**Heterogeneous geographic patterns of diversity dynamics across terrestrial vertebrates**

Héctor Tejero-Cicuéndez, Iris Menéndez, Fernando Blanco, Elizabeth Steell, Guillermo Navalón, Jiří Šmíd

Abstract

Evolutionary and ecological dynamics differ across regions of Earth and across clades of the tree of life.

Introduction

The evolutionary and ecological processes underlying patterns of biodiversity have always been a central subject of study for natural historians and evolutionary biologists (de Candolle 1859; Matthew 1915; Moore 1920; Ruthven 1920; Allee 1926; Dobzhansky 1950; Fischer 1960; MacArthur 1965; Anderson 1974). The study of global geographic patterns of species diversity has led the macroecological discussion from the very beginning of evolutionary biology as a discipline, being among the major topics in the works that paved the way for the modern evolutionary theory (Humboldt and Bonpland 1807; Darwin 1859; Wallace 1876). The biodiversity levels in a given area are ultimately determined by three fundamental processes: lineage origination (generally represented by speciation in macroevolutionary studies of extant taxa), extinction, and dispersal (Ricklefs 2004; Mittelbach et al. 2007; Wiens 2011). These processes, and therefore the differences in richness across geographic and phylogenetic contexts, might be subjected to multiple biotic and abiotic factors operating at regional and local scales (Ricklefs 1987, 2006; Rabosky 2009), such as ecological interactions (Schemske et al. 2009), evolutionary time (Wallace 1878; Stephens and Wiens 2003), ecomorphological dynamics (Heard and Hauser 1995; Freeman et al. 2022), environmental conditions (Currie et al. 2004; Allen et al. 2006), climatic trends (Thompson et al. 2023), or topography and plate tectonics (Hoorn et al. 2010; Badgley et al. 2017; Tejero-Cicuéndez et al. 2022).

In recent years, the emergence and development of what is known as spatial phylogenetics (Earl et al. 2021; Mishler 2023) has fostered the advancement of our understanding of macroecological dynamics by integrating the phylogenetic component into the study of geographic biodiversity patterns. Specifically, the use of phylogeny-based metrics of biodiversity such as phylogenetic diversity (PD) allows for the investigation of the relatedness of biodiversity across geographic scales (high PD indicates the presence of species distantly related in the phylogeny, while low PD is the result of closely related species in a given area). This, in turn, may greatly enhance our ability to understand the evolutionary, ecological, and environmental factors that shape diversity dynamics (Davies and Buckley 2011; Tucker et al. 2017), as well as being an essential source of information for conservation purposes (Faith 1992; Redding and Mooers 2006).

Even though richness and PD are in general positively correlated (i.e., regions of high and low richness have generally high and low PD, respectively), spatial patterns of the two are not necessarily coincidental (Tucker and Cadotte 2013). In other words, there are geographic areas that harbor higher and lower PD than expected for their richness levels – i.e., areas where species are more distantly or more closely related, respectively, than would be predicted by the number of species (Fig. 1). Identifying these deviations of PD from richness (residual PD; Velasco and Pinto-Ledezma 2022) is key to understanding the processes underlying diversity patterns and investigating evolutionary scenarios plausible with such existing patterns.

At local or regional scales, levels of residual PD might reflect the existence of biotic or abiotic filters in the community assembly. In this case, low residual PD could reflect an assembly governed by strong abiotic (e.g., habitat) filtering, leading to the coexistence of closely related species which, considering niche conservatism principles, would presumably be ecologically similar (Romdal et al. 2013; Pyron et al. 2015; Chazot et al. 2021). In contrast, high residual PD would primarily reflect biotic (e.g., competition) filtering, resulting in the coexistence of species with different ecological affinities and likely more distantly related phylogenetically (Gause 1934; Hardin 1960; Macarthur and Levins 1967; Chesson 2000; HilleRisLambers et al. 2012). At broader scales, geographic differences in residual PD may arise due to the differential persistence of lineages through time, which can result in some regions having a higher proportion of older, more evolutionarily distinct lineages than others. This, in turn, can be affected by a variety of factors, such as differences in habitat stability, dispersal events, or diversification rates. More specifically, regions of high residual PD (i.e., with species more distantly related to each other than predicted by richness) might result from gradual accumulation of species, either by dispersal from other areas (immigration) or by low levels of speciation and extinction (low turnover rate), acting as a reservoir of ancient lineages. This could reflect what has been commonly known in the evolutionary biology literature as a “museum” or “sanctuary” of biodiversity (Dobzhansky 1950; Stebbins 1974). However, high levels of residual PD might also arise with a different combination of processes, such as high speciation rates in the past followed by low extinction of those ancient lineages, or exceptionally high extinction rates of young lineages. Conversely, regions of low residual PD (i.e., with species more closely related than expected by richness) can result from exceptionally high speciation and extinction rates maintained through time (high turnover rate), which constitute the original conceptualization of a “cradle” of biodiversity (Stebbins 1974). However, again, low residual PD can also be the result of other scenarios, such as reduced extinction rates of recent lineages or increased extinction of ancient clades. This multiplicity of scenarios generating patterns of lineage and phylogenetic diversity highlights the importance of investigating the underlying evolutionary processes rather than focusing the discussion on dichotomously elucidating whether specific regions are cradles or museums of biodiversity (Vasconcelos et al. 2022).

The increasing availability of global distribution and phylogenetic data for large clades of the tree of life allows for the exploration of large-scale diversity patterns and evolutionary processes. For example, in the last decade, the geographic distribution of residual phylogenetic diversity has been addressed for the major clades of terrestrial vertebrates: mammals (Davies and Buckley 2011), amphibians (Fritz and Rahbek 2012), birds (Voskamp et al. 2017), and squamates (Gumbs et al. 2020; Vásquez-Restrepo et al. 2023). However, a comprehensive exploration including mapping residual PD and identifying similarities and differences across vertebrate clades, as well as analyzing the potential effect of different factors on such patterns, is still lacking. In this study, we characterize geographic patterns of current tetrapod diversity dynamics by inferring species and phylogenetic diversity, and test hypotheses related to the impact of multiple factors on regional levels of residual PD: recent speciation rates, evolutionary time, and environmental conditions. This allows us to identify regions in which the evolutionary history has been potentially subjected to different processes shaping the observed patterns across clades. Ultimately, this constitutes a step forward in our understanding of evolutionary dynamics and, importantly, might provide an impactful insight into how to confront the challenges imposed by the global environmental crisis.

