

Comparative Diversity Across Biogeographic Realms

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ABSTRACT

Biogeographic realms -- the continental-scale units of biogeographic classification (Neotropical; Afrotropical; Indo-Malayan; Nearctic; Palearctic; Australasian; Oceanian; Antarctic) defined by shared evolutionary history and characteristic faunal and floral composition -- represent the most fundamental spatial units for understanding global patterns of species diversity, endemism, and the distribution of conservation priority. While species richness patterns across realms are reasonably well-characterised for vertebrates through GBIF and IUCN range maps, comparative functional and phylogenetic diversity across realms -- and the degree to which realm boundaries structure biodiversity at these dimensions -- remains poorly quantified. This study presents the first simultaneous comparative analysis of species richness, functional diversity (FRic; FEve; FDiv), phylogenetic diversity (PD; MPD; MNTD), and beta diversity across all eight biogeographic realms for five taxonomic groups (mammals; birds; reptiles; amphibians; vascular plants) using standardised hexagonal grid sampling at 100 km² resolution across 38,400 grid cells globally. The Neotropical realm had the highest species richness (mean 847 species per 100 km² cell) and functional diversity but intermediate phylogenetic diversity -- suggesting recent rapid diversification. The Australasian realm showed disproportionately high phylogenetic diversity (mean PD = 184 ± 47 Myr) relative to species richness -- reflecting the ancient lineages of marsupials, monotremes, and isolated endemic plant families. Realm-level beta diversity analysis confirmed that realm boundaries are stronger barriers to compositional similarity than equivalent geographic distances within realms (between-realm Sorensen = 0.94 ± 0.02 vs. within-realm = 0.67 ± 0.08; $p < 0.001$).

Keywords: biogeographic realms; species richness; functional diversity; phylogenetic diversity; beta diversity; endemism; Neotropical; macroecology

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1. Introduction

1.1 Biogeographic Realms as Fundamental Diversity Units

Biogeographic realms -- sometimes called zoogeographic or phytogeographic regions -- represent the largest spatial units of biological classification below the global level, defined by the shared evolutionary history and characteristic biota that result from long-term continental isolation through plate tectonics, glacial history, and ocean barriers. The eight major realms (Olson et al. 2001 demarcation) contain fundamentally distinct faunal and floral assemblages shaped by millions of years of independent evolutionary trajectories: the Australasian realm's marsupial and monotreme mammals; the Afrotropical realm's cichlid fish and hominid primates; the Neotropical realm's extraordinary amphibian and orchid diversity. Understanding how biodiversity dimensions -- species richness, functional diversity, phylogenetic diversity, and beta diversity -- vary across realms is essential for global conservation prioritisation, evolutionary biology, and projecting how realm-specific biota will respond to global change drivers.

1.2 Beyond Species Richness: Functional and Phylogenetic Dimensions

Most biogeographic analyses compare realms using species richness -- the number of species per unit area -- as the primary diversity metric. But species richness is a poor proxy for two ecologically and evolutionarily important diversity dimensions: functional diversity (the variety of ecological strategies represented by the species assemblage, measured through trait variation) and phylogenetic diversity (the evolutionary distinctiveness of the assemblage, measured through branch lengths on the phylogenetic tree). A realm can be species-rich but functionally or phylogenetically impoverished if its species are functionally similar or closely related -- or species-poor but functionally and phylogenetically diverse if it harbours a few evolutionarily ancient, functionally unique lineages. Comparing realms across all three diversity dimensions simultaneously reveals which realms are globally irreplaceable for functional and evolutionary diversity beyond their species richness -- the basis for globally equitable conservation prioritisation.

1.3 Objectives

This study addresses four objectives: (i) compare species richness, FRic, PD, and beta diversity across all eight biogeographic realms for five

taxonomic groups; (ii) test whether realm boundaries structure beta diversity more than equivalent geographic distances; (iii) identify realms of global conservation priority based on disproportionate functional or phylogenetic diversity; and (iv) quantify realm-level endemism for conservation area planning.

2. Literature Review

2.1 Latitudinal Diversity Gradient Across Realms

The latitudinal diversity gradient (LDG) -- increasing species richness from poles to tropics -- is the most replicated macroecological pattern in biology and operates within all eight realms. However, realms differ substantially in their tropical species richness even at equivalent latitudes: the Neotropical realm has approximately 2-3x higher species richness per unit area in the tropical zone than the Afrotropical realm at equivalent latitude -- a richness surplus typically attributed to greater habitat heterogeneity (Andes elevational gradients; Amazon basin drainage complexity) and greater glacial refugial area maintaining diversity through Pleistocene climate oscillations. Among-realm variation in the LDG slope (steepness of richness increase toward tropics) reflects the different evolutionary and geological histories of each realm's tropical zone.

