diversity and within-region variation in these parameters is not important.

We used Akaike information criterion (AIC, Burnham & Anderson, 2002) to select top-ranked models and included all models within 2 units in our inference (Arnold, 2010). We checked for over-dispersion by dividing the Pearson goodness-of-fit statistic by the residual degrees of freedom and found no values greater than one suggesting that our data were not over-dispersed (McCullagh & Nelder, 1989). We inspected the residual vs. fitted plots of each model to confirm that residuals were approximately randomly distributed with respect to fitted values. We assumed sites on different farms were independent, and tested for spatial dependence in the residuals using a Moran's I test (Cliff & Ord, 1981), finding no evidence of spatial autocorrelation. We undertook all analyses using the *MuMIn* package in R (Bartoń, 2009).

RESULTS

We recorded 57 species of reptiles from ten families (Table S2). Species richness ranged from one to 10 species per site, with a decline in richness with increasing latitude (slope= -0.061±0.018, p<0.001) corresponding to approximately one less species for every five degrees of latitude (Fig. S2). Species accumulation curves for each study region and the whole study area approached an asymptote (Fig. S3), ranging between 72.4% and 92.9% of the estimated true richness (Table S3).

The top-ranked model for species richness across the study area included a positive effect of growth index, log cover, native groundcover richness and rock cover with lesser negative effects of elevation, native overstorey cover, and northerly (sunlit) aspect (Table 1, Fig. 2). Region was included in the model although its effects were weak with no interaction effect apparent.

Rare species richness was explained across the study area by a positive effect of rock cover and, to a lesser extent, a negative effect of native overstorey cover (Table 1, Fig. 2). Rare species richness was negatively associated with elevation in the Southern Highlands and Northern Slopes regions, and positively in the remaining regions. An interactive effect of region also occurred with native groundcover richness, which was positively associated in all but the Northern region.

Reptile abundance was explained across the study area by a positive effect of rock cover and interactions of region with elevation, northerly (sunlit) aspect and native groundcover richness (Table 1, Fig. 2). Reptile species evenness was explained across the study area by positive effects of growth index and, to a lesser extent, positive effects of rock cover and native groundcover richness and negative effects of elevation (Table 1, Fig. 2). There was no interaction effect of region.

Standardizing predictor variables for all diversity measures revealed the same result, with evenness revealing an additional effect of region (Table S4), indicating environmental terms had similar effects at the within-region and between-region scales.

DISCUSSION

We used an information-theoretic approach to assess how incorporating spatial variation in habitat requirements can assist large-scale conservation planning. Our study revealed that environmental features important in driving reptile diversity differed for each region. Critically, two of the four measures of reptile diversity responded at the regional-scale, in some cases reversing the direction of effect. Our work provides empirical support for incorporating regional-scale criteria into conservation planning, addressing an emerging need in conservation science (Lüscher *et al.*, 2015).

Biological interpretation of the models

To understand the appropriate regional-level conservation planning and management outcomes of this study, it is important to consider the mechanisms behind region-specific responses to environment by reptiles. We found two abiotic variables (elevation, aspect) and one biotic variable (native groundcover richness) were important drivers of abundance and rare species richness that varied in effect at the regional level (Fig. 2b). In two of the southern (colder) regions, lower elevation corresponded with lower numbers of reptiles and rare species, while in the warmer Northern and Northern Slopes regions the pattern was reversed. This is consistent with known thermoregulatory limits which reptiles experience at higher elevations (Fischer and Lindenmayer, 2005; McCain, 2010). In contradiction to this idea was the positive effect of elevation on rare species richness in the Southern Slopes (Fig. 2b). However, this might reflect extensive native vegetation loss in the fertile lower slopes of this region compared with hilltops where native vegetation is often retained (Fischer *et al.*, 2010).

Northerly (sunlit) aspects generally supported higher reptile abundance, although this also differed by region. At cooler (higher) latitudes, higher reptile abundance on northerly (sunlit) aspects within the Northern Slopes and Southern Highlands regions is consistent with reptile thermal requirements (Brown *et al.*, 2011). This effect also could be expected for the cooler Southern Slopes, although similar preference by livestock for these north-facing warmer and more productive pastures may contribute to lower reptile abundance observed here based on the demonstrated impact of grazing on reptiles (Dorrough *et al.*, 2012; Howland *et al.*, 2014). Higher abundance on southerly (shaded) aspects in the warmer Northern region may reflect a preference for species to occupy mesic refugia when thermoregulatory processes are not limiting, a recognised pattern in reptiles (Duckett & Stow, 2013).

Native groundcover richness influenced rare reptile species richness and abundance at the regional-level, with positive effects in all but the Northern region. This regional effect probably reflects differences in climate (Hutchinson *et al.*, 2005) and cultivation histories (Hoekstra *et al.*, 2005) between the regions, with a greater reliance on native groundcover richness by reptiles in the more intensively cultivated southern regions. This is consistent with the well-established negative impact of agricultural land-use recognised for reptiles globally (Fabricius, Burger & Hockey, 2003; Ribeiro *et al.*, 2009).

Five of the seven environmental features identified in top models for reptile diversity were linked to reptile thermoregulatory behaviour. Ground-layer structural attributes related to reptile basking, including cover of rocks (Seebacher & Franklin, 2005) and overstorey (Pike, Webb & Shine, 2011), as well as broad thermally-relevant climatic variables of growth index, elevation and aspect were important in driving reptile diversity. This suggests inclusion of features that influence thermoregulatory environments enhances regional effectiveness of conservation programs for reptiles.

Implications for conservation

To facilitate adaptive learning (sensu Perkins *et al.*, 2010) from the Environmental Stewardship Programme that was the focus of this investigation, we present a summary of suggested management actions to inform future programs. We summarise features important for conserving overall reptile diversity, and identify features important at the regional-level for conserving rare species within this Programme (Table 2). To help guide conservation planning more generally, we identify four key management recommendations that emerge from our study.

