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Citation for final published version:

Jins, V. J., Panigrahi, Madhumita, Jayapal, Rajah and Bishop, Tom R. 2021. Elevational gradients of reptile richness in the southern Western Ghats of India: Evaluating spatial and bioclimatic drivers. Biotropica 53 (1) , pp. 317-328. 10.1111/btp.12878

Publishers page: https://doi.org/10.1111/btp.12878

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1	Elevational gradients of reptile richness in the southern Western Ghats of India:
2	evaluating spatial and bioclimatic drivers
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ABSTRACT

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Exploring elevational patterns in species richness and their underlying mechanisms is a major goal in biogeography and community ecology. Reptiles can be powerful model organisms to examine biogeographical patterns. In this study, we examine the elevational patterns of reptile species richness and test a series of hypotheses that may explain them. We sampled reptile communities along a tropical elevation gradient (100-1500 m a.s.l.) in the Western Ghats of India using time constrained visual encounter surveys at each 100m elevation zone for a period of three years. First, we investigated species richness patterns across elevation and the support of mid-domain effect and Rapport's rule. Second, we tested whether a series of bioclimatic (temperature and tree density) and spatial (middomain effect and area) hypotheses explained species richness. We used linear regression and AICc to compare competing models for all reptiles and each of the subgroups: snakes, lizards and Western Ghats' endemics. Overall reptile richness and lizard richness both displayed linear declines with elevation which was best explained by temperature. Snake richness and endemic species richness did not systematically vary across elevation, and none of the potential hypotheses explained variation in them. This is the first standardized sampling of reptiles along an elevational gradient in the Western Ghats, and our results agree with the global view that temperature is the primary driver of ectotherm species richness. By establishing strong reptile diversity-temperature associations across elevation, our study also has implications for the impact of future climate change on range-restricted species in the Western Ghats.

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Data availability statement: Data used in this study will be archived in Dryad, as per the Biotropica policy. Code for analyses will be supplied with datasets.

- 51 **Keywords:** Herpetofauna, altitude, mid-domain effect, Rapoport's rule, range size,
- 52 distribution patterns, Agasthyamalai Biosphere Reserve, tropical mountain

1 INTRODUCTION

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55 Why are there different numbers of species in different places? The answer to this question is a major goal in ecology and biogeography (Pianka, 1966; MacArthur, 1972; 56 57 Brown, 2014). Exploring this question provides us with a greater understanding of how 58 the natural world is organized, but is also a critical activity in a range of conservation 59 planning contexts (Ricketts et al., 1999; Pimm & Brown, 2004). This aim is increasingly 60 important as we enter the Anthropocene and species must either move or evolve if they 61 are to survive (Pecl et al., 2017). Numerous studies across the globe are describing patterns of species diversity and testing them against mechanistic hypotheses (Hudson et 62 63 al., 2014; Peters et al., 2016). Despite this effort, however, our understanding of species 64 diversity patterns is taxonomically and geographically biased – focusing on patterns of 65 bird and mammal diversity in Europe and the Americas (Hudson et al., 2014). To address 66 this, we explore the variation in species richness of reptiles along an elevational gradient 67 in one of the world's "hottest biodiversity hotspots": The Western Ghats (Nair, 1991; 68 Myers et al., 2000). 69 Mountain regions contain disproportionate numbers of species relative to their geographic 70 area (Rahbek et al., 2019a), and many of the global biodiversity hotspots exist within 71 them (Kozak & Wiens, 2010; Guo et al., 2013). In terms of understanding general 72 mechanisms underlying variation in species diversity, elevational gradients have long 73 been recognized as useful "microcosms" of broader latitudinal patterns in species richness 74 (Stevens, 1992). Latitudinal gradients themselves are challenging to study due to their 75 large spatial extent, but in the case of elevation gradients, individual mountain ranges can 76 act as replicated transects. This provides opportunities to test the underlying causes of 77 species diversity patterns (Sanders & Rahbek, 2012). Finally, while elevational gradients

78 have a wide diversity of topographies and climates (Rahbek et al., 2019b), a key feature 79 of them is the existence of a strong thermal gradient. Temperature, a factor known to 80 influence the distribution and functioning of life across organizational scales (Brown, 81 2014), universally declines with increasing elevation. Temperature is particularly 82 important for reptiles; as ectotherms, they rely on ambient temperature to regulate their 83 body heat and allow them to function (Angilletta, 2009). 84 Elevational patterns in species richness tend to take one of three main forms: (1) a 85 monotonic increase, (2) a monotonic decline and (3) a mid-elevation peak (Rahbek, 86 1995). The prevalence of these patterns can vary across different taxonomic groups and 87 biogeographical regions (Peters et al., 2016), although the hump-shaped, mid-elevational 88 peak is reported to be the most common relationship (Rahbek, 2005). There are several 89 hypotheses which may explain these different richness-elevation patterns, and these can 90 be broadly grouped into two main categories: bioclimatic or spatial hypotheses (Grytnes 91 & McCain, 2007). 92 Variation in biologically important variables such as temperature, rainfall or productivity 93 represent climatic hypotheses. In these cases, it is hypothesized that the covariation of 94 these factors along elevational gradients is the cause for various richness-elevation 95 patterns. Compared to endotherms, ectotherm metabolism is highly dependent on ambient 96 temperature (Angilletta, 2009). In consequence, declines in ectotherm richness along 97 elevational gradients have been repeatedly linked to concurrent declines in temperature 98 across space and time (Bishop et al., 2014; Peters et al., 2016), and these patterns can 99 further be explained by the availability of water (Szewczyk & McCain, 2016). 100 The second category of hypotheses seeking to explain elevational gradients in species 101 richness are spatial. A common explanation for richness-elevation patterns is the