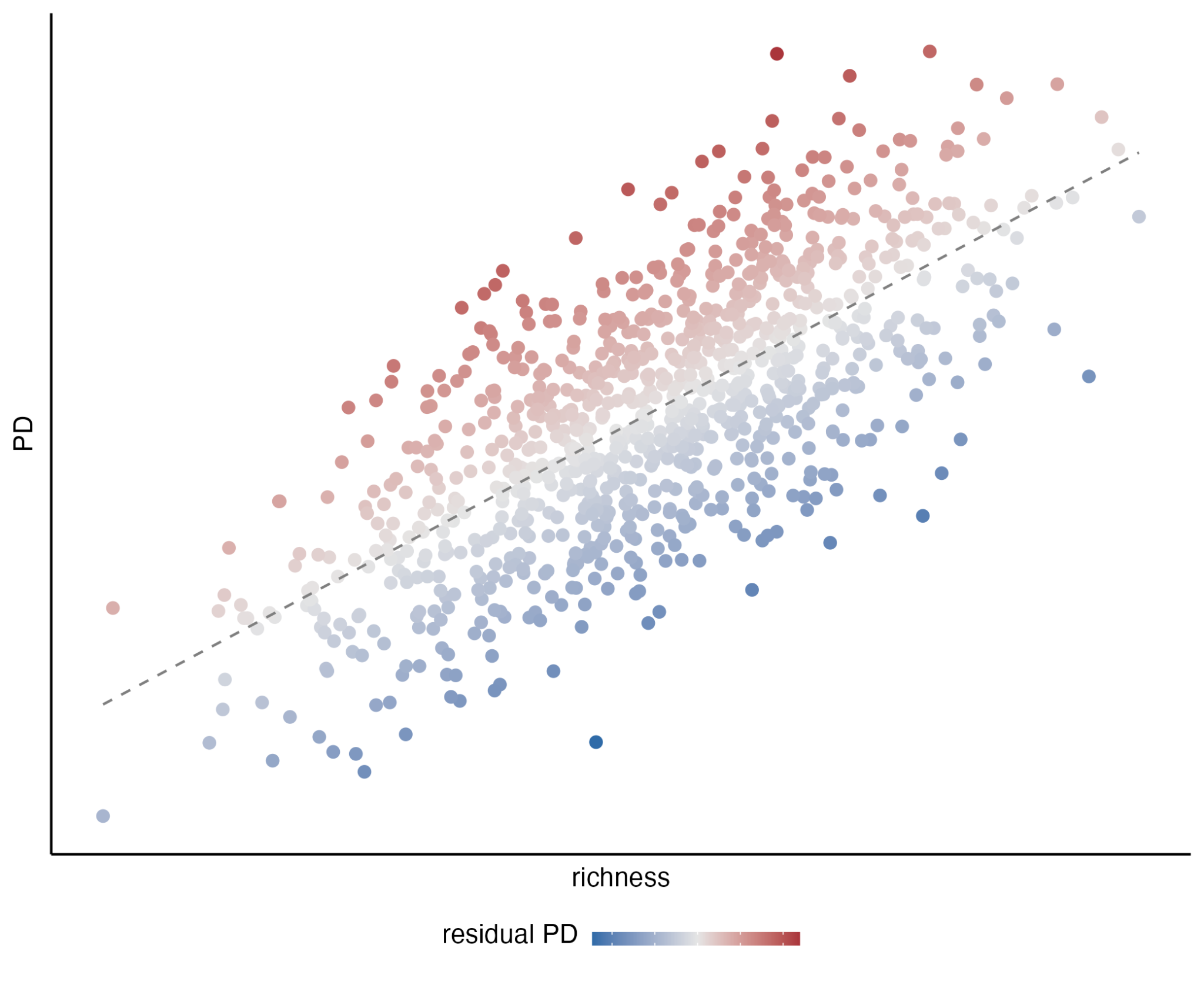


Fig. 1. Schematic representation of the relationship between species richness (X-axis) and phylogenetic diversity (Y-axis), with color representing residual phylogenetic diversity.

Materials and Methods

**Vertebrate data**. We obtained distribution vector data for amphibians and terrestrial mammals from IUCN (IUCN 2022), for birds from BirdLife International (http://www.birdlife.org/) and for squamates from Roll et al. (2021). Range maps for all groups were downloaded on 1 May 2022.

Phylogenetic data for all groups were downloaded from VertLife (<https://data.vertlife.org/>). This includes consensus and posterior phylogenetic trees for amphibians (Jetz and Pyron 2018), birds (Jetz et al. 2012; we used the phylogeny built based on the backbone from Hackett et al. 2008), mammals (Upham et al. 2019), and squamates (Tonini et al. 2016).

After matching both distribution and phylogenetic data, the final datasets contained a total of 28,270 species: 5832 amphibians, 7995 birds, 5164 mammals, and 9279 squamates. These were the datasets used in subsequent analyses.

**Residual phylogenetic diversity**. For each vertebrate group, we first produced a hexagonal 100-km-resolution species richness grid using the epm package v1.1.1 (Title et al. 2022) in R 4.3.0 (R Core Team 2023), with the polygon distribution data transformed into an equal-area Behrmann projection as input and the ‘centroid’ approach. The resulting grid contains the information of the species present in each hexagonal cell, and was the base cell grid for subsequent analyses.

We obtained an average phylogenetic diversity (PD) grid after calculating PD grids for 100 trees from the posterior distribution. With the per-grid values of species richness and PD, we performed a local regression analysis (LOESS) and obtained the residuals from it. We then mapped these residuals onto the hexagonal grid to visualize the geographic distribution of the deviation of PD relative to richness (residual PD). High residual values indicate high PD for a given number of species (i.e., the species within a grid cell are more distantly related to each other than expected by richness), and, conversely, low residual PD indicates that the species present in a grid cell are more closely related to each other than predicted by richness.

Additionally, we set a threshold at 10% and another one at 90% of the distribution of residual PD values to visualize the grid cells with lowest and highest residual PD, respectively, for each vertebrate clade. We then identified focal regions with the greatest geographic extents of contiguous high and low residual PD grid cells to investigate whether there are differences between them in speciation rates, lineage accumulation patterns, and environmental conditions.

**Recent speciation rates**. We estimated recent speciation rates (tip rates) calculating the average DR metric (Jetz et al. 2012) across 100 trees from the posterior distribution for each vertebrate clade. We then mapped per-cell mean DR values onto the hexagonal cell grids (see above), and implemented a linear regression model of per cell mean DR against residual PD. Additionally, we tested for differences in DR between the species present in regions of highest and lowest residual PD. To do this, we performed linear models with randomized residual permutations with the RRPP package v1.3.1 (Collyer and Adams 2018, 2022), first to globally compare grid cells of high and low residual PD and then to individually compare among the focal regions we identified (see above).

**Evolutionary time and lineage accumulation**. To explore whether there are differences in the age or the lineage accumulation patterns between regions of high and low residual PD, we calculated the number of lineages through time with the ape package v5.7.1 (Paradis and Schliep 2019), with the aid of the additional packages geiger v2.0.11 (Pennell et al. 2014) and phytools v1.5.1 (Revell 2012) for phylogenetic data handling. We then visually compared lineage-through-time (LTT) plots to determine whether our data reflect two main expectations: i) regions of high residual PD might act as reservoirs of older diversity than regions of low residual PD (and therefore the ancestral origin of the lineages in high-PD regions should be older), and ii) the pattern of lineage accumulation might be different between regions of high and low residual PD.

**Environmental variables**. One of the factors that may affect evolutionary processes and therefore shape geographic patterns of biodiversity is the environment in which species live. We tested the relationship between residual PD and different environmental variables: mean annual temperature, temperature seasonality, annual precipitation, precipitation seasonality, net primary productivity (NPP), and terrain roughness index (TRI, a variable representing the topographic complexity). Temperature and precipitation data were collected at a 10-minute spatial resolution (~18.5 km) from the summary data for the period between the years 1970 and 2000 contained in the WoldClim v2.1 dataset (Fick and Hijmans 2017). Net primary productivity data summarized over the period between 1981 and 2015 was obtained at 5-arc-minute resolution from the NDVI3g time series (Pinzon and Tucker 2014). The topography data were based on Wilson et al. (2007) and obtained from the ENVIREM dataset (Title and Bemmels 2018) at a spatial resolution of 10 arc-minutes. For the latter, we compared current topography values with estimated Holocene and Last Glacial Maximum values, and we did not find considerable differences, so we report only the analyses with the current values. All the environmental variables were resampled to match the spatial resolution of the hexagonal cell grid built for species richness and phylogenetic diversity (100 km), so that we could have per-cell values for every variable in order to implement regression models. Additionally, we generated three climatic spaces: one defined by temperature and precipitation, another one defined by temperature seasonality and precipitation seasonality, and a third one defined by NPP and TRI, and mapped the grid cells with lowest and highest 10% of the residual PD onto those climatic spaces to explore for potential segregation between them. Finally, we also explored how residual PD is distributed across the latitudinal gradient, to compare residual PD patterns with species richness.

Results

**Geographic patterns of residual phylogenetic diversity.** We found some regions with consistent patterns of residual PD across vertebrate clades, and some other regions of different levels of residual PD for different clades (Supp. Fig. 1). The African continent harbors overall high residual PD (i.e., species more distantly related to each other than expected for the species richness) for all vertebrates, with the exception of the Sahara desert for mammals and the rainforest in central Africa for squamates. Conversely, large parts of South America contain low residual PD (species more closely related to each other than predicted by richness) for all clades. In fact, Africa and South America constitute focal regions of highest and lowest residual PD, respectively, for all vertebrate clades (Fig. 2). Australia is a low-residual-PD region for amphibians and especially squamates, while it harbors high residual PD for birds and mammals. Residual PD in the Indomalayan region is generally high for birds and squamates and relatively low for amphibians, while for mammals it is a heterogeneous area with high levels in India and regions of low and high levels in Southeast Asia. North America is a region of low residual PD for birds and squamates, and of relatively high residual PD for amphibians. For mammals, there is a clear segregation in residual PD patterns between eastern (high values) and western (low values) North America. Eurasia is also a heterogeneous region across vertebrates, with generally low levels of residual PD for mammals and birds, high levels for amphibians, and areas of high and low levels for squamates. The Arabian Peninsula contains exclusively high levels of residual PD for squamates, but for mammals and birds it shows relatively low levels across the interior and high levels in the mountainous regions of the south and west (Supp. Fig. 1).

**The effect of speciation rates**. We found a significant negative relationship between recent speciation rates and residual PD for all vertebrate clades (*P* <<< 0.001; Fig. 3). In other words, there are in average higher recent speciation rates in regions of low residual PD (i.e., in regions where species are more related to each other than predicted by richness), while regions of high residual PD have in general lower speciation rates. However, this negative relationship was found to be somewhat weak, with low R2 and slope coefficient values (Supp. Table 1; R2amphibians = 0.005, R2birds = 0.047, R2mammals = 0.076, R2squamates = 0.13).