1) <u>Incorporating regional-level responses of species diversity to environmental features allows greater sophistication in conservation program design</u>

The results of our study suggest conservation programs will be more effective if they incorporate regional variation in important environmental features. The identification of regional patterns for reptile abundance and rare species is of specific value for conservation managers. This is because bolstering existing populations and increasing species of conservation concern is fundamental to arresting biodiversity erosion in fragmented agricultural landscapes (Gonthier *et al.*, 2014). Our work addresses the need to shift beyond the ‘one-size-fits-all’ approach commonly applied to large-scale programs (Whittingham *et al.*, 2007; Batáry *et al.*, 2011), underscoring the value of considering the disproportionate benefit some environmental features provide in certain contexts. Managers can apply regional-level biodiversity information either by selecting sites containing certain attributes, or for targeted restoration activities. For example, restoration of native groundcover (e.g. Lindenmayer *et al.*, 2010) would be most effectively applied for restoring rare reptile diversity in southern regions of this study (Fig. 2b). Although similar studies across a suite of taxonomic groups are needed, the habitat recommendations identified in this study are largely consistent with, and unlikely to be detrimental for, many other ground-dependent fauna including mammals and amphibians (McElhinny *et al.*, 2006).

2) Rare species need special consideration

Despite the overarching objectives of many conservation programs to conserve targeted ecological communities, it is evident that rare and threatened taxa may continue to decline (Kleijn *et al.*, 2006), or show time-lags in response to conservation programs (Michael *et al.*, 2014). Procedures for ensuring robust protection of rare and threatened species in land-stewardship conservation programs are limited (Whittingham, 2011; Batáry *et al.*, 2011) and have not previously involved recommendations for management at the regional-level (Table 2). An explicit recommendation from our study is to incorporate regional environmental features important for conserving rare species at the site selection stage and focus management actions at this level. Applying this approach for rare species in other taxonomic groups may help identify important features for preventing multi-taxon species decline in agricultural landscapes. Where recommendations for different taxonomic groups clash (e.g. positive for reptiles while negative for birds), other approaches such as multi-criteria decision analyses (Huang, Keisler & Linkov, 2011) could be used to consider a range of contrasting management options.

3) There is a need to prioritize variables that cannot be managed

Some of the most important drivers of diversity at the site level are environmental attributes that cannot be influenced by site management, such as aspect, elevation and growth index. Despite their importance for diversity, these abiotic attributes are rarely considered when designing conservation programs (Kleijn *et al.*, 2006). Because these features cannot be managed, their integration at the initial site selection stages of conservation planning, particularly at the regional-level, would enhance species diversity and therefore effectiveness of conservation programs. Although large programs may inadvertently capture these features, a targeted approach would be more effective. This could be achieved by ensuring sufficient representation of these variables in the preliminary stages of program development, but then tailoring site selection to include key features relevant to particular regions.

4) Programs can be tailored to better support species groups at higher conservation risk

Many conservation programs differ in effectiveness among species and fail to support species-groups at higher conservation risk. For example, land-stewardship conservation programs are more effective for plants and some invertebrate groups (Whittingham, 2011) with no demonstrable benefit for other rapidly declining groups such as reptiles (Michael *et al.*, 2014). However, we contend that refining programs by incorporating environmental features can benefit these at-risk groups. Our study shows that reptiles, a group experiencing global decline (Böhm *et al.*, 2013), are positively associated with features important for thermoregulation (e.g. aspect, elevation, rock cover). Maintaining important thermoregulatory features, either through site-selection (by considering elevation and aspect) or proposed management actions (such as maintaining rock cover as a non-renewable resource), would help reptiles and possibly other thermoregulating species-groups (e.g. amphibians, invertebrates; Cossins & Bowler, 1987).

The management recommendations we have identified were developed with the goal of enhancing effectiveness of the large-scale land-stewardship conservation programs. Such programs have become one of the most used tools globally for conserving biodiversity in agricultural landscapes (European Commission, 2014; USDA, 2014). By examining difference between regions, for an important yet poorly studied taxonomic group, we have identified new opportunities for better conservation management in agricultural landscapes that can improve effectiveness of large-scale conservation programs globally.

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SUPPORTING INFORMATION

Additional Supporting Information may be found in the online version of this article at the publisher's web-site:

Appendix S1. Calculation of Growth Index

Fig. S1. Example of a typical woodland site from our study.

Fig. S2. Relationship between reptile species richness and latitude.

Fig. S3. Accumulation curves of observed species richness for the study area and four study regions.

Table S1. Additional description of each study region.

Table S2. List of all reptile individuals surveyed.

Table S3. Observed and estimated species richness for the whole study area and each of the four study regions.

Table S4. GLMMs for the four measures of reptile community assembly in relation to eight environmental and habitat predictors.

TABLES

Table 1. Summary of the best model for reptile diversity response (species richness, rare species richness, abundance, evenness) as predicted by eight environmental variables: growth index (Gr_id), northerly aspect (Asp_N), elevation (Elev), native groundcover richness (NGR), length of log cover (LogLth), rock cover (Rock), bare ground cover (BG) and native overstorey cover (NOS_cvr) plus interaction with region (Reg). The Northern Region is incorporated in the intercept as the reference category against which all regions, and their interactions, are measured. Unstandardized models are provided (these match the standardized models). Direction of response is given (sign)

Response	Model terms	Direction	Estimate	SE	F	P
Species Richness	Reg + Rock + NGR + Gr_id + Asp_N + Elev + LogLth + NOS_cvr					
	(Intercept)		0.294	0.517	0.567	0.5705
	Reg(NS)	+	0.006	0.218	0.025	0.9798