influence of available area (Lomolino, 2001). This hypothesis is analogous to the wellknown species-area relationship which suggests that more individuals will exist in elevational zones that have more available area, which in turn are more likely to come from a larger species pool (Sanders, 2002; Romdal & Grytnes, 2007). The mid-domain effect (MDE) is another popular spatial hypothesis describing species richness patterns. The MDE predicts mid-elevational peaks in richness, purely as a result of the geometry of a bounded domain, such as that between a mountain top and the coast (Colwell & Hurtt, 1994; Colwell & Lees, 2000; Jetz & Rahbek, 2001). Through the random placement of varying species ranges, there is a high probability of greater range overlap, and therefore higher species richness, at the centre of the bounded domain (Colwell & Lees, 2000). Although MDE predictions are purely based on geometric constraints on range sizes, recent analyses have modelled this effect in conjunction with bioclimatic variables (Colwell et al., 2016). There is mixed empirical support for the influence of MDE on elevation-richness patterns (Hawkins & Diniz-Filho, 2002; Currie & Kerr, 2008; McCain, 2009). Rapoport's rule on elevational range sizes can also be seen as a "spatial" hypothesis (Stevens, 1992), although it derives from some degree of climatic control (Kendall & Haedrich, 2006). Rapoport's rule hypothesizes that species at higher elevations have larger range sizes than those at lower elevations. This is due to the broader climatic tolerances required to survive in variable high elevation conditions. There is an underlying assumption that most species have relatively small ranges and cannot tolerate a broad range of climatic conditions. Consequently, ranges accumulate in the climactically stable lowlands to generate a monotonic decline in species richness with increasing elevation (Stevens, 1992; Rahbek, 1997). Like the MDE, support for

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126 Rapoport's rule as general phenomenon is mixed (Gaston & Chown, 1999; Sanders, 127 2002; McCain & Knight, 2013). 128 In this study, we are interested in describing and understanding the elevational diversity 129 patterns of reptiles in the Western Ghats of India. Overall, richness-elevation patterns of 130 herpetofauna (reptiles and amphibians) tend to show monotonic declines (Heatwole, 131 1982; Cadle & Patton, 1988; Woinarski & Gambold, 1992; Hofer et al., 1999, 2000; 132 Nathan & Werner, 1999; Chettri et al., 2010). This taxonomic group is largely 133 understudied within India especially on elevational diversity patterns (but see 134 Naniwadekar & Vasudevan, 2007; Chettri et al., 2010). This demands an immediate 135 attention because the Indian subcontinent, and the Western Ghats in particular, is a global 136 hotspot of biodiversity. The unique bioclimatic conditions, topographic features and 137 habitat heterogeneity makes the Western Ghats particularly rich in biodiversity and high 138 in species endemism (Nair, 1991; Myers et al., 2000). In fact, 47.13% of the reptiles that 139 occur here are endemic to the Western Ghats (Srinivasulu et al., 2014). Recent studies 140 have also indicated that each mountain range in the Western Ghats possibly has many 141 local endemics and basal lineages – especially in case of reptiles (Cyriac et al., 2018; Pal 142 et al., 2018; Chaitanya et al., 2019; Mallik et al., 2019; Deepak et al., 2020). 143 Consequently, there is a need to better document and explain patterns of species richness 144 in this region. 145 In this context, we ask the following questions: (1) how is reptile species richness distributed across elevation in the southern Western Ghats? (2) What bioclimatic and 146 147 spatial hypotheses explain these patterns? We use temperature and tree density as 148 measures of bioclimatic niche variables of relevance to reptiles. We predict that both will 149 relate positively to reptile species richness in this region: reptile metabolism is tightly

linked to ambient temperature, and we hypothesize that higher tree densities will provide a greater number of niches that different reptile species can exploit. Tree density is often used as a surrogate of habitat heterogeneity and habitat complexity (McCoy & Bell, 1991) and has been repeatedly shown to alter reptile community structure (Hever and Berven, 1973, Scott, 1976, Voris, 1977, Gillespie et al., 2015). In our case, we hypothesize that more reptiles will be present in areas of higher tree densities. We test each hypothesis separately for the two main subgroups of reptile: snakes and lizards. This is typically done in studies of reptile diversity (Fu et al., 2007, Kryštufek et al., 2008, Chettri et al., 2010) because of their different morphology and life-history strategies (Shine & Charnov, 1992). Snakes tend to occupy higher trophic positions compared to lizards, and being limbless they move through the environment very differently s (Gove, 1979, Parker & Plummer, 1987, Da Silva et al., 2018). Furthermore, snakes tend to have larger range sizes compared to lizards, which may be an indication of their higher dispersal abilities (Böhm et al., 2013). In general, large-ranged and smallranged species tend to show different responses to the mid-domain effect (Dunn et al., 2006, Dunn et al., 2007), with small-ranged taxa less likely to conform to the predictions of the MDE. In this context, we predict that the differences in life-history strategies and range sizes between snakes and lizards will result in different elevation-richness patterns, specifically that snakes, with their larger ranges, will be more likely to conform to a mid-elevational peak. We also predict that endemic species will show a mid-elevational peak or a monotonic increase in richness with elevation. Previous studies on herpetofauna have found mid-elevational peaks in endemic richness (Fu et al., 2006), while globally, increases in endemism with elevation may be explained by the greater topographic