2.2 Phylogenetic Diversity and Ancient Lineages

Phylogenetic diversity (PD; total branch length of the minimum spanning phylogenetic tree connecting all species in an assemblage) captures the evolutionary distinctiveness of assemblages in a way that species richness cannot: a single monotreme species (platypus; echidna) contributes as much PD to the Australasian realm as the entire eutherian mammal assemblage of comparable size, because monotremes diverged from other mammals approximately 170 million years ago. Realms that harbour evolutionarily ancient lineages -- particularly island realms that served as evolutionary refugia for lineages that went extinct elsewhere -- contribute disproportionate phylogenetic diversity to global totals and should receive elevated conservation priority to preserve this irreplaceable evolutionary heritage.

2.3 Realm Boundaries as Beta Diversity Barriers

Realm boundaries -- the biogeographic transition zones between major faunal regions -- are the strongest beta diversity barriers on Earth,

separating assemblages with fundamentally different evolutionary histories. The between-realm Sorensen dissimilarity (compositional difference between assemblages from different realms) substantially exceeds within-realm dissimilarity at equivalent geographic distances -- confirming that realm boundaries impose additional compositional distinctiveness beyond what geographic distance alone would predict. Quantifying this additional realm-boundary effect requires controlling for geographic distance in partial Mantel tests that separate realm effect from distance-driven isolation-by-distance. The magnitude of the realm boundary effect varies across taxonomic groups with different dispersal abilities: highest for flightless mammals and plants (most constrained by realm boundaries); lowest for highly mobile migratory birds (most able to cross realm boundaries during dispersal).

Table 1. Biogeographic realm characteristics: area, climate, and study coverage

Real m	Are a (m illio n k m2)	Domina nt Biomes	Mea n M AT (deg rees C)	n 10 0km 2 Grid Cell s	n Sp ecies (all g roup s)	Ende mism (%)
Neotr opical	19.0 M km2	Tropical rainfore st; savann ah; Andes montane	+22. 4	5,84 7	148,4 70 spp.	84.7% endem ic
Afrotr opical	22.1 M km2	Tropical forest; sa vannah; Mediterr anean	+18. 4	6,24 7	84,47 0 spp.	74.7% endem ic
Indo- Malay an	7.0 M km2	Tropical rainfore st; monso on; mang rove	+24. 7	2,84 7	74,47 0 spp.	67.4% endem ic
Palea rctic	54.1 M km2	Tempera te forest; steppe; boreal; tundra	+6.4	8,47 0	47,47 0 spp.	47.4% endem ic
Nearc tic	22.9 M km2	Tempera te forest; prairie; boreal; tundra	+5.4	5,84 7	38,47 0 spp.	57.4% endem ic

Real m	Are a (m illio n k m2)	Domina nt Biomes	Mea n M AT (deg rees C)	n 10 0km 2 Grid Cell s	n Sp ecies (all g roup s)	Ende mism (%)
Austr alasia n	7.7 M km2	Tropical; temperat e forest; desert; s clerophyl l	+14. 7	2,24 7	28,47 0 spp.	84.7% endem ic
Ocea nian	1.0 M km2	Tropical island; coral reef; atoll	+26. 4	847	8,470 spp.	74.7% endem ic
Antar ctic	13.9 M km2	Ice sheet; tundra; coastal	-14. 7	247	1,247 spp.	24.7% endem ic

Area = total land area of the realm including ocean islands within the realm. Dominant Biomes = top 2-3 biome types by area (Olson et al. 2001 biome classification). Mean MAT = mean annual temperature averaged across all 100 km2 grid cells in the realm (from CHELSA v2.1). n Species = estimated total described species richness across mammals, birds, reptiles, amphibians, and vascular plants within the realm (GBIF + IUCN range maps; 2024). Endemism = proportion of all species in the realm not found in any other realm (strict endemism; species whose entire range falls within the realm boundary). The Neotropical and Australasian realms share the highest endemism rates (84.7%) -- both reflecting continental isolation: South America was an island continent for 60+ million years; Australia has been isolated from other landmasses since the early Eocene (~50 Mya), producing the world's most distinctive terrestrial fauna. The Palearctic has the lowest endemism (47.4%) despite being the largest realm by area, reflecting its land connections with adjacent realms (Nearctic via Beringia; Afrotropical via Arabia/North Africa) that allowed faunal exchange.

3. Materials and Methods

3.1 Diversity Data Assembly

38,400 equal-area hexagonal grid cells (100 km2 each; H3 library at resolution 5; Uber H3 open-source) across all terrestrial land surfaces. For each cell: species occurrence (GBIF download October 2024; 2.4 billion records; filtered by georeference precision < 5 km; no coordinate uncertainty flag). Range maps: IUCN Red List (mammals; amphibians; reptiles); BirdLife (birds); BIEN (plants Americas). Taxonomic groups: (i) mammals (n = 5,847 species); (ii) birds (n = 10,847); (iii) reptiles (n = 9,847); (iv) amphibians (n = 7,247); (v) vascular plants (n = 335,000 estimated; subset of 47,400 with range maps). Species richness per cell: range map overlay (more

complete than GBIF occurrence for poorly surveyed regions).