Response	Model terms	Direction	Estimate	SE	F	P
	Reg(SH)	+	0.347	0.264	1.318	0.1876
	Reg(SS)	+	0.192	0.230	0.836	0.4029
	Rock	+	0.021	0.007	3.072	0.0021
	NGR	+	0.021	0.008	2.722	0.0065
	Gr_id	+	6.815	3.184	2.14	0.0323
	Asp_N	–	-0.106	0.058	-1.82	0.0686
	Elev	–	-0.001	3.17 x 10^{-04}	-2.01	0.0443
	LogLth	+	0.004	0.002	2.038	0.0415
	NOS_cvr	–	-0.003	0.002	-1.56	0.1198
Rare species richness	Reg + Elev + Reg*Elev + Rock + NOS_cvr + Reg*NGR + NGR					
	(Intercept)		-0.161	0.840	-0.191	0.8482
	Reg(NS)	+	0.340	0.991	0.343	0.7315
	Reg(SH)	+	2.169	1.107	1.960	0.0500
	Reg(SS)	–	-0.811	0.936	-0.866	0.3862
	Rock	+	0.025	0.011	2.326	0.0200
	NOS_cvr	–	-0.005	0.003	-1.742	0.0815
	Elev	+	0.002	0.001	1.296	0.1951
	Reg(NS)*Elev	–	-0.003	0.002	-2.019	0.0435
	Reg(SH)*Elev	–	-0.004	0.002	-2.497	0.0125
	Reg(SS)*Elev	+	4.19 x 10^{-04}	0.001	0.280	0.7791
	NGR	–	-0.049	0.055	-0.889	0.3741
	Reg(NS)*NGR	+	0.119	0.061	1.949	0.0513
	Reg(SH)*NGR	+	0.068	0.057	1.190	0.2339
	Reg(SS)*NGR	+	0.085	0.059	1.452	0.1465
Abundance	Reg + Reg*NGR + NGR + Rock + Elev + Reg*Elev + Asp_N + Reg*Asp_N					
	(Intercept)		1.282	0.518	2.475	0.0133
	Reg(NS)	+	1.469	0.685	2.144	0.0320
	Reg(SH)	+	1.734	0.870	1.993	0.0462
	Reg(SS)	+	0.628	0.596	1.054	0.2918
	Rock	+	0.023	0.007	3.149	0.0016
	NGR	–	-0.025	0.027	-0.920	0.3575
	Reg(NS)*NGR	+	0.035	0.034	1.037	0.2998
	Reg(SH)*NGR	+	0.044	0.030	1.445	0.1484
	Reg(SS)*NGR	+	0.101	0.029	3.435	0.0006
	Elev	+	0.002	0.001	1.978	0.0480
	Reg(NS)*Elev	–	-0.005	0.001	-4.029	0.0001
	Reg(SH)*Elev	–	-0.004	0.001	-3.042	0.0023
	Reg(SS)*Elev	–	-0.004	0.001	-3.612	0.0003
	Asp_N	–	-0.347	0.150	-2.312	0.0208
	Reg(NS)*Asp_N	+	0.322	0.211	1.530	0.1260
	Reg(SH)*Asp_N	+	0.096	0.205	0.467	0.6402
	Reg(SS)*Asp_N	+	0.533	0.170	3.138	0.0017
Evenness	Rock + NGR + Elev + Gr_id					
	(Intercept)		0.477	0.116	4.124	0.0000
	Rock	+	0.009	0.005	1.890	0.0588
	NGR	+	0.007	0.004	1.587	0.1141
	Elev	–	-2.25 x 10^{-04}	1.39 x 10^{-04}	-1.624	0.1044
	Gr_id	+	2.620	0.875	2.996	0.0027

Table 2. Recommendations for scheme development, particularly targeting site prioritisation aiming to enhance overall reptile richness and rare species richness for sites included in the four study regions within the study area

Region	**To conserve overall richness**	**To conserve rare reptiles**
Whole study	• Target high (>3%) rock cover • Target high (>300m/ha) log cover • Target open (<20%) overstorey • Target sites at low (<500m) elevation • Target high (1.0) growth index • Target high (>0.033 species/m^2) native groundcover richness	• Target high (>3%) rock cover • Target open (<20%) overstorey
Northern	• As for whole study	• Target sites at high (<540m) elevation • Target southerly (shaded) aspect • Target low (<0.037 species/m^2) native groundcover richness
Northern Slopes	• As for whole study	• Target sites at low (<430m) elevation • Target high (>0.037 species/m^2) native groundcover richness
Southern Slopes	• As for whole study	• Target sites at high (>430m) elevation • Target southerly (shaded) aspect • Target high (>0.033 species/m^2) native groundcover richness
Southern Highlands	• As for whole study	• Target sites at low (<730m) elevation • Target northerly (sunlit) aspect • Target high (>0.038 species/m^2) native groundcover richness