For all clades, we found significantly lower speciation rates in the species present in grid cells with the lowest residual PD relative to those present in cells with the highest residual PD (*P* = 0.001 in all cases), especially for squamates, although, attending to the effect sizes (Z) and the overall distribution of DR values, this difference appears to be mild (Fig. 4).

Likewise, we found significant differences in species’ DR rates among focal regions of highest and lowest residual PD, with low residual PD broadly corresponding to higher speciation rates, but these differences are overall not prominently apparent (Supp. Fig. 2, Supp. Table 2). Furthermore, we did not find clearly greater differences in DR effect size (Z) between focal regions of highest and lowest residual PD than between different regions of high residual PD and between different regions of low residual PD (*P* = 0.467; Supp. Fig. 3), indicating that the differences in DR rates between regions of high and low residual PD, though significant, are not of large magnitude.

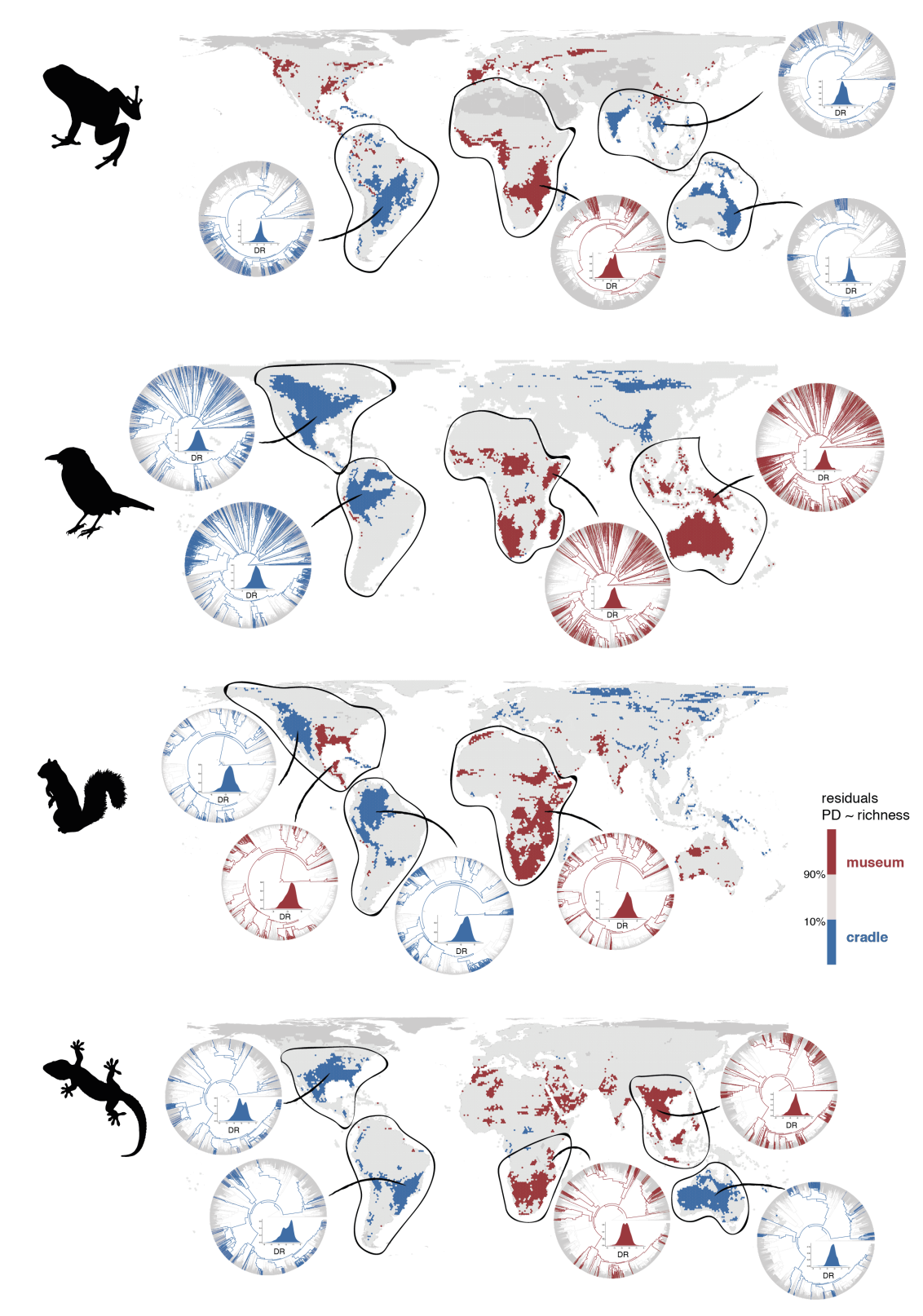


Fig. 2. Geographic distribution of areas with the 10% lowest (in blue) and highest (in red) residual PD for terrestrial vertebrates. The phylogenetic relationships of species present in focal regions are also shown to illustrate the evolutionary differences of regions with high and low residual PD. Silhouettes extracted from 'phylopic' (www.phylopic.org).

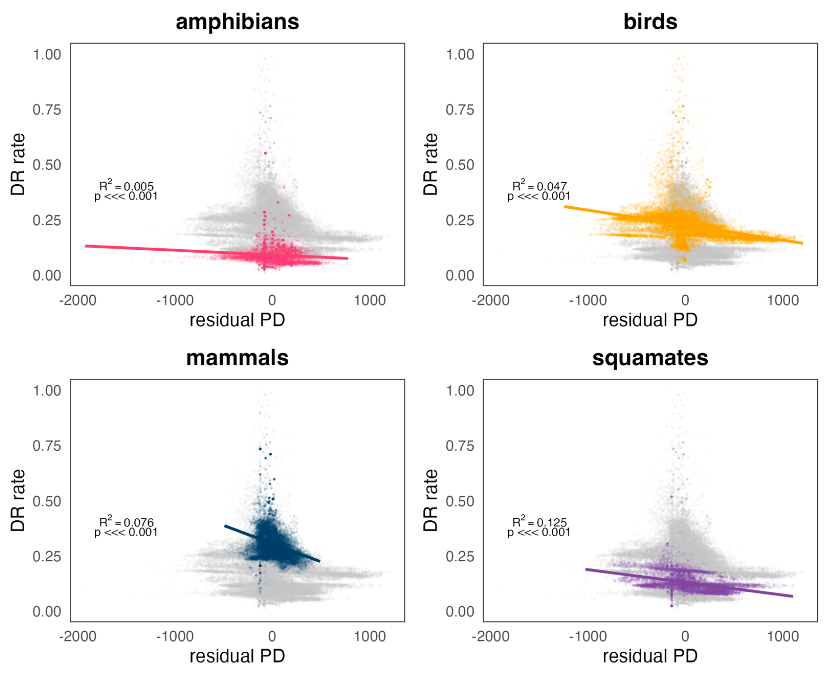


Fig. 3. Relationship between DR rates and residual PD for all four groups of terrestrial vertebrates.