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174	isolation of these areas which promotes speciation and endemicity (Steinbauer et al.,
175	2016). Finally, given previous work on reptiles which found limited global support for a
176	series of spatial hypotheses (McCain, 2010), we expect to find more support for climatic
177	hypotheses at this local scale in the Western Ghats. Simultaneous tests of these
178	hypotheses have not yet been undertaken for reptiles in the biodiversity hotspot of the
179	Western Ghats. Here, we provide a test.

2 METHODS

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182 2.1 Study area Our study was located within the Agasthyamalai Hills (8.4° to 8.8° N and 77.0° to 77.4° E) 183 184 which is part of the Agasthyamalai Biosphere Reserve (ABR) on the southern tip of the 185 Western Ghats. We covered only the western slope (windward side) of the Agasthyamalai 186 Hills which comprised of two major protected areas: Neyyar and Peppara wildlife 187 sanctuaries in the Kerala State (Figure 1). The mean temperature of the coldest month in 188 the region ranges from 13 °C to 23°C (Pascal, 1982). The windward side of the 189 Agasthyamalai Hills receives high rainfall: varying between 2000-5000 mm annually 190 with only two to three dry months (Ramesh et al., 1997; Varghese & Balasubramanyan, 191 1998). 192 The Agasthyamalai region is well-known for its high plant diversity and endemism 193 (Nayar, 1996; Ramesh et al., 1997; Manju et al., 2009). The vegetation of the area 194 changes significantly along elevation. Champion & Seth (1968) identified four major 195 vegetation types in the area: southern moist mixed deciduous forest (<400 m a.s.l.), west 196 coast semi-evergreen (400-600 m a.s.l.), west coast tropical evergreen (600-1200 m a.s.l.) 197 and southern hilltop tropical evergreen (>1200 m a.s.l.). The deciduous or evergreen 198 forests up to 1200m a.s.l. are comprised of taller trees with canopy height ranging from 199 10-35 m however, the hill top forest is of a dense, stunted evergreen type with canopy 200 height reaching a maximum up to 10 m, mixed with open rocky and grass areas 201 (Varghese & Balasubramanyan, 1998). Apart from human settlements in the lower 202 elevations (<400 m a.s.l.), trekking and pilgrimage activities also exert significant 203 pressure on the natural habitats of the region (Ramesh et al., 1997). Although we

observed some level of habitat disturbance along the main trekking route, our sampling was mostly restricted to undisturbed patches along the elevational gradient.

The focal study area encompasses approximately 250 km², spread across an elevational range of 50 to 1868 m a.s.l.. The coast is 30 km from the site - this makes the landscape ideal for testing mid-domain effects as it has geometric constraints on both ends, the mountain summit at the top and the coastline at the bottom.

2.2 Data collection

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2.2.1 Reptile richness

We surveyed reptiles in the Agasthyamalai Hills from April 2012 through to December 2014 along an elevation gradient, covering both wet and dry seasons. The total elevational range was categorized into fourteen 100 m wide elevational bands, beginning at 100 m a.s.l. and rising to 1500 m a.s.l.. We did not sample at the coast due to the lack of adequate undisturbed habitat, and we did not sample higher than 1500 m a.s.l. due to logistical constraints. Transects of approximately 2000 m in length and 250-300 m in width were laid in each elevational band based on topography and accessibility. We performed time constrained visual encounter surveys (VES) to sample the reptile communities in each elevational band. The VES method surveys an area for a prescribed time, systematically searching for animals in all possible microhabitats covering different vertical strata (Campbell & Christman, 1982, Crump & Scott, 1994). This is an appropriate and well-understood method for both species inventorying and monitoring, and is suitable for examining landscape level patterns especially in mountains. The method is also known for having a higher detection rate of rare species (Crump & Scott, 1994) and has successfully been applied before in the Western Ghats (Bhupathy & Nixon, 2011) and Eastern Himalayas (Chettri et al., 2010)

We used the transects laid in each elevational band as an approximate spatial guide for our VES sampling. We gradually searched along each transect for reptiles using VES during daylight, from 0800 to 1800 hours, and the search included turning stones and fallen logs, moving leaf litter, scanning the vegetation and, searching on stems and barks of trees. In this sense, VES explores all possible microhabitats from the ground level to the tree branches of approximately 3 m above the ground. Even though active microhabitat search was not possible in higher vertical strata (above 3 m), simple visual scanning of vegetation and tree branches to a maximum height was carried out wherever possible. Repetition of sampling in the same spatial area was avoided as the VES method involves the alteration of microhabitats (turning stones and logs etc.). In our dataset, a single VES "sample" within an elevational band consisted of two person hours (1 hour \times 2 people searching = 2 person hours). We were unable to perform equal sampling effort across the elevations, however, due to the differences in spatial and temporal accessibility to some elevational zones (Table S1). We identified all reptiles to species level where possible and assigned a distinct morphospecies identifier where full identification was not possible.