FIGURES

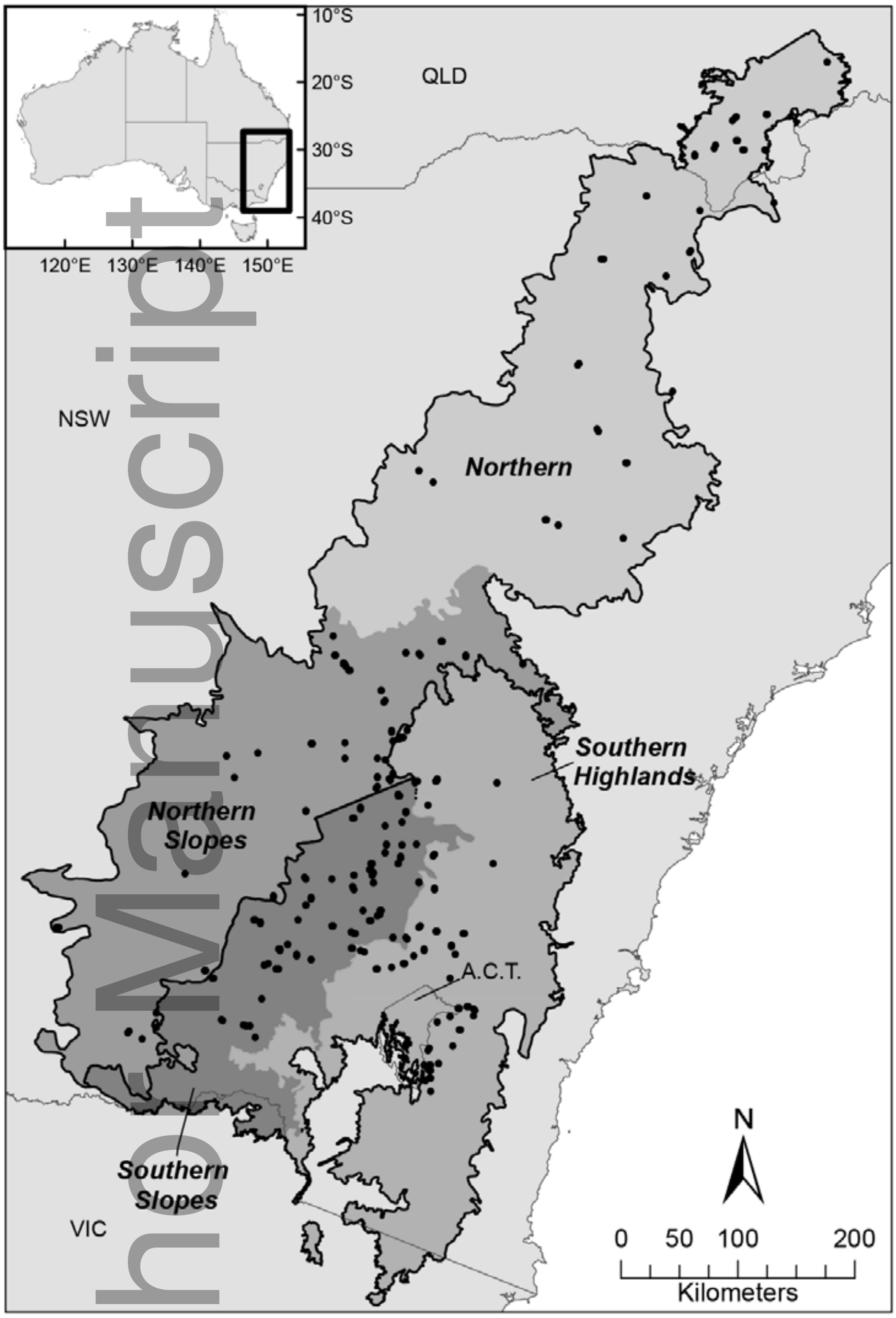

Fig. 1. Location of the study area spanning New South Wales (NSW) and southern Queensland (QLD) of south-eastern Australia showing the location of monitoring sites (n=234) surveyed across the four study regions (greyed fill) and two agro-climatic systems (black boundary).

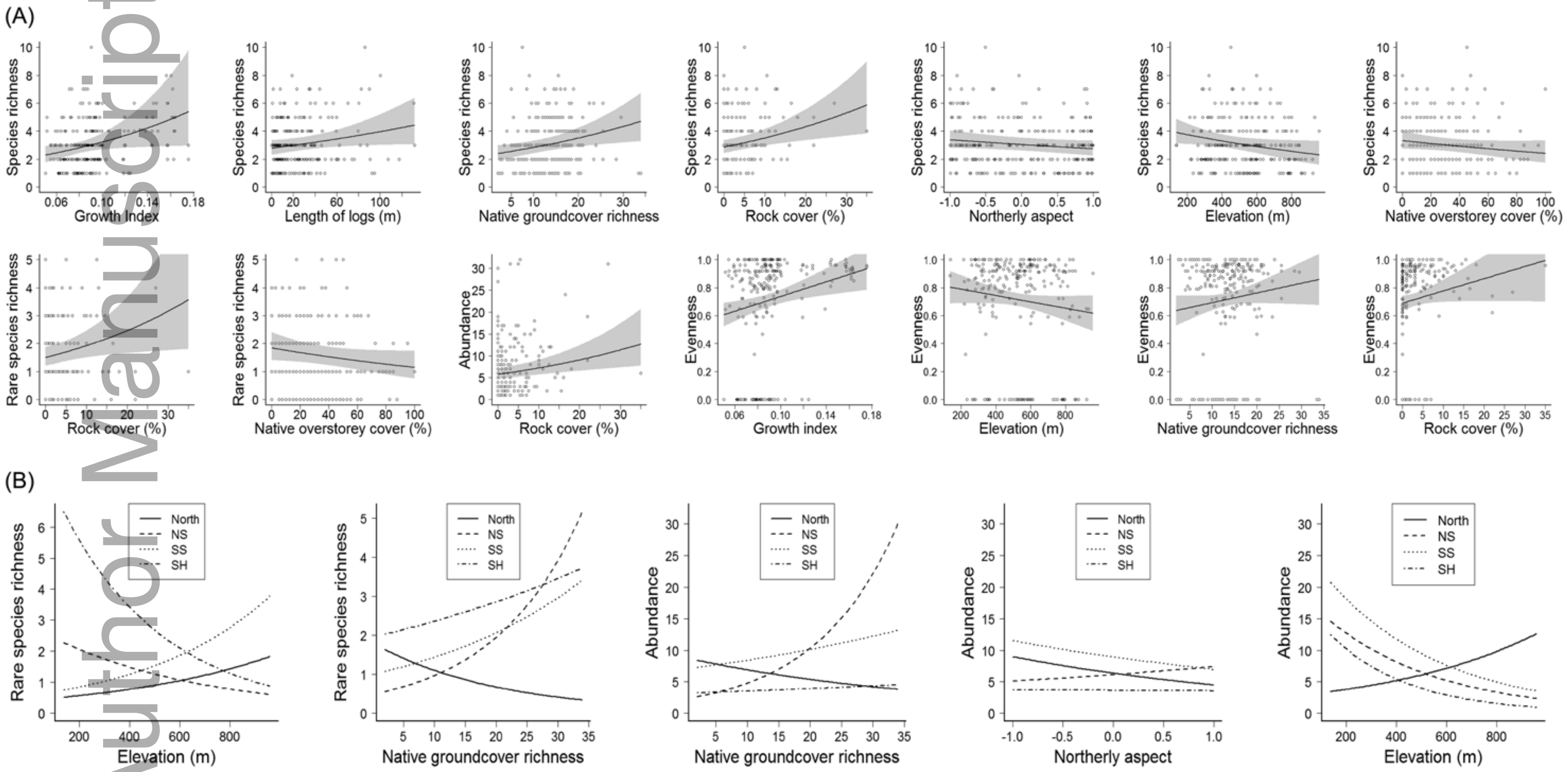
(A)
Species richness
Growth Index
Length of logs (m)
Native groundcover richness
Rock cover (%)
Northerly aspect
Elevation (m)
Native overstorey cover (%)
Rare species richness
Rock cover (%)
Native overstorey cover (%)
Abundance
Rock cover (%)
Evenness
Growth index
Elevation (m)
Native groundcover richness
Rock cover (%)
(B)
Rare species richness
Elevation (m)
Rare species richness
Native groundcover richness
Abundance
Native groundcover richness
Abundance
Northerly aspect
Abundance
Elevation (m)
North
NS
SS
SH