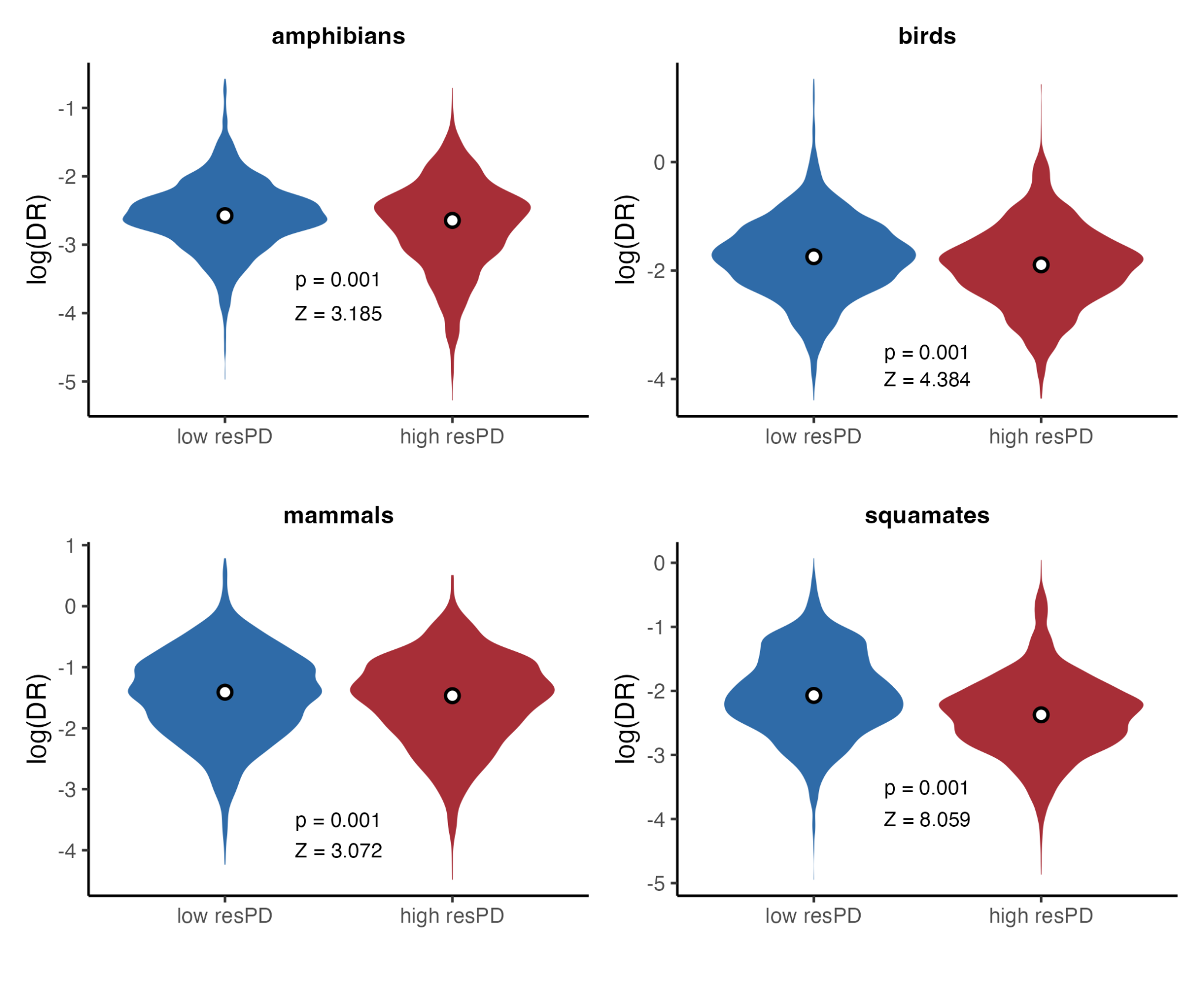


Fig. 4. Differences in DR rates between areas of 10% lowest (in blue) and highest (in red) residual PD.

**Evolutionary time and lineage accumulation**. We did not find notable differences between focal regions of high and low residual PD in the time of origin or the pattern of accumulation of the lineages they harbor (Supp. Figs. 4-7). Specifically, we did not find the expected older age in regions of high residual PD, and the pace of lineage accumulation is also not clearly distinguishable between regions of both types. Even though some regions of low residual PD do harbor younger diversity than regions of high residual PD (e.g., amphibians in Oceania relative to amphibians in Africa, Supp. Fig. 4), this is the opposite in other cases (e.g., mammals in high residual PD Africa have actually younger ancestors than in low residual PD regions of North and South America, Supp. Fig. 6), and in most cases the age of origin of the lineages leading to the current species is similar in regions of high and low residual PD.

**Environmental variables**. We found overall low to no relationship between residual PD and environmental variables (Supp. Figs. 8-13). There is a negative and very mild relationship between annual precipitation and residual PD for all groups (Supp. Fig. 8), while the relationship with mean annual temperature is negative for amphibians and positive for the rest of vertebrate clades (Supp. Fig. 9), with mammals showing the highest amount of residual PD variance explained in both cases (precipitation R2mammals = 0.017; temperature R2mammals = 0.138). For precipitation seasonality and temperature seasonality, amphibians show an opposite trend to that of the other clades, although the variance explained is very low overall (Supp. Figs. 10 and 11). In amphibians, the correlation of residual PD with precipitation seasonality is negative (Supp. Fig. 10) and with temperature seasonality positive (Supp. Fig. 11), while for the rest of vertebrates these correlations are positive and negative, respectively. There is an extremely low correlation of residual PD with net primary productivity (NPP) for all clades (Supp. Fig. 12). With current topographic complexity (terrain roughness index, TRI), the correlation is also very low overall, but there is a somewhat clearer negative trend in birds and mammals (Supp. Fig. 13).

In the environmental space defined by mean annual temperature and annual precipitation, we found some segregation between regions of low and high PD for birds and mammals, but not for amphibians and squamates (Fig. 5). In both birds and mammals, low residual PD regions are characterized by two combinations: low precipitation with low to moderate temperature (which roughly correspond to areas of tundra, cold deserts and temperate grasslands; Whittaker 1975), and high precipitation with high temperature (i.e., tropical rainforest and savannah). Most of the high residual PD regions for birds and mammals, on the other hand, are found in environments with both low to moderate precipitation and high temperature (i.e., subtropical desert and savannah).

The patterns of distribution of regions with high and low residual PD across the environmental space defined by precipitation seasonality and temperature seasonality, or by NPP and TRI, do not follow clearly interpretable trends, and there is not an apparent segregation of high and low residual PD regions in neither of them (Supp. Figures 14 and 15), except perhaps for birds in the climate seasonality space, where high residual PD regions tends to be at lower temperature seasonality than regions of low residual PD (Supp. Fig. 14). Likewise, there is not an apparent latitudinal gradient in residual PD for any vertebrate clade, in contrast to species richness (Supp. Fig. 16). Notably, although there appears to be no clear relationship between richness and residual PD (which is expected given that richness and PD are highly correlated), for birds regions of high richness across different latitudinal bands coincide with low residual PD levels (Supp. Fig. 16).

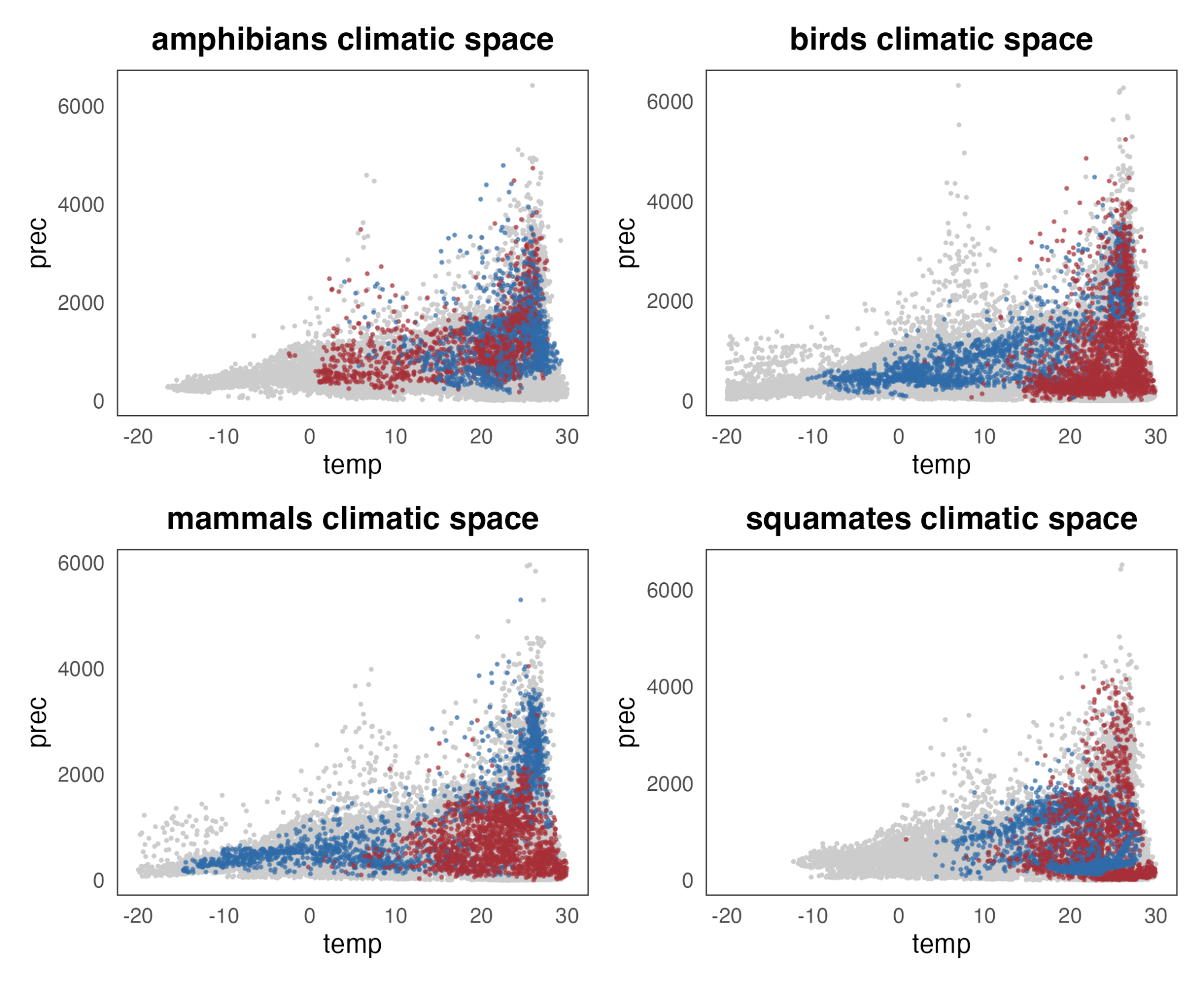


Fig. 5. Climatic space (mean annual temperature vs. annual precipitation) occupied by regions of highest (in red) and lowest (in blue) residual PD for each vertebrate clade.