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2.2.2 Tree density

We laid 10×10 m quadrats along each elevational transect, each quadrat separated by 250 m. This gave 8 quadrats on most transects, although space constraints restricted us from laying 8 quadrats at all elevations. All elevations had at least four quadrats. We counted the number of trees in each quadrat to estimate tree density per hectare.

251	2.2.3 Elevation and available area
252	Elevation for each VES was determined during the sampling using an altimeter and GPS.
253	We extracted ASTER global digital elevation model-Version 3 (source:
254	https://earthdata.nasa.gov/, downloaded on 10 January 2020) and calculated the available
255	area of each 100 m elevational band using QGIS Version 3.10. Only the western slope of
256	the Agasthyamalai Hills was considered for this area calculation as it comprises the entire
257	area of the study.
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259	2.2.4 Environmental variables
260	We downloaded bioclimatic variables for the study area from the Chelsa` climatic
261	database (http://www.chelsa-climate.org/) which is a fine-scale (i.e. 1×1 km), long-term
262	(1979 to 2013) climate dataset with global coverage based on statistical downscaling
263	(Karger et al., 2017). Due to its high resolution, the Chelsa dataset is reported to be more
264	effective for modelling species distributions in geographically complex regions such as
265	mountainous landscapes (Maria & Udo, 2017). Out of the available 19 bioclimatic
266	variables, we retained only mean annual temperature (MAT) and mean annual
267	precipitation (MAP) for analysis as they are most ecologically important for the
268	distribution of reptiles. QGIS Version 3.10 was used for extracting the data from the
269	bioclimatic layer and we used the central point of each elevational transect to represent
270	the climate of each elevation.
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272	2.3 Data analysis

All analyses took place within the R environment (R Core Team, 2018).

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2.3.1 Species richness

We used rarefaction to generate standardized species richness estimates because sampling effort (hours of VES) varied across the elevational bands. We used the *iNEXT* package in R (Hsieh et al., 2016) to do this. Specifically, we used the function *estimateD* in "incidence_freq" mode (because our raw data are incidences of species in variable numbers of samples from each elevation). We used *estimateD* to estimate species richness for each elevation at the median sampling effort (38 two-person hours). This involved extrapolating richness estimates for elevations that were not sampled for 38 two-person hours, and interpolating samples that were sampled for more than 38 two-person hours. We employed this procedure using four different data subsets: reptiles (all species), snakes, lizards and endemics (of the Western Ghats). We use these estimated species richness values in all the analyses that follow. We assigned status of endemism of each species based on recent assessment of reptiles of the Western Ghats (Srinivasulu et al., 2014). We provide sample completeness estimates from *iNEXT* in Table S1.

2.3.2 Describing elevational patterns

We used linear regressions with Gaussian errors to test whether the species richness of each taxonomic subset had a linear, curvilinear or no relationship with elevation. We used Gaussian errors because the sample size corrected species richness values were not integers. For the linear models, we used only elevation as a predictor variable. For the curvilinear models, we used elevation and elevation² as predictor variables. The null models included only an intercept. We compared models using bias corrected Akaike information criteria (AICc). We calculated the difference in AICc (Δ AICc) between the

three models, relative to the one with the lowest AICc, and extracted R^2 adjusted for small sampled sizes. Where competing models are within 2 Δ AICc of each other, we opt to interpret and present the simplest model. We present the model with the lowest AICc along with its adjusted R^2 for each taxonomic subset. None of the models deviated from the model assumptions based on our interpretation of the model diagnostic and residual plots.

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2.3.3 Testing species richness drivers

We use an information-theoretic approach to assess the relative evidence for different hypothesized drivers of variation in reptile species richness (Burnham & Anderson, 2002) . We did not build a "global model" and analyse all possible sub-models. Rather, we split our explanatory variables into three classes representing separate, competing hypotheses, and ranked them using AICc. We did this because we do not consider models containing MDE along with other explanatory variables to be biologically meaningful – these hypotheses operate at completely different spatiotemporal scales to those concerning temperature or precipitation, for example. Our goal was to assess the relative weight of evidence in favour of a given hypothesis (represented by one or more actual statistical models). These classes were environmental, area, and mid-domain effects (MDE). Plots of their variation across elevation are presented in Figure S1. Environmental drivers: We used mean annual temperature (°C) and tree density (n/ha) to represent environmental drivers. We did not include precipitation because models containing precipitation as well as temperature and tree density, had variance inflation factors (VIF) above 2 (Fox & Monette, 1992). In total there were three environmental models: temperature, tree density and temperature + tree density. We hypothesised that