Fig. 2. Relationships of all linear predictors (plus confidence intervals) in the top-ranked models for (A) the different reptile assemblage measures within the whole study area, and (B) important interactions with the four study regions: Northern (North), Northern Slopes (NS), Southern Slopes (SS) and Southern Highlands (SH) regions

SUPPORTING INFORMATION

Appendix S1. Calculation of Growth Index variable

The Growth Index is calculated within the GROCLIM package of ANUCLIM (Xu & Hutchinson, 2013). The Growth Index is a measure that summarises several broad environmental and climatic variables into one biologically-meaningful productivity-related metric. Designed initially as a generalized growth model for vegetation response to light, thermal and water regimes, growth index calculates weekly indices of light, temperature, moisture availability and applies them to models of plant growth based on input climate surfaces for Australia. The output is a comprehensive set of raster layers, which can be built under current, or projected future climates.

For ecological examinations, the use of the growth index metric presents significant advantages over other environmental and climatic measures available including latitude, longitude, temperature and rainfall and hence was used in this study. First, although geographically descriptive, the use of latitude/longitude has limited ecological and biological meaning. Latitude/longitude is often used to reflect gradients in temperature, aridity and ecosystem change however in our study these gradients were better represented using the combined model of growth index. Second, combining environmental and climatic measures into one productivity-based model of growth index allowed us to combine the likely influences of several variables into one variable suitable for modelling. Third, the measures of growth index (daylight, temperature, and moisture) are relevant to reptiles as thermoregulatory ectotherms sensitive to basking opportunity, thermal conditions and moisture-limiting attributes like vegetation cover and prey availability.

Table S1. Description of each region including the broad agro-climate (from Hutchinson *et al.*, 2005), topographic and dominant land use features (from OEH, 2014).

Region	Agro-climate	Annual Temp. (^{o}C)	Annual rainfall (mm)	Mean elevation (m a.s.l)	General Topography	Dominant Land Use
Northern Region	Most plant growth in summer, although summers are moisture limiting. Temperature limits plant growth in winter	10-19	449-1015	540	Inland Slopes	Summer crops; native pasture grazing

Northern Slopes	Most plant growth in summer, although summers are moisture limiting. Temperature limits plant growth in winter	10-16	500 – 1150	431	Tablelands / Plains	Winter cereals and summer crops; native pasture grazing
Southern Slopes	Moisture availability high in winter-spring, moderate in summer, most plant growth in spring	9-15	500 – 1150	427	Inland Slopes	Spring crops; improved and native pastures
Southern Highlands	Moisture availability high in winter-spring, moderate in summer, most plant growth in spring	6-16	460-1883	733	Elevated Ranges	Horticulture; improved and native pasture grazing

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Table S2. List of all reptile individuals surveyed for each species, summed for the entire study area (Study) and each study region: Northern (North), Northern Slopes (NS), Southern Slopes (SS), Southern Highlands (SH).

Family	Scientific name	Totals				
		Study	North	NS	SH	SS
Agamidae	*Amphibolurus burnsi*	1	1	0	0	0
	Amphibolurus muricatus	6	1	0	5	0
	Diporiphora nobbi	1	1	0	0	0
	Intellagama lesueurii	1	1	0	0	0
	Pogona barbata	18	3	2	8	5
Carphodactylidae	*Underwoodisaurus milii*	11	0	0	0	11
Cheluidae	*Chelodina longicollis*	2	0	0	2	0