Discussion

The integration of phylogenetic metrics in the analysis of diversity allows for a more informed understanding of the evolutionary and ecological processes underlying current spatial patterns of biodiversity. Here we addressed the geographic distribution of richness-corrected phylogenetic diversity (residual PD) for four major vertebrate clades (amphibians, birds, mammals, and squamates), identifying the areas of greatest concentration of high and low residual PD and finding consistently low levels (more closely related species than predicted by richness) in America and high levels (more distantly related species) in Africa for all groups (Fig. 2). Further, we found a negative but weak relationship of recent speciation rates with residual PD (Figs. 3 and 4), indicating some role, though limited, of recent speciation in generating this pattern. Finally, our results show ambiguous and low to no effect of evolutionary time and climatic variables on the differentiation of regions with highest and lowest residual PD (Fig. 5).

There are multiple processes that can drive patterns of residual PD, and therefore the specific processes underlying such patterns might vary from one region to another and among different taxonomic groups (Davies and Buckley 2011). Here we discuss some of the processes that could be generating the patterns we found, attending to historical, biogeographic, and ecological dynamics of vertebrates in different continents. We found that the American continent is consistently a region of low residual PD across vertebrate clades. Likewise, Africa consistently harbors high levels of residual PD for all groups. Previous work on mammals (Davies and Buckley 2011) suggested that the high residual PD found in Africa might reflect that many of the extant mammal clades have an African origin (Lillegraven et al. 1987). While this is a plausible explanation, we argue that the consistencies among vertebrate clades with disparate biogeographic origins might indicate that the factors generating this pattern are common for all groups, regardless of their geographic origin or historical biogeographic dynamics. Following this reasoning, attending to the environmental and geologic histories of different regions that have potentially affected all vertebrates in a similar manner might provide deeper insights into the generation of this geographic pattern. Namely, the fact that America, and particularly South America, has low levels of residual PD relative to the consistently high values in Africa for all groups (Fig. 2) likely reflects the recent diversification of multiple current clades following migrations after the formation of the Isthmus of Panama coupled with the extinction of ancient lineages (Webb 1976; Weir et al. 2009; Davies and Buckley 2011; Carrillo et al. 2020). This is consistent with the ubiquitous negative relationship observed between residual PD and recent speciation rates which, although weak, reflects that recent speciation is likely one of the processes at play in the unfolding of vertebrate diversity dynamics (Fig. 3). Taken together, these results might point at recent climatic or geographic events (e.g., reconfiguration of continents) as a primary driver of spatial patterns of diversity dynamics in some regions by affecting, at least in part, recent levels of speciation.

However, the heterogeneity in residual PD patterns among vertebrate groups in other parts of the world (e.g., Eurasia and Australia; Fig. 2) indicates that species’ intrinsic (i.e., physiological, ecological, or morphological) characteristics might also have a role in the generation of these patterns. For example, the Malay Archipelago shows especially high residual PD for birds relative to the other vertebrates, while parts of Australia present low residual PD for amphibians and squamates but high residual PD for mammals and especially birds (Fig. 2). One explanation for these differences may reside in the ecological and functional differences among clades, which may have determined their biogeographic and evolutionary history. The high vagility of birds, which enabled the repeated colonization of the islands in Southeast Asia and Australia (Jønsson and Fjeldså 2006; Sheldon et al. 2015), might be the cause of the higher values of residual PD found in the region for this clade resulting from the arrival and relictual permanence of lineages with different phylogenetic origins (Jønsson et al. 2007), as opposed to isolated radiations which might be more frequent in organisms with lower dispersal abilities (Inger and Voris 2001; Siler et al. 2012). High residual PD of squamates in this area might be related to multiple waves of island colonization during intervals of low sea levels and environmental change (How and Kitchener 1997; Voris 2000; Brown et al. 2013; Husson et al. 2020), although this also affected mammals (Van Den Bergh et al. 2001; Meijaard 2003; Mercer and Roth 2003) and amphibians (Brown et al. 2013), which do not show comparable patterns of residual PD (perhaps due to a greater effect of environmental fluctuations promoting turnover in these taxa; e.g., Wilting et al. 2012). On the other hand, the low residual PD of squamates in arid Australia and of amphibians in the temperate woodlands of the northern and eastern coasts of Australia is likely the result of a few massive radiations (see the phylogenetic trees in Fig. 2) facilitated by the adaptation to the environmental conditions and specialization within those biomes, which have led to a community assembly driven by proportionally more closely related species (Pianka 1981; Rabosky et al. 2007; Skinner et al. 2011; Vidal-García and Keogh 2015; Brennan et al. 2023). Finally, geographic patterns of residual PD might also be partially generated by ancient evolutionary lineages that inhabit certain regions. This could be the case of dibamid reptiles in Southeast Asia (Townsend et al. 2011), palaeognath birds in Australia (Yonezawa et al. 2017), or marsupial mammals in Australia and North America (May-Collado et al. 2015).

Apart from differences in trait- and environment-mediated speciation and dispersal, extinction might also be a major driver of diversity, diversification and biogeographic patterns (Jablonski 2001; Seeholzer and Brumfield 2023). Specifically, extinction events are known not only to underlie current patterns of species richness (Pyron 2014a; Meseguer and Condamine 2020) but also to importantly affect other facets of biodiversity (Erwin 2008; Pimiento et al. 2020; Brocklehurst et al. 2021). Extinction might act generating both increasing and decreasing phylogenetic diversity, depending on the age of the lineages more prone to extinction (Daru et al. 2017). High residual PD regions might result from the extinction of species from relatively recent radiations, mainly reducing communities to species with a distant evolutionary relationship, while low residual PD may arise in regions where extinction rates are higher for relatively old diversity (Vasconcelos et al. 2022). The exploration of extinction dynamics and, critically, the inclusion of fossil data, will help to further disentangle the factors underlying this and other geographic patterns of vertebrate diversity.

The variety of factors that might be generating residual PD geographic patterns is consistent with previous results indicating that the distribution of diversity is strongly subjected both to extrinsic (e.g., the paleogeographic history) and intrinsic (e.g., ecomorphological or niche-related) factors (Pyron 2014b; Menéndez et al. 2021). In this sense, mountainous regions (a universally recognized driver of diversity and evolutionary processes; Hoorn et al. 2010; Rahbek et al. 2019; Perrigo et al. 2020) can have very different ecological roles depending on how the species’ ecological preferences relate to environmental features. Namely, they can act as a source of new diversity, promoting speciation due to habitat diversity across an elevational gradient (especially in the tropics; Cadena et al. 2011) or constituting dispersal barriers (e.g., Miller et al. 2008), and they have also been reported as important refugia and reserves of cold- or humid-adapted diversity during periods of climate warming and aridification events (Hampe and Jump 2011; Fjeldså et al. 2012). Likewise, deserts, which have been recurrently considered sinks of diversity (i.e., regions harboring distantly related species due to a lack of within-system diversification; Crisp et al. 2009) might in fact harbor low levels of residual PD, like the Australian deserts for squamates and the North American deserts for birds, mammals and squamates (Fig. 2), which in many cases might reflect large radiations of certain clades adapted to the arid conditions (e.g., Wiens et al. 2013; Rabosky et al. 2014).

This ecological versatility of physiographic features might be responsible for the lack of a clear relationship between environmental variables and residual PD (Supp. Figs. 8-13), although some segregation is apparent in the climate space between the regions of highest and lowest residual PD, especially in birds and mammals (Fig. 5), which might be explained by fundamental physiologically imposed differences in how endotherms and ectotherms interact with the environment (Buckley et al. 2012). Additionally, the fact that multiple processes can lead to similar patterns of residual PD probably explain why we did not find a clear effect of evolutionary time or lineage accumulation dynamics on the differences between regions of high and low residual PD (Supp. Figs. 4-7). While time has been reported as a primary driver of diversity gradients in some systems (e.g., Miller and Román-Palacios 2021) and might be reflected in age differences among biotas in different regions, here we did not find the expected relationship between more closely related lineages (low residual PD) and younger ages. Likewise, a differential pattern of lineage accumulation between regions of high and low residual PD would be a plausible expectation. Specifically, as potential scenarios, we could expect a relatively linear or constant accumulation of species in regions of high residual PD, maybe resulting in the maintenance of ancient lineages, while in regions of low residual PD we might expect a community build-up marked by alternating periods of high diversification and stasis in lineage dynamics. However, our results show an ambiguous pattern in this respect, without a clear segregation between regions of low and high residual PD. This, together with the mild differences in recent speciation between species from low and high residual PD regions (Figs. 3 and 4), might be an indicative that the phylogenetic patterns of extant species alone cannot account for the evolutionary dynamics we found across vertebrate clades, which in turn suggests that dispersal and/or deep-time diversification might be key for understanding these results.