322 each variable may positively influence reptile species richness independently, or in 323 combination. 324 Area: We used available elevational area (as described above) to represent the species-325 area hypothesis. 326 Mid-domain effect: For MDE, we used the R package rangemodelR (Marathe, 2019) to 327 simulate artificial, random range distributions 1000 times. We took the average species 328 richness estimate across the repetitions as the prediction of the MDE hypothesis. This 329 package uses the approach of Wang & Fang (2012), itself an extension of the classic 330 MDE model of Colwell et al. (2004). This model shuffles range midpoints while 331 maintaining range sizes. Midpoints can be shuffled anywhere within the geometric 332 constraints of a bounded domain. We used this procedure separately for each taxonomic 333 subset. Species ranges were interpolated between the highest and lowest elevations we 334 observed them, species recorded at only a single elevation were given a range size of 0. 335 We modelled each class of drivers separately (1 model for each class, except for the 336 environmental class where there were three candidate models). We constructed linear 337 regressions with Gaussian errors to do this. We compared and ranked all models, including the null intercept only model, using AICc and calculated adjusted R² values. 338 339 We consider the "best" model to be the one with the lowest AICc, but also interpret 340 models within 2 \triangle AICc of the top ranked model. We also interpret our models 341 considering the size and direction of the effect sizes (by standardising all explanatory 342 variables prior to running the regressions (Schielzeth, 2010) and the proportion of 343 variance explained (R²). For example, models for the MDE hypotheses should have a 344 slope of ~1 if they are predicting similar richness-elevation patterns to our observed data. 345 We performed this modelling procedure four times, once for each of the taxonomic 346 subsets of all reptiles, snakes, lizards and endemic species. 347 Finally, we tested Rapoport's rule by correlating species range sizes with their range midpoints (Kwon et al., 2014). We interpolated species ranges, assuming them to be 348 349 present at all elevations between the highest and lowest observed sighting to generate 350 these data. We performed this test for each subset of reptiles: all, snakes, lizards and 351 endemics. 352 353 **RESULTS** 354 We sampled 47 species of reptiles across the elevational gradient, including 24 lizards, 22 355 snakes and one tortoise. Twenty-five of these species are endemic to the Western Ghats. 356 Our full dataset and R code are made available in the public data archiving platform, 357 Dryad. 358 359 2.4 **Elevational patterns** For reptiles and lizards, species richness declined linearly with increasing elevation 360 361 (Figure 2a, c; ΔAICc to next best model was 3.99 and 3.86, respectively). In each case, elevation explained a large fraction of the variation in species richness (reptiles adjusted 362 $R^2 = 0.74$, lizards adjusted $R^2 = 0.85$). Neither the linear or curvilinear models fitted well 363 364 to the patterns of snake and endemic species richness, suggesting that there was no clear 365 systematic variation of species richness with elevation in these groups (Figure 2b, d; 366 \triangle AICc to next best model was 2.46 and 1.56, respectively). Full model details can be

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found in Table S2.

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The best supported models explaining overall reptile species richness were those for temperature and temperature + tree density (Table 1). Both were positively related to reptile species richness (Figure 3ab). The inclusion of tree density however, did not explain any additional variance compared to the model containing only temperature: it's Δ AICc was greater than 2, and it's standardised slope was much smaller than that of temperature in the same model (Table 1). None of the tested hypotheses appear to drive snake species richness (Table 2). The best model was the one containing only an intercept, and none of the candidate models had high R² values (expanded version of Table 1 in the supplementary material, Table S3). For lizard species richness, temperature was the clear best model (Table 1). Lizard species richness was positively related to temperature (Figure 3c). The model containing temperature + tree density was ranked second but, again, the inclusion of this variable did not increase the R² and the AICc values clearly indicated that this model was poorer than the one containing only temperature (Table 1). Furthermore, the slope estimate for tree density was smaller than that for temperature and its confidence interval overlapped zero (Table 1). Endemic species richness was not modelled well by the candidate hypotheses. The best ranked model was the null model containing only an intercept (Table 1). The second ranked model, within a ΔAICc of 2, was for the mid-domain effect. The MDE model had the highest R^2 (0.14) of the candidates and was positively related to endemic species richness (Figure 3d). The unstandardized slope of this model, however, deviated from the expectation of a 1:1 relationship ($b = 0.27 \pm 0.33$, Figure 3d).

Finally, there was no evidence for a positive correlation between species elevational
ranges and elevational midpoints, as Rapoport's rule would predict. The Pearson's
correlation coefficient was -0.16, -0.12, -0.27 and -0.22 for all reptiles, snakes, lizards and
endemics, respectively. All correlations were insignificant ($p > 0.6$ in all cases).

3 DISCUSSION

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398 Our study is the first analysis of reptile diversity along an elevational gradient within the 399 Western Ghats. We find a linear decline of reptile richness with increasing elevation 400 (Figure 3a). This pattern is repeated in lizards (Figure 3c), who make up the largest 401 fraction of overall reptile diversity in this area, but not for snakes (Figure 3b) or for 402 endemic species (Figure 3d). We find no clear relationships between snake and endemic 403 species richness with elevation. Furthermore, our data do not support a range of spatial hypotheses concerning the underlying drivers of reptile species richness (i.e. low R²s and 404 405 high \triangle AICcs of these models, Table 1, Table S3). Instead, our data suggest that 406 temperature is the primary factor driving the diversity of reptiles in this area. 407 Our headline result is the monotonic decline in reptile and lizard species richness which 408 appears to be driven by temperature (Table 2). Fewer reptiles (and lizards) are found in 409 the colder, high elevations (Figure 3, Figure 4). These findings echo results from both the 410 global and the local scale. For example, McCain (2010) found that the most common 411 richness-elevation pattern in reptiles across the globe was a monotonic decline, and that 412 this was largely explained by temperature. Similar findings have been reported for 413 Himalayan reptiles (Chettri et al., 2010), the Costa Rican herpetofauna (Fauth et al., 414 1989), reptiles in the Dinaric Alps (Kryštufek et al., 2008) and a suite of other ectotherms 415 from around the globe (Bishop et al., 2014; Peters et al., 2016). Although negative 416 richness-temperature relationships are reported for many taxa, including endotherms such 417 as birds and bats (McCain, 2007, 2009), a monotonic decline pattern is most reported for 418 ectothermic taxa (McCain, 2010). Consequently, our results in the Western Ghats feed 419 into the general narrative that temperature is the primary driver of reptile species richness 420 gradients worldwide.