Diplodactylidae	*Amalosia rhombifer*	1	1	0	0	0
	Lucasium steindachneri	1	1	0	0	0
	Nebulifera robusta	3	3	0	0	0
	Oedura tryoni	1	1	0	0	0
	Strophurus intermedius	2	0	2	0	0
Elapidae	*Cryptophis nigrescens*	2	2	0	0	0
	Demansia psammophis	3	2	1	0	0
	Furina diadema	1	1	0	0	0
	Notechis scutatus	1	0	0	1	0
	Parasuta dwyeri	27	5	6	7	9
	Pseudechis porphyriacus	2	0	0	1	1
	Pseudonaja textilis	17	1	6	1	9
Gekkonidae	*Christinus marmoratus*	46	0	13	9	24
	Diplodactylus vittatus	37	2	6	8	21
	Gehyra dubia	1	0	1	0	0
	Gehyra variegata	7	0	2	4	1
	Heteronotia binoei	7	7	0	0	0
Pygopodidae	*Aprasia parapulchella*	32	0	9	14	9
	Delma inornata	14	2	2	2	8
	Delma plebeia	9	7	2	0	0
	Delma tincta	2	2	0	0	0
Scincidae	*Acritoscincus platynotum*	6	0	0	6	0
	Anomalopus leuckartii	15	10	5	0	0
	Carlia pectoralis	1	1	0	0	0
	Carlia sp	10	10	0	0	0
	Carlia tetradactyla	88	12	11	10	55
	Carlia vivax	3	3	0	0	0
	Cryptoblepharus pannosus	67	2	16	0	49
	Cryptoblepharus pulcher	34	34	0	0	0
	Cryptoblepharus sp	92	14	48	0	30
	Ctenotus spaldingi	163	36	41	10	76
	Ctenotus taeniolatus	39	0	2	15	22
	Egernia cunninghami	27	1	7	9	10
	Egernia striolata	49	14	7	0	28
	Eulamprus quoyii	1	1	0	0	0
	Hemiergis talbingoensis	134	28	0	87	19
	Lampropholis delicata	123	8	10	74	31
	Lampropholis guichenoti	22	8	0	13	1
	Lerista bougainvillii	5	0	1	1	3
	Lerista timida	13	6	7	0	0
	Lygisaurus foliorum	9	8	1	0	0
	Menetia greyii	12	7	0	4	1
	Morethia boulengeri	438	34	61	78	265
	Saiphos equalis	1	1	0	0	0

	Tiliqua rugosa ssp aspera	10	0	0	3	7
	Tiliqua scincoides ssp scincoides	13	4	1	6	2
Typhlopidae	*Ramphotyphlops nigrescens*	2	1	1	0	0
	Ramphotyphlops sp	1	1	0	0	0
	Ramphotyphlops wiedii	5	5	0	0	0
Varanidae	*Varanus varius*	2	0	1	0	1

Table S3. Observed species richness, estimated richness and the percentage of observed to the estimated species richness (pcnt value) for the whole study area and each of the four study regions.

	Observed richness	Estimated richness	Pcnt value
Whole study area	57	72	79.7%
Northern	43	59	72.4%
Northern Slopes	28	34	82.9%
Southern Slopes	26	30	87.5%
Southern Highlands	25	27	92.9%

Table S4. The best-ranked generalised linear mixed models (GLMMs) investigating the role of eight predictor variables (growth index [Gr_id], northerly aspect [Asp_N], elevation [Elev], richness of native groundcover [NGR], length of log cover [LgL], rock cover [Rock], bare ground cover [BG] and native overstorey cover [NOS]) plus interaction with region (Reg) as predictors of four measures of reptile community assembly (total richness, rare species richness, abundance, evenness) for the whole study area. Outputs from both the (i) unstandardized and (ii) standardized variables are given. Selected models are indicated by bold text.

(i) Unstandardized

Response	**Included variables**																**Model rank**		
	(Int)	**Asp_N**	**Reg**	**BG**	**Elev**	**Gr_id**	**LgL**	**NGR**	**NOS**	**Rock**	**Reg* Elev**	**Reg* Asp_N**	**Reg* NGR**	**Reg* LgL**	**df**	**logLik**	**AICc**	**delta**	**weight**
Species	1.09	-0.06			-0.07	0.10	0.10	0.11	-0.08	0.10					9	-419.47	857.7	0.00	0.108
Richness	1.09	-0.07				0.12	0.09	0.08	-0.07	0.10					8	-420.70	858	0.30	0.093
	1.09	-0.06				0.12	0.06	0.07		0.11					7	-421.84	858.2	0.45	0.087
	1.09				-0.07	0.11	0.11	0.11	-0.07	0.10					8	-420.80	858.2	0.50	0.084
	1.09	-0.06			-0.06	0.12	0.06	0.09		0.11					8	-420.90	858.4	0.71	0.076
	1.09				-0.06	0.12	0.07	0.09		0.11					7	-422.03	858.6	0.83	0.072
	1.09	-0.08				0.14		0.07		0.11					6	-423.16	858.7	0.95	0.067
	1.09					0.13	0.07	0.07		0.11					6	-423.21	858.8	1.05	0.064
	1.09					0.12	0.10	0.08	-0.06	0.10					7	-422.28	859.1	1.33	0.056
	1.09	-0.07			-0.06	0.13		0.09		0.11					7	-422.29	859.1	1.35	0.055
	0.92	**-0.07**	**+**		**-0.12**	**0.19**	**0.09**	**0.12**	**-0.07**	**0.10**					**12**	**-416.85**	**859.1**	**1.37**	**0.055**
	0.92	-0.08	+		-0.11	0.21		0.10		0.11					10	-419.08	859.1	1.41	0.053
	0.94	-0.07	+		-0.11	0.19	0.05	0.10		0.11					11	-418.07	859.3	1.60	0.049
	1.09	-0.06				0.13	0.06			0.12					6	-423.62	859.6	1.87	0.042
	0.90	-0.23	+		-0.10	0.21		0.10		0.12		+			13	-416.087	859.8	2.1	0.038
Rare	-0.18		+		0.17			0.17	-0.09	0.11	+				12	-333.21	691.8	0.00	0.149
Species	-0.15		+		0.16			0.15		0.12	+				11	-334.44	692.1	0.24	0.132
Richness	-0.20		+		0.16		0.07	0.17	-0.13	0.10	+				13	-332.75	693.2	1.32	0.077
	-0.18	-0.05	+		0.18			0.17	-0.10	0.11	+				13	-332.87	693.4	1.55	0.069

	-0.06		**+**		**0.28**			**-0.27**	**-0.11**	**0.12**	**+**		**+**		**15**	**-330.61**	**693.4**	**1.59**	**0.067**
	-0.39		+		0.19	0.11		0.16	-0.10	0.11	+				13	-332.97	693.6	1.76	0.062
	-0.15		+		0.18			0.18	-0.11		+				11	-335.21	693.6	1.78	0.061
	-0.21		+	0.04	0.19			0.17	-0.09	0.11	+				13	-333.08	693.8	1.97	0.056
	-0.19		+	0.05	0.19			0.15		0.12	+				12	-334.21	693.8	1.99	0.055
	-0.33		+		0.18	0.09		0.14		0.12	+				12	-334.279	694	2.13	0.051