The study of phylogenetic diversity patterns and their underlying causes is not only important to understanding how different factors operate and shape the evolutionary history. Our results might also be especially relevant from a conservation perspective. In fact, the need of integrating the evolutionary relationships of the species at the regional scale to inform conservation policies has been stated for decades (Faith 1992), in opposition to conservation approaches that focus on hotspots of species richness and endemism (Myers et al. 2000). The geographic deviations of phylogenetic diversity from species richness (i.e., patterns of residual PD) might provide essential information to develop proper conservation strategies. Regions with highest residual PD maximize the conservation of phylogenetically distinct lineages, helping to preserve larger portions of evolutionary history. However, it might not be sufficient to prioritize those areas, since regions with lowest residual PD, on the other hand, potentially act like sources of diversity, where new species are originating (Meseguer et al. 2020). Thus, combining the conservation of regions both with high and low residual PD might be an effective way to attend to past as well as future diversification arenas. Considering additional factors, such as the stability or turnover of communities, and therefore the degree of opportunity for their permanence or demise, might prove a critical practice to integrate in the decision of where to invest conservation resources. Studying geographic patterns of diversity dynamics is the baseline to carry out these practices, which in turn might stand as the only valid approach to mitigate the effects of the undergoing global environmental change.

References

Allee W.C. 1926. Distribution of Animals in a Tropical Rain-Forest with Relation to Environmental Factors. Ecology. 7:445–468.

Allen A.P., Gillooly J.F., Savage V.M., Brown J.H. 2006. Kinetic effects of temperature on rates of genetic divergence and speciation. Proceedings of the National Academy of Sciences of the United States of America. 103:9130–9135.

Anderson S. 1974. Patterns of Faunal Evolution. The Quarterly Review of Biology. 49:311–332.

Badgley C., Smiley T.M., Terry R., Davis E.B., DeSantis L.R.G., Fox D.L., Hopkins S.S.B., Jezkova T., Matocq M.D., Matzke N., McGuire J.L., Mulch A., Riddle B.R., Roth V.L., Samuels J.X., Strömberg C.A.E., Yanites B.J. 2017. Biodiversity and Topographic Complexity: Modern and Geohistorical Perspectives. Trends in Ecology and Evolution. 32:211–226.

Brennan I.G., Lemmon A.R., Lemmon E.M., Hoskin C.J., Donnellan S.C., Keogh J.S. 2023. Populating a Continent: Phylogenomics Reveal the Timing of Australian Frog Diversification. Systematic Biology.:syad048.

Brocklehurst N., Panciroli E., Benevento G.L., Benson R.B.J. 2021. Mammaliaform extinctions as a driver of the morphological radiation of Cenozoic mammals. Current Biology. 31:2955-2963.e4.

Brown R.M., Siler C.D., Oliveros C.H., Esselstyn J.A., Diesmos A.C., Hosner P.A., Linkem C.W., Barley A.J., Oaks J.R., Sanguila M.B., Welton L.J., Blackburn D.C., Moyle R.G., Townsend Peterson A., Alcala A.C. 2013. Evolutionary processes of diversification in a model island archipelago. Annual Review of Ecology, Evolution, and Systematics. 44:411–435.

Buckley L.B., Hurlbert A.H., Jetz W. 2012. Broad-scale ecological implications of ectothermy and endothermy in changing environments. Global Ecology and Biogeography. 21:873–885.

Cadena C.D., Kozak K.H., Gómez J.P., Parra J.L., McCain C.M., Bowie R.C.K., Carnaval A.C., Moritz C., Rahbek C., Roberts T.E., Sanders N.J., Schneider C.J., VanDerWal J., Zamudio K.R., Graham C.H. 2011. Latitude, elevational climatic zonation and speciation in New World vertebrates. Proceedings of the Royal Society B: Biological Sciences. 279:194–201.

de Candolle A.L.P.P. 1859. On the Causes which Limit Vegetable Species Towards the North, in Europe and Similar Regions. Annual Report of the Board of Regents of the Smithsonian Institution for the Year 1858.:237–245.

Carrillo J.D., Faurby S., Silvestro D., Jaramillo C., Bacon C.D., Antonelli A. 2020. Disproportionate extinction of South American mammals drove the asymmetry of the Great American Biotic Interchange. Proceedings of the National Academy of Sciences.:1–7.

Chazot N., Condamine F.L., Dudas G., Peña C., Matos-Maraví P., Freitas A.V.L., Willmott K.R., Elias M., Warren A., Aduse-Poku K., Lohman D.J., Penz C.M., DeVries P., Kodandaramaiah U., Fric Z.F., Nylin S., Müller C., Wheat C., Kawahara A.Y., Silva-Brandão K.L., Lamas G., Zubek A., Ortiz-Acevedo E., Vila R., Vane-Wright R.I., Mullen S.P., Jiggins C.D., Slamova I., Wahlberg N. 2021. Conserved ancestral tropical niche but different continental histories explain the latitudinal diversity gradient in brush-footed butterflies. Nature Communications. 12:5717.

Chesson P. 2000. Mechanisms of Maintenance of Species Diversity. Annual Review of Ecology and Systematics. 31:343–366.

Collyer M.L., Adams D.C. 2018. RRPP: An r package for fitting linear models to high-dimensional data using residual randomization. Methods in Ecology and Evolution. 9:1772–1779.

Collyer M.L., Adams D.C. 2022. RRPP: Linear Model Evaluation with Randomized Residuals in a Permutation Procedure. .

Crisp M.D., Arroyo M.T.K., Cook L.G., Gandolfo M.A., Jordan G.J., McGlone M.S., Weston P.H., Westoby M., Wilf P., Linder H.P. 2009. Phylogenetic biome conservatism on a global scale. Nature. 458:754–756.

Currie D.J., Mittelbach G.G., Cornell H.V., Field R., Guégan J.-F., Hawkins B.A., Kaufman D.M., Kerr J.T., Oberdorff T., O’Brien E., Turner J.R.G. 2004. Predictions and tests of climate-based hypotheses of broad-scale variation in taxonomic richness. Ecology Letters. 7:1121–1134.

Daru B.H., Elliott T.L., Park D.S., Davies T.J. 2017. Understanding the Processes Underpinning Patterns of Phylogenetic Regionalization. Trends in Ecology & Evolution. 32:845–860.

Darwin C. 1859. On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life. London, UK: John Murray.

Davies T.J., Buckley L.B. 2011. Phylogenetic diversity as a window into the evolutionary and biogeographic histories of present-day richness gradients for mammals. Philosophical Transactions of the Royal Society B: Biological Sciences. 366:2414–2425.

Dobzhansky T. 1950. Evolution in the tropics. American Scientist. 38:209–221.

Earl C., Belitz M.W., Laffan S.W., Barve V., Barve N., Soltis D.E., Allen J.M., Soltis P.S., Mishler B.D., Kawahara A.Y., Guralnick R. 2021. Spatial phylogenetics of butterflies in relation to environmental drivers and angiosperm diversity across North America. iScience. 24:102239.

Erwin D.H. 2008. Extinction as the loss of evolutionary history. Proceedings of the National Academy of Sciences. 105:11520–11527.

Faith D.P. 1992. Conservation evaluation and phylogenetic diversity. Biological Conservation. 61:1–10.

Fick S.E., Hijmans R.J. 2017. WorldClim 2: new 1-km spatial resolution climate surfaces for global land areas. International Journal of Climatology. 37:4302–4315.

Fischer A.G. 1960. Latitudinal variations in organic diversity. Evolution. 14:64–81.

Fjeldså J., Bowie R.C.K., Rahbek C. 2012. The Role of Mountain Ranges in the Diversification of Birds. Annual Review of Ecology, Evolution, and Systematics. 43:249–265.

Freeman B.G., Weeks T., Schluter D., Tobias J.A. 2022. The latitudinal gradient in rates of evolution for bird beaks, a species interaction trait. Ecology Letters. 25:635–646.

Fritz S.A., Rahbek C. 2012. Global patterns of amphibian phylogenetic diversity. Journal of biogeography. 39:1373–1382.

Gause G.F. 1934. The struggle for existence. Baltimore, Maryland: Williams and Wilkins.

Gumbs R., Gray C.L., Böhm M., Hoffmann M., Grenyer R., Jetz W., Meiri S., Roll U., Owen N.R., Rosindell J. 2020. Global priorities for conservation of reptilian phylogenetic diversity in the face of human impacts. Nat Commun. 11:2616.