Despite this overall finding, however, we do not detect any systematic patterns in snake or endemic richness patterns (Figure 3b, d). For snakes, at least, this may be a consequence of our sampling. Compared to lizards, snakes are rare and can be difficult to observe during VES. This results from their cryptic behaviours, frequent use of inaccessible microhabitats (e.g., burrows, boulders and tree holes) and low rates of activity (Parker & Plummer, 1987, Durso et al., 2011). In our dataset, 40% of snake species were recorded at only a single site, whereas this was the case for only 12% of lizards. This high proportion of singleton observations suggests that this sampling difficulty may well be obscuring any systematic patterns in snake richness. Consequently, we suggest that further standardised and repeated sampling across the Western Ghats is needed to fully disentangle the issue of snake elevational-diversity patterns in the region. Note, even at a global-scale, data scarcity is a major issue in deriving broad scale diversity patterns in snakes and in assessing their conservation status or extinction risks (Böhm et al., 2013, Böhm et al., 2017). In terms of endemic species, this potential sampling issue is unlikely to explain our results. Of the species we sampled, 53% were endemic which closely matches the proportion of endemic reptiles in the Western Ghats which is 47% (Srinivasulu et al., 2014), and only 20% were found at a single site. Consequently, we are more confident that the patterns we describe for endemic species are reflecting reality – that the number of endemic species does not systematically vary across elevation. An interesting contrast with endemics can be seen in frogs from the Hengduan Mountains, China. In this case, endemics were not influenced by environmental factors, but did fit MDE predictions (Fu et al., 2006). While we do not find strong evidence that endemic species follow the MDE, our data agree with that of Fu et al., (2006) in that the diversity patterns of endemic species do not appear to be driven by bioclimatic variables.

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How representative are our results in the Agasthyamalai Hills of the Western Ghats as a whole? The Western Ghats largely consist of conical shaped mountains, as do the hills sampled here (Elsen & Tingley, 2015). Compared to the windward side we focused in the present study, the ranges towards the leeward side of the Ghats slightly differ in their habitat types and rainfall intensities (Nair & Daniel, 1986; Nair, 1991), but are unlikely to differ in their temperature-elevation patterns. Critically, the unique high elevation tropical montane cloud forest known as Shola, a natural matrix of forests and grasslands (found only above 1500m a.s.l) is scarce in the Agasthyamalai landscape compared to most of the northern hill ranges (e.g. Anaimalai Hills- 2695m a.s.l.). Sholas are known for the presence of some endemic reptiles (Deepak & Vasudevan, 2008), and this has been further proved by recent discoveries (Deepak et al., 2020). Consequently, studies exploring such high elevation habitats could alter the endemic-elevation pattern that we see here. Finally, a recent phylogeographic analysis of frogs highlighted that the Palghat Gap (a natural biogeographical barrier within the Western Ghats) could potentially be a barrier to dispersal and influence larger macroevolutionary patterns (Vijayakumar et al., 2016). Whether this biogeographical barrier also causes differences in the patterns and drivers of reptile richness, however, remains to be tested – we suspect that it is unlikely. In this study, we have not analyzed beta diversity across elevation because our sampling effort differed across the gradient. For alpha diversity (species richness) we could correct for this using known interpolation and extrapolation techniques (Hsieh et al., 2016). While similar corrections exist for beta diversity (Chao et al., 2005), this is beyond the scope of the current manuscript. Regardless, there is a clear opportunity and need for more comparative analyses of elevational patterns (including beta diversity) between different ranges within the Western Ghats. Regardless, considering the largely similar habitat types across the region and the repeated temperature-elevation gradients, we

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suggest that our alpha diversity analyses are likely to be representative of the entire

Western Ghats.

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In summary, we provide the first evidence of reptile species richness-elevation patterns in the Western Ghats, a global biodiversity hotspot. Despite the strong geometric constraints (mountain summit and coastline) present in the study range, the observed richness patterns were not shaped by the mid-domain effect or the available-area effect in the Agasthyamalai Hills. Temperature is the clear driver of these patterns for reptiles, and for lizards but not for snakes and endemic species. These temperature relationships result in a monotonic decline in reptile and lizard richness with increasing elevation. These findings agree with those at the global scale which report a tight link between temperature and reptile diversity patterns (McCain, 2010). Since external temperatures directly determine metabolic rates in ectotherms (such as reptiles and amphibians), they show higher affinities with temperature and are more vulnerable to changing climates than endotherms (i.e. birds and mammals) (Rolland et al., 2018). This becomes a critical issue for the large number of range-restricted reptiles in the Western Ghats where many species are endemic and confined to certain hill ranges. As global temperatures rise, these species may find themselves pushed to new elevational ranges, or they may run out of appropriate thermal environments entirely (Colwell et al., 2008). The next steps are to extend this kind of standardized sampling, throughout the Western Ghats, to confirm if the patterns are repeatable and to further generalize our understanding of how biodiversity is maintained in these ancient landscapes.

ACKNOWLEDGEMENTS

improving the MS at different stages.