Response	**Included variables**														**Model rank**				
											Reg*	**Reg***	**Reg***	**Reg***					
	(Int)	**Asp_N**	**Reg**	**BG**	**Elv**	**Gr_id**	**LgL**	**NGR**	**NOS**	**rck**	**Elev**	**Asp_N**	**NGR**	**LgL**	**df**	**logLik**	**AICc**	**delta**	**weight**
Abundance	**1.85**	**-0.24**	**+**		**0.29**			**-0.14**		**0.11**	**+**	**+**	**+**		**18**	**-680.94**	**1401.1**	**0.00**	**0.223**
	1.47	-0.23	+		0.31	0.19		-0.13		0.11	+	+	+		19	-679.95	1401.5	0.39	0.183
	1.85	-0.23	+		0.29			-0.13	-0.02	0.11	+	+	+		19	-680.849	1403.2	2.19	0.075
Evenness	0.72					0.08				0.05					5	-78.55	167.4	0.00	0.138
	0.72				**-0.04**	**0.07**		**0.04**		**0.04**					**7**	**-76.69**	**167.9**	**0.52**	**0.107**
	0.72				-0.03	0.08				0.05					6	-77.93	168.2	0.86	0.09
	0.72					0.08		0.02		0.04					6	-78.01	168.4	1.01	0.083
	0.72					0.08	0.02			0.05					6	-78.12	168.6	1.24	0.074
	0.72	-0.02				0.08				0.05					6	-78.23	168.8	1.47	0.066
	0.72				-0.04	0.08		0.04							6	-78.44	169.2	1.87	0.054
	0.72				-0.04	0.07	0.02	0.04		0.04					8	-76.31	169.3	1.88	0.054
	0.72			0.01		0.08				0.05					6	-78.47	169.3	1.94	0.052
	0.72					0.08			0.01	0.05					6	-78.47	169.3	1.95	0.052
	0.72					0.09									4	-80.58	169.3	1.97	0.051
	0.72				-0.03	0.07	0.02			0.05					7	-77.518	169.5	2.16	0.047

(ii) Standardized

Response	**Included variables**														**Model rank**				
	(Int)	**Asp_N**	**Reg**	**BG**	**Elv**	**Gr_id**	**LgL**	**NGR**	**NOS**	**rck**	**Reg***	**Reg***	**Reg***	**Reg***	**df**	**logLik**	**AICc**	**delta**	**weight**

											Elev	Asp_N	NGR	LgL					
Species	**1.38**	**-0.07**	**+**		**-0.08**	**0.08**	**0.09**	**0.11**	**-0.07**	**0.10**					**12**	**-416.85**	**859.1**	**0.00**	**0.092**
Richness	1.39	-0.08	+		-0.07	0.09		0.10		0.11					10	-419.08	859.1	0.04	0.09
	1.38	-0.07	+		-0.08	0.08	0.05	0.10		0.11					11	-418.07	859.3	0.23	0.082
	1.37	-0.23	+		-0.07	0.09		0.09		0.12		+			13	-416.09	859.8	0.73	0.064
	1.39		+		-0.08	0.08	0.07	0.09		0.11					10	-419.56	860.1	1.00	0.056
	1.38		+		-0.08	0.08	0.10	0.11	-0.07	0.10					11	-418.51	860.2	1.10	0.053
	1.37		+		-0.10	0.06	0.18	0.11		0.11				+	13	-416.39	860.4	1.34	0.047
	1.37		+		-0.11		0.20	0.11		0.11				+	12	-417.52	860.4	1.34	0.047
	1.39	-0.08	+			0.10		0.08		0.11					9	-420.84	860.5	1.38	0.046
	1.39	-0.08	+		0.02	0.09		0.09		0.11	+				13	-416.48	860.6	1.51	0.043
	1.37	-0.23	+			0.10		0.07		0.12		+			12	-417.62	860.6	1.55	0.042
	1.37		+		-0.11		0.23	0.13	-0.07	0.11				+	13	-416.53	860.7	1.61	0.041
	1.37	-0.24	+		0.04	0.09		0.09		0.12	+	+			16	-413.13	860.8	1.66	0.04
	1.36		+		-0.10	0.06	0.21	0.12	-0.06	0.10				+	14	-415.43	860.8	1.68	0.04
Response	**Included variables**														**Model rank**				
											Reg*	**Reg***	**Reg***	**Reg***					
	(Int)	**Asp_N**	**Reg**	**BG**	**Elv**	**Gr_id**	**LgL**	**NGR**	**NOS**	**rck**	**Elev**	**Asp_N**	**NGR**	**LgL**	**df**	**logLik**	**AICc**	**delta**	**weight**
	1.36	-0.06	+		-0.10	0.06	0.19	0.12	-0.07	0.11				+	15	-414.33	860.9	1.77	0.038
	1.36	-0.05	+		-0.10	0.06	0.16	0.11		0.11				+	14	-415.49	860.9	1.80	0.037
	1.39	-0.08	+		-0.07	0.09		0.10	-0.03	0.10					11	-418.87	860.9	1.83	0.037
	1.38	-0.08	+		0.01	0.08	0.08	0.11	-0.08	0.10	+				15	-414.38	861	1.86	0.036
	1.38	-0.07	+			0.09	0.08	0.09	-0.07	0.10					11	-418.92	861	1.92	0.035
	1.36	-0.05	+		-0.11		0.22	0.13	-0.07	0.11				+	14	-415.63	861.2	2.07	0.033
Rare	-0.07		+		0.12			0.16	-0.09	0.11		+			12	-333.21	691.8	0.00	0.149
Species	-0.07		+		0.11			0.14		0.12		+			11	-334.44	692.1	0.24	0.132
	-0.07		+		0.11		0.06	0.16	-0.13	0.10		+			13	-332.75	693.2	1.32	0.077
	-0.07	-0.05	+		0.13			0.16	-0.10	0.11		+			13	-332.87	693.4	1.55	0.069
	-0.07		**+**		**0.19**			**-0.26**	**-0.11**	**0.12**		**+**	**+**		**15**	**-330.61**	**693.4**	**1.59**	**0.067**
	-0.07		+		0.13	0.05		0.16	-0.10	0.11		+			13	-332.97	693.6	1.76	0.062