Hackett S.J., Kimball R.T., Reddy S., Bowie R.C.K., Braun E.L., Braun M.J., Chojnowski J.L., Cox W.A., Han K.-L., Harshman J., Huddleston C.J., Marks B.D., Miglia K.J., Moore W.S., Sheldon F.H., Steadman D.W., Witt C.C., Yuri T. 2008. A Phylogenomic Study of Birds Reveals Their Evolutionary History. Science. 320:1763–1768.

Hampe A., Jump A.S. 2011. Climate Relicts: Past, Present, Future. Annual Review of Ecology, Evolution, and Systematics. 42:313–333.

Hardin G. 1960. The Competitive Exclusion Principle: An idea that took a century to be born has implications in ecology, economics, and genetics. Science. 131:1292–1297.

Heard S.B., Hauser D.L. 1995. Key evolutionary innovations and their ecological mechanisms. Historical Biology. 10:151–173.

HilleRisLambers J., Adler P.B., Harpole W.S., Levine J.M., Mayfield M.M. 2012. Rethinking Community Assembly through the Lens of Coexistence Theory. Annual Review of Ecology, Evolution, and Systematics. 43:227–248.

Hoorn C., Wesselingh F.P., ter Steege H., Bermudez M.A., Mora A., Sevink J., Sanmartín I., Sanchez-Meseguer A., Anderson C.L., Figueiredo J.P., Jaramillo C., Riff D., Negri F.R., Hooghiemstra H., Lundberg J., Stadler T., Särkinen T., Antonelli A. 2010. Amazonia Through Time: Andean Uplift, Climate Change, Landscape Evolution, and Biodiversity. Science. 330:927–931.

How R.A., Kitchener D.J. 1997. Biogeography of Indonesian snakes. Journal of Biogeography. 24:725–735.

Humboldt A. von, Bonpland A. 1807. Essai sur la géographie des plantes. Paris, France: Schoell.

Husson L., Boucher F.C., Sarr A.-C., Sepulchre P., Cahyarini S.Y. 2020. Evidence of Sundaland’s subsidence requires revisiting its biogeography. Journal of Biogeography. 47:843–853.

Inger R.F., Voris H.K. 2001. The biogeographical relations of the frogs and snakes of Sundaland. Journal of Biogeography. 28:863–891.

IUCN. 2022. The IUCN Red List of Threatened Species. Version 2022-2. Available from https://www.iucnredlist.org.

Jablonski D. 2001. Lessons from the past: Evolutionary impacts of mass extinctions. Proceedings of the National Academy of Sciences. 98:5393–5398.

Jetz W., Pyron R.A. 2018. The interplay of past diversification and evolutionary isolation with present imperilment across the amphibian tree of life. Nature Ecology and Evolution. 2:850–858.

Jetz W., Thomas G.H., Joy J.B., Hartmann K., Mooers A.O. 2012. The global diversity of birds in space and time (Sup). Nature. 491:444–448.

Jønsson K.A., Fjeldså J. 2006. Determining biogeographical patterns of dispersal and diversification in oscine passerine birds in Australia, Southeast Asia and Africa. Journal of Biogeography. 33:1155–1165.

Jønsson K.A., Fjeldså J., Ericson P.G.P., Irestedt M. 2007. Systematic placement of an enigmatic Southeast Asian taxon *Eupetes macrocerus* and implications for the biogeography of a main songbird radiation, the Passerida. Biology Letters. 3:323–326.

Lillegraven J.A., Thompson S.D., McNab B.K., Patton J.L. 1987. The origin of eutherian mammals. Biological Journal of the Linnean Society. 32:281–336.

Macarthur R., Levins R. 1967. The Limiting Similarity, Convergence, and Divergence of Coexisting Species. The American Naturalist. 101:377–385.

MacArthur R.H. 1965. Patterns of Species Diversity. Biological Reviews. 40:510–533.

Matthew W.D. 1915. Climate and evolution. Annals of the New York Academy of Sciences. 24:171–318.

May-Collado L.J., Kilpatrick C.W., Agnarsson I. 2015. Mammals from ‘down under’: a multi-gene species-level phylogeny of marsupial mammals (Mammalia, Metatheria). PeerJ. 3:e805.

Meijaard E. 2003. Mammals of south-east Asian islands and their Late Pleistocene environments. Journal of Biogeography. 30:1245–1257.

Menéndez I., Gómez Cano A.R., Cantalapiedra J.L., Peláez-Campomanes P., Álvarez-Sierra M.Á., Hernández Fernández M. 2021. A multi-layered approach to the diversification of squirrels. Mammal Review. 51:66–81.

Mercer J.M., Roth V.L. 2003. The Effects of Cenozoic Global Change on Squirrel Phylogeny. Science. 299:1568–1572.

Meseguer A.S., Antoine P.-O., Fouquet A., Delsuc F., Condamine F.L. 2020. The role of the Neotropics as a source of world tetrapod biodiversity. Global Ecology and Biogeography. 29:1565–1578.

Meseguer A.S., Condamine F.L. 2020. Ancient tropical extinctions at high latitudes contributed to the latitudinal diversity gradient. Evolution. 74:1966–1987.

Miller E.C., Román-Palacios C. 2021. Evolutionary time best explains the latitudinal diversity gradient of living freshwater fish diversity. Global Ecology and Biogeography. 30:749–763.

Miller M.J., Bermingham E., Klicka J., Escalante P., do Amaral F.S.R., Weir J.T., Winker K. 2008. Out of Amazonia again and again: episodic crossing of the Andes promotes diversification in a lowland forest flycatcher. Proceedings of the Royal Society B: Biological Sciences. 275:1133–1142.

Mishler B.D. 2023. Spatial phylogenetics. Journal of Biogeography. n/a.

Mittelbach G.G., Schemske D.W., Cornell H.V., Allen A.P., Brown J.M., Bush M.B., Harrison S.P., Hurlbert A.H., Knowlton N., Lessios H.A., McCain C.M., McCune A.R., McDade L.A., McPeek M.A., Near T.J., Price T.D., Ricklefs R.E., Roy K., Sax D.F., Schluter D., Sobel J.M., Turelli M. 2007. Evolution and the latitudinal diversity gradient: Speciation, extinction and biogeography. Ecology Letters. 10:315–331.

Moore B. 1920. The Ecological Society and Its Opportunity. Science. 51:67–68.

Myers N., Mittermeier R.A., Mittermeier C.G., da Fonseca G.A.B., Kent J. 2000. Biodiversity hotspots for conservation priorities. Nature. 403:853–858.

Paradis E., Schliep K. 2019. ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R. Bioinformatics. 35:526–528.

Pennell M.W., Eastman J.M., Slater G.J., Brown J.W., Uyeda J.C., Fitzjohn R.G., Alfaro M.E., Harmon L.J. 2014. Geiger v2.0: An expanded suite of methods for fitting macroevolutionary models to phylogenetic trees. Bioinformatics. 30:2216–2218.

Perrigo A., Hoorn C., Antonelli A. 2020. Why mountains matter for biodiversity. Journal of Biogeography.:315–325.

Pianka E.R. 1981. Diversity and adaptive radiations of Australian desert lizards. Ecological biogeography of Australia. p. 1376–1392.

Pimiento C., Bacon C.D., Silvestro D., Hendy A., Jaramillo C., Zizka A., Meyer X., Antonelli A., Bacon C.D. 2020. Selective extinction against redundant species buffers functional diversity. Proceedings of the Royal Society B: Biological Sciences. 287:20201162.

Pinzon J.E., Tucker C.J. 2014. A non-stationary 1981-2012 AVHRR NDVI3g time series. Remote Sensing. 6:6929–6960.

Pyron R.A. 2014a. Temperate extinction in squamate reptiles and the roots of latitudinal diversity gradients. Global Ecology and Biogeography. 23:1126–1134.

Pyron R.A. 2014b. Biogeographic analysis reveals ancient continental vicariance and recent oceanic dispersal in amphibians. Systematic Biology. 63:779–797.

Pyron R.A., Costa G.C., Patten M.A., Burbrink F.T. 2015. Phylogenetic niche conservatism and the evolutionary basis of ecological speciation. Biological Reviews. 90:1248–1262.

R Core Team. 2023. R: A Language and Environment for Statistical Computing. Vienna, Austria: R Foundation for Statistical Computing.

Rabosky D.L. 2009. Ecological limits and diversification rate: Alternative paradigms to explain the variation in species richness among clades and regions. Ecology Letters. 12:735–743.

Rabosky D.L., Donnellan S.C., Talaba A.L., Lovette I.J. 2007. Exceptional among-lineage variation in diversification rates during the radiation of Australia’s most diverse vertebrate clade. Proceedings of the Royal Society B: Biological Sciences. 274:2915–2923.