This publication is an outcome of a larger project on reptiles and birds of Agasthyamalai Hills funded by Department of Biotechnology (DBT), Govt. of India. We dedicate this work to late Dr. S. Bhupathy of SACON who was the principal investigator of the project and Ph.D. supervisor to J.V.J initially. We are grateful to Kerala Forest Department for all the research permissions and logistic support in the field. We thank Director, SACON for the support at different stages of the study. Special thanks to Dr. P.V. Karunakaran, SACON for his help in vegetation sampling. Dr. Nathan J. Sanders, University of Vermont, USA gave comments on earlier drafts of MS and facilitated collaborations. We thank Dr. Arun P. R, SACON and Dr. Bhoj K. Acharya, Sikkim University for the guidance and constant support to J.V.J. We appreciate the help provided by the field assistants and local communities during the field study.

Author contribution statement: J.V.J conceived the questions and designed the study.

J.V.J and M.P conducted field data collection. J.V.J along with T.R.B designed MS, carried out data analysis and led the writing. R.J and M.P provided comments for

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786 TABLES

Table 1. Results of modelling to test hypotheses of species richness drivers. For each taxonomic subset, summaries of the top three linear regression models are shown. AICc is the bias corrected Akaike information criterion. \triangle AICc is calculated relative to the top ranked model for each taxonomic subset. R² is adjusted R². Standardised slopes are also given \pm the 95% CIs. Slope 1 refers to the first, or only explanatory variable. Slope 2 refers to the second, where applicable, which is always tree density.

Taxon subset	Explanatory variable	Slope 1	Slope 2	AICc	ΔAICc	\mathbb{R}^2
	Temperature	4.27±1.54		72.08	0	0.73
Reptiles	Temperature + tree density	4.87 ± 2.07	0.91 ± 2.07	74.97	2.9	0.73
	Area	2.52 ± 2.65		87.39	15.31	0.2
	Null			55.89	0	0
Snakes	Temperature	0.48 ± 1.13		58.39	2.49	-0.01
	Tree density	0.09 ± 1.17		59.33	3.44	-0.09
	Temperature	3.63±0.99		59.78	0	0.83
Lizards	Temperature + tree density	3.45 ± 1.38	-0.26 ± 1.38	63.61	3.83	0.82
	Tree density	-2.54 ± 1.9		78.11	18.33	0.36
	Null			57.93	0	0
Endemics	MDE	0.9 ± 1.12		58.14	0.21	0.15
	Tree density	-0.7±1.18		59.51	1.58	0.06

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FIGURES

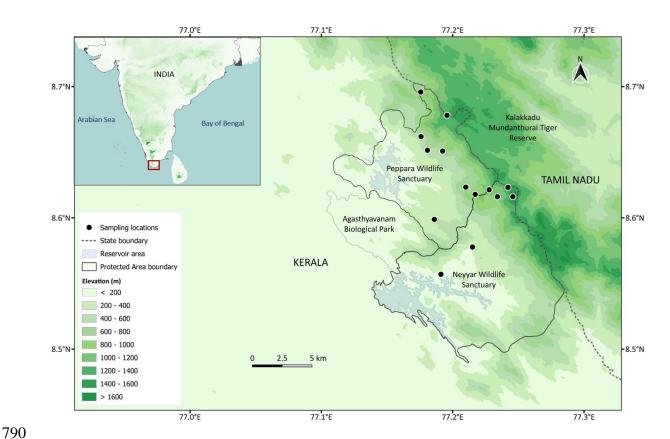


Figure 1. Sampling locations along the elevation gradient. Inset: location of

Agasthyamalai Hills in the Indian subcontinent.

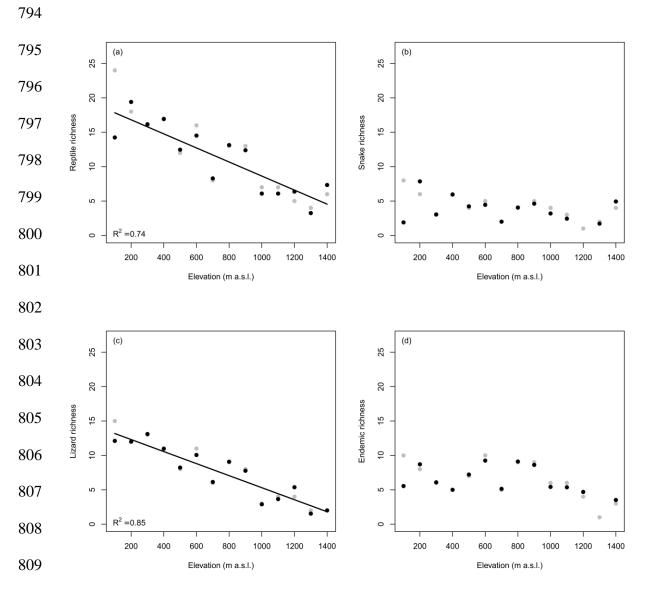


Figure 2. Patterns of species richness across elevation for (a) all reptiles, (b) snakes, (c) lizards and (d) endemic species. Data points represent elevational sampling sites. Black points are the analysed data, interpolated or extrapolated to correct for sampling biases. Grey points represent the raw, observed species richness values. Lines represent linear regression lines.