	-0.06		+		0.12			0.17	-0.11			+		11	-335.21	693.6	1.78	0.061
	-0.07		+	0.03	0.13			0.16	-0.09	0.11		+		13	-333.08	693.8	1.97	0.056
	-0.07		+	0.04	0.13			0.14		0.12		+		12	-334.21	693.8	1.99	0.055
	-0.07		+		0.12	0.04		0.14		0.12		+		12	-334.28	694	2.13	0.051
Abundance	**1.87**	**-0.23**	**+**		**0.20**			**-0.13**		**0.11**	**+**	**+**	**+**	**18**	**-680.94**	**1401.1**	**0.00**	**0.223**
	1.87	-0.23	+		0.22	0.08		-0.13		0.11	+	+	+	19	-679.95	1401.5	0.40	0.183
	1.87	-0.23	+		0.21			-0.13	-0.02	0.11	+	+	+	19	-680.85	1403.2	2.19	0.075
Evenness	**0.86**		**+**		**-0.04**	**0.05**		**0.03**		**0.04**				**10**	**-75.50**	**172**	**0.00**	**0.119**
	0.86		+		-0.04	0.06				0.05				9	-76.61	172	0.03	0.118
	0.86		+			0.06				0.05				8	-77.82	172.3	0.28	0.104
	0.86		+		-0.04	0.05	0.03			0.05				10	-75.95	172.9	0.90	0.076
	0.86		+		-0.05	0.05	0.02	0.03		0.05				11	-74.94	173.1	1.08	0.07
	0.86		+			0.06		0.02		0.04				9	-77.25	173.3	1.30	0.062
	0.86	-0.02	+		-0.04	0.05		0.03		0.04				11	-75.09	173.4	1.39	0.06
	0.86	-0.02	+		-0.04	0.06				0.05				10	-76.21	173.4	1.41	0.059
	0.86		+			0.05	0.02			0.05				9	-77.32	173.4	1.45	0.058
	0.86		+		-0.04	0.06		0.04						9	-77.37	173.5	1.55	0.055
	0.86	-0.02	+			0.06				0.05				9	-77.45	173.7	1.71	0.051
	0.86		+		-0.04	0.06			0.01	0.05				10	-76.51	174	2.01	0.044

Fig. S1: Example of a site from our study area showing the open woodland structure that is typical of the box-gum grassy woodland ecological community.

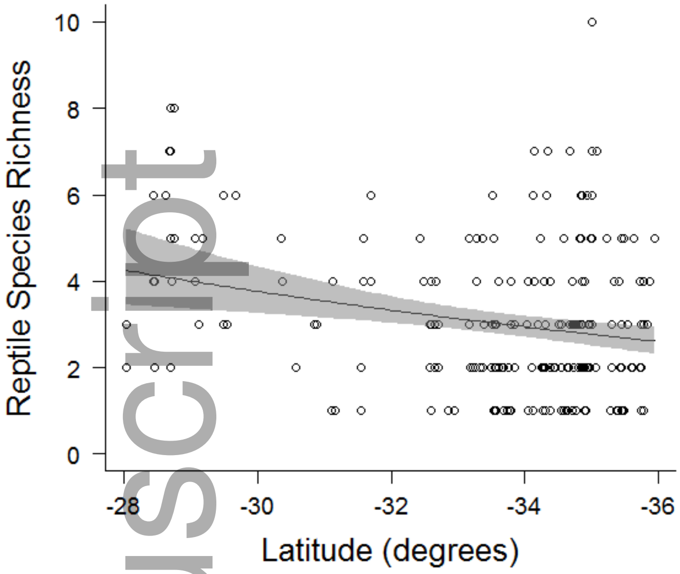

Fig. S2. Relationship between reptile species richness and latitude (degrees) gradient evident across the whole study, indicating confidence interval (shaded) and raw data (points)

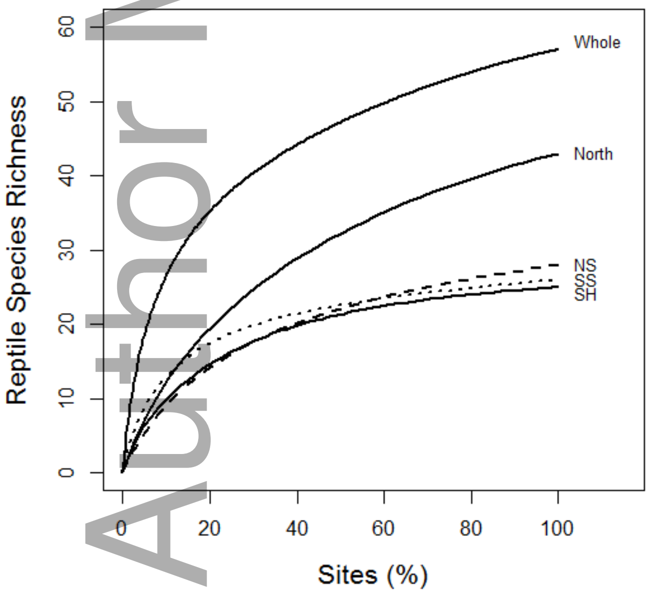

Fig. S3. Species accumulation curves for the observed species richness for the whole study and the four study regions.