Rabosky D.L., Hutchinson M.N., Donnellan S.C., Talaba A.L., Lovette I.J. 2014. Phylogenetic disassembly of species boundaries in a widespread group of Australian skinks (Scincidae: *Ctenotus*). Molecular Phylogenetics and Evolution. 77:71–82.

Rahbek C., Borregaard M.K., Antonelli A., Colwell R.K., Holt B.G., Nogues-Bravo D., Rasmussen C.M.Ø., Richardson K., Rosing M.T., Whittaker R.J., Fjeldså J. 2019. Building mountain biodiversity: Geological and evolutionary processes. Science (New York, N.Y.). 365:1114–1119.

Redding D.W., Mooers A.O. 2006. Incorporating evolutionary measures into conservation prioritization. Conservation Biology. 20:1670–1678.

Revell L.J. 2012. phytools: An R package for phylogenetic comparative biology (and other things). Methods in Ecology and Evolution. 3:217–223.

Ricklefs R.E. 1987. Community Diversity: relative roles of local and regional processes. Science. 235:167–171.

Ricklefs R.E. 2004. A comprehensive framework for global patterns in biodiversity. Ecology Letters. 7:1–15.

Ricklefs R.E. 2006. Evolutionary diversification and the origin of the diversity-environment relationship. Ecology. 87:3–13.

Roll U., Meiri S., Farrell M., Davies J., Gittleman J., Wiens J., Stephens P. 2021. GARD 1.5 range shapefiles used in: Global diversity patterns are explained by diversification rates at ancient, not shallow, timescales. .

Romdal T.S., Araújo M.B., Rahbek C. 2013. Life on a tropical planet: niche conservatism and the global diversity gradient. Global Ecology and Biogeography. 22:344–350.

Ruthven A.G. 1920. The Environmental Factors in the Distribution of Animals. Geographical Review. 10:241–248.

Schemske D.W., Mittelbach G.G., Cornell H.V., Sobel J.M., Roy K. 2009. Is There a Latitudinal Gradient in the Importance of Biotic Interactions? Annual Review of Ecology, Evolution, and Systematics. 40:245–269.

Seeholzer G.F., Brumfield R.T. 2023. Speciation-by-Extinction. Systematic Biology.:syad049.

Sheldon F.H., Lim H.C., Moyle R.G. 2015. Return to the Malay Archipelago: the biogeography of Sundaic rainforest birds. J Ornithol. 156:91–113.

Siler C.D., Oaks J.R., Welton L.J., Linkem C.W., Swab J.C., Diesmos A.C., Brown R.M. 2012. Did geckos ride the Palawan raft to the Philippines? Journal of Biogeography. 39:1217–1234.

Skinner A., Hugall A.F., Hutchinson M.N. 2011. Lygosomine phylogeny and the origins of Australian scincid lizards. Journal of Biogeography. 38:1044–1058.

Stebbins G.L. 1974. Flowering plants: evolution above the species level. Harvard University Press.

Stephens P.R., Wiens J.J. 2003. Explaining species richness from continents to communities: The time-for-speciation effect in emydid turtles. American Naturalist. 161:112–128.

Tejero-Cicuéndez H., Patton A.H., Caetano D.S., Šmíd J., Harmon L.J., Carranza S. 2022. Reconstructing Squamate Biogeography in Afro-Arabia Reveals the Influence of a Complex and Dynamic Geologic Past. Systematic Biology. 71:261–272.

Thompson J.B., Davis K.E., Dodd H.O., Wills M.A., Priest N.K. 2023. Speciation across the Earth driven by global cooling in terrestrial orchids. Proceedings of the National Academy of Sciences. 120:e2102408120.

Title P.O., Bemmels J.B. 2018. ENVIREM: an expanded set of bioclimatic and topographic variables increases flexibility and improves performance of ecological niche modeling. Ecography. 41:291–307.

Title P.O., Swiderski D.L., Zelditch M.L. 2022. EcoPhyloMapper: An r package for integrating geographical ranges, phylogeny and morphology. Methods in Ecology and Evolution. 13:1912–1922.

Tonini J.F.R., Beard K.H., Ferreira R.B., Jetz W., Pyron R.A. 2016. Fully-sampled phylogenies of squamates reveal evolutionary patterns in threat status. Biological Conservation. 204:23–31.

Townsend T.M., Leavitt D.H., Reeder T.W. 2011. Intercontinental dispersal by a microendemic burrowing reptile (Dibamidae). Proceedings of the Royal Society B: Biological Sciences. 278:2568–2574.

Tucker C.M., Cadotte M.W. 2013. Unifying measures of biodiversity: understanding when richness and phylogenetic diversity should be congruent. Diversity and Distributions. 19:845–854.

Tucker C.M., Cadotte M.W., Carvalho S.B., Davies T.J., Ferrier S., Fritz S.A., Grenyer R., Helmus M.R., Jin L.S., Mooers A.O., Pavoine S., Purschke O., Redding D.W., Rosauer D.F., Winter M., Mazel F. 2017. A guide to phylogenetic metrics for conservation, community ecology and macroecology. Biological Reviews. 92:698–715.

Upham N.S., Esselstyn J.A., Jetz W. 2019. Inferring the mammal tree: Species-level sets of phylogenies for questions in ecology, evolution, and conservation. PLoS Biology. 17:1–44.

Van Den Bergh G.D., De Vos J., Sondaar P.Y. 2001. The Late Quaternary palaeogeography of mammal evolution in the Indonesian Archipelago. Palaeogeography, Palaeoclimatology, Palaeoecology. 171:385–408.

Vasconcelos T., O’Meara B.C., Beaulieu J.M. 2022. Retiring “Cradles” and “Museums” of Biodiversity. The American Naturalist. 199:195–204.

Vásquez-Restrepo J.D., Ochoa-Ochoa L.M., Flores-Villela O., Velasco J.A. 2023. Deconstructing the dimensions of alpha diversity in squamate reptiles (Reptilia: Squamata) across the Americas. Global Ecology and Biogeography. 32:250–266.

Velasco J.A., Pinto-Ledezma J.N. 2022. Mapping species diversification metrics in macroecology: Prospects and challenges. Frontiers in Ecology and Evolution. 10.

Vidal-García M., Keogh J.S. 2015. Convergent evolution across the Australian continent: ecotype diversification drives morphological convergence in two distantly related clades of Australian frogs. Journal of Evolutionary Biology. 28:2136–2151.

Voris H.K. 2000. Maps of Pleistocene sea levels in Southeast Asia: shorelines, river systems and time durations. Journal of Biogeography. 27:1153–1167.

Voskamp A., Baker D.J., Stephens P.A., Valdes P.J., Willis S.G. 2017. Global patterns in the divergence between phylogenetic diversity and species richness in terrestrial birds. Journal of Biogeography. 44:709–721.

Wallace A.R. 1876. The geographical distribution of animals. New York, USA: Harper and Brothers.

Wallace A.R. 1878. Tropical nature, and other essays. Macmillan and Company.

Webb D.S. 1976. Mammalian faunal dynamics of the great American interchange. Paleobiology. 2:220–234.

Weir J.T., Bermingham E., Schluter D. 2009. The Great American Biotic Interchange in birds. Proceedings of the National Academy of Sciences. 106:21737–21742.

Whittaker R.H. 1975. Communities and ecosystems. Macmillan Publishing.

Wiens J.J. 2011. The causes of species richness patterns across space, time, and clades and the role of “ecological limits.” Quarterly Review of Biology. 86:75–96.

Wiens J.J., Kozak K.H., Silva N. 2013. Diversity and niche evolution along aridity gradients in North American lizards (Phrynosomatidae). Evolution. 67:1715–1728.

Wilson M.F.J., O’Connell B., Brown C., Guinan J.C., Grehan A.J. 2007. Multiscale Terrain Analysis of Multibeam Bathymetry Data for Habitat Mapping on the Continental Slope. Marine Geodesy. 30:3–35.

Wilting A., Sollmann R., Meijaard E., Helgen K.M., Fickel J. 2012. Mentawai’s endemic, relictual fauna: is it evidence for Pleistocene extinctions on Sumatra? Journal of Biogeography. 39:1608–1620.

Yonezawa T., Segawa T., Mori H., Campos P.F., Hongoh Y., Endo H., Akiyoshi A., Kohno N., Nishida S., Wu J., Jin H., Adachi J., Kishino H., Kurokawa K., Nogi Y., Tanabe H., Mukoyama H., Yoshida K., Rasoamiaramanana A., Yamagishi S., Hayashi Y., Yoshida A., Koike H., Akishinonomiya F., Willerslev E., Hasegawa M. 2017. Phylogenomics and Morphology of Extinct Paleognaths Reveal the Origin and Evolution of the Ratites. Current Biology. 27:68–77.