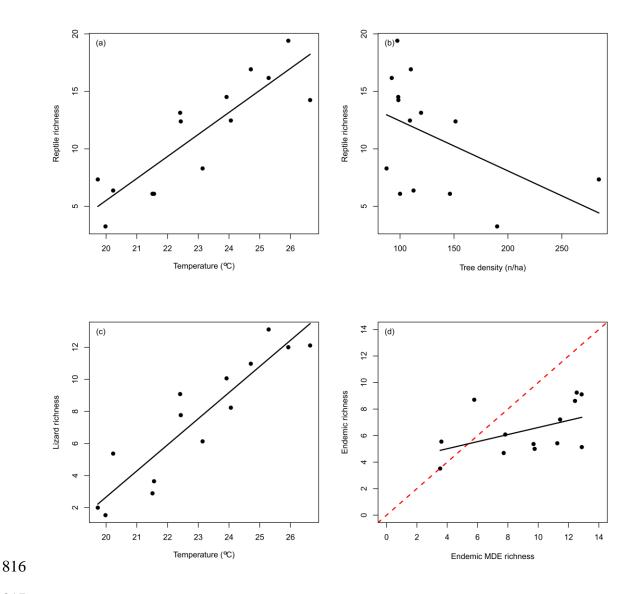


Figure 3. Select relationships between species richness of different reptile subsets and different potential drivers. Data points are elevational sampling sites. Black solid lines represent linear regression lines. Red dashed line in (d) represents a 1:1 relationship, which would be expected if the mid-domain effect (MDE) predictions of species richness match observed richness patterns. Relationships displayed here were top-ranked by AICc, or within Δ AICc of the top-ranked models and are displayed here for illustration.

SUPPLEMENTARY MATERIAL

Table S1. Table showing sample completeness calculated using the iNEXT function in the iNEXT package of R. Sampling effort is recorded in two-person hours (1 = 2 people searching for 1 hour).

Elevation (m)	Sampling effort	Species observed	Sample completeness
100	152	24	0.9639
200	27	18	0.9056
300	35	16	0.9054
400	37	17	0.9628
500	32	12	0.9413
600	44	16	0.9106
700	31	8	0.9539
800	35	13	0.8651
900	39	13	0.8109
1000	54	7	0.9378
1100	50	7	0.9129
1200	22	5	0.6818
1300	47	4	0.4086
1400	26	6	0.6753

Table S2. Table showing modelling details for elevational diversity patterns.

P *****				
Taxon subset	Elevational model	AICc	ΔAICc	\mathbb{R}^2
Reptiles	Linear	71.88	0	0.74
Reptiles	Curvilinear	75.88	3.99	0.76
Reptiles	Null	88.36	16.48	0
Snakes	Null	55.89	0	0
Snakes	Linear	58.36	2.47	0.07
Snakes	Curvilinear	62.69	6.80	0
Lizards	Linear	58.25	0	0.85
Lizards	Curvilinear	62.12	3.87	0.86
Lizards	Null	82.26	24.00	0
Endemics	Null	57.93	0	0
Endemic	Curvilinear	59.49	1.56	0.38
Endemics	Linear	59.50	1.57	0.13
		_		

Table S3. Expanded version of table 2 in the main text. Results of modelling to test hypotheses of species richness drivers. For each taxonomic subset, summaries of the top three linear regression models are shown. AICc is the bias corrected Akaike information criterion. \triangle AICc is calculated relative to the top ranked model for each taxonomic subset. R^2 is adjusted R^2 . Standardised slopes are also given \pm the 95% CIs. Slope 1 refers to the first, or only explanatory variable. Slope 2 refers to the second, where applicable, which is always tree density.

Taxon subset	Explanatory driver	Slope 1	Slope 2	AICc	ΔAICc	\mathbb{R}^2
Reptile	Temperature	1.92±0.69		72.08	0	0.73
Reptile	Temperature + tree density	2.19±0.93	0.02 ± 0.04	74.97	2.9	0.73
Reptile	Area	0.13±0.14		87.39	15.31	0.2
Reptile	Tree density	-0.04±0.05		88.21	16.13	0.15
Reptile	Null			88.36	16.29	0
Reptile	MDE	0.03±0.52		91.65	19.58	-0.08
Snake	Null			55.89	0	0
Snake	Temperature	0.22±0.52		58.39	2.49	-0.01
Snake	Tree density	0±0.02		59.33	3.44	-0.09
Snake	MDE	-0.03±0.5		59.35	3.45	-0.09
Snake	Area	0±0.06		59.35	3.46	-0.09
Snake	Temperature + tree density	0.55±0.76	0.02±0.03	60.66	4.76	0.05
Lizard	Temperature	1.63±0.44		59.78	0	0.83
Lizard	Temperature + tree density	1.55±0.62	0±0.03	63.61	3.83	0.82
Lizard	Tree density	-0.05±0.04		78.11	18.33	0.36
Lizard	Area	0.13±0.1		78.96	19.18	0.32
Lizard	Null			82.26	22.48	0
Lizard	MDE	0.03±0.68		85.56	25.78	-0.08

Endemic	Null			57.93	0	0
Endemic	MDE	0.27±0.33		58.14	0.21	0.15
Endemic	Tree density	-0.01±0.02		59.51	1.58	0.06
Endemic	Temperature	0.33±0.55		59.52	1.59	0.06
Endemic	Area	0±0.06		61.4	3.47	-0.09
Endemic	Temperature + tree density	0.2±0.73	-0.01±0.03	63.35	5.42	0