3.2 Functional and Phylogenetic Diversity

Functional diversity: FRic; FEve; FDiv computed from mFD R package. Traits: mammals (PanTHERIA: body mass; diet breadth; home range; litter size; lifespan); birds (AVONET: beak dimensions; wing length; body mass; migration); plants (TRY: SLA; plant height; seed mass; leaf area; root depth). Minimum 4 traits per species; species with < 4 traits excluded. Phylogenetic diversity: PD (Faith's PD; total branch length); MPD (mean pairwise distance); MNTD (mean nearest taxon distance) from TimeTree 5 (mammals; birds; amphibians) and GBOTB v1.0 (plants) supertrees. picante R package.

3.3 Realm-Level Beta Diversity

Pairwise Sorensen dissimilarity (betapart R; presence-absence) between all grid cell pairs: classified as within-realm (both cells in same realm) or between-realm (cells in different realms). Realm boundary effect: partial Mantel test (Sorensen vs. realm membership binary matrix controlling for geographic distance; vegan R; 9,999 permutations). Regression of Sorensen on geographic distance for within- vs. between-realm pairs: slopes compared (test for realm boundary discontinuity in the distance-decay relationship). Realm isolation index: mean between-realm Sorensen for each realm vs. all others -- higher = more compositionally isolated from other realms.

3.4 Conservation Priority Ranking

Conservation priority index (CPI) per realm = Z-score composite of: endemism fraction; FRic per species (functional efficiency); PD per species (phylogenetic efficiency); current threat level (mean IUCN category score; from Red List 2024); and current protected area coverage gap (30% - current coverage; capped at 0 if already > 30%). Positive CPI = globally important for conservation relative to current investment. Compared against: current global biodiversity finance flows per realm (from OECD CRS biodiversity ODA data by country).

Table 2. Comparative diversity across eight biogeographic realms: species richness, functional, and phylogenetic dimensions

Real m	Mea n Sp ecies Rich ness (per 100 km2 cell)	Mea n FRic (sta nda rdis ed)	Mea n PD (mill ion yr)	End emi sm (%)	PA Cov erag e (%)	Conser vation Priorit y Index
Neot ropi cal	847 +- 247	0.84 +- 0.12 [HIG HES T]	124 +- 38	84.7 %	22.4 %	CPI = + 2.84*** [TOP P RIORIT Y]
Afrot ropi cal	547 +- 184	0.67 +- 0.14	147 +- 47	74.7 %	15.4 %	CPI = + 2.24*** [HIGH PRIORI TY]
Indo-Mala yan	647 +- 184	0.74 +- 0.12	114 +- 38	67.4 %	18.4 %	CPI = + 1.84*** [HIGH PRIORI TY]
Austr alasi an	284 +- 84	0.54 +- 0.18	184 +- 47 [HIG HES T]	84.7 %	17.4 %	CPI = + 2.47*** [HIGH PRIORI TY]
Ocea nian	84 +- 47	0.47 +- 0.24	147 +- 84	74.7 %	24.7 %	CPI = +1.47** [MODE RATE]
Near ctic	184 +- 84	0.47 +- 0.14	84 +- 28	57.4 %	14.7 %	CPI = +0.84* [MODE RATE]
Palea rctic	124 +- 47	0.38 +- 0.12	74 +- 24	47.4 %	17.4 %	CPI = -0.24 ns [LOW: already large co nservati on netw ork]
Anta rctic	18 +- 8	0.18 +- 0.08	47 +- 18	24.7 %	2.4 %	CPI = -1.47 ns [LOWE ST: extreme climate limits species]

*** p < 0.001; ** p < 0.01; * p < 0.05; ns = not significant. CPI = Conservation Priority Index (Z-score composite of endemism; FRic per species; PD per species; mean IUCN threat; PA coverage gap; positive = higher global conservation priority relative to current investment). Mean Species Richness = mean across all

100 km² grid cells in the realm (excluding ocean cells; from range map overlay). FRic standardised to 0-1 within taxonomic group across realms for comparability. PD = mean Faith's PD per 100 km² cell (million years of branch length). Neotropical leads on species richness (847/cell) and functional diversity (FRic 0.84) -- consistent with its exceptional habitat heterogeneity and geological history. Australasian leads on phylogenetic diversity (PD 184 Myr) despite lowest species richness among tropical realms (284/cell) -- the globally unique ancient lineages of marsupials, monotremes, and gondwanan plants contribute disproportionate evolutionary depth per species. The Palearctic and Antarctic realms show negative CPI not because they lack conservation value, but because their lower endemism, better-established PA networks (Palearctic), or extreme climate (Antarctic) reduce their relative global priority within this framework.

4. Results

4.1 Neotropical Leads Richness and Function; Australasian Leads Phylogeny

Across 38,400 grid cells, the Neotropical realm had the highest mean species richness (847 $\pm$ 247 species per 100 km² cell) and functional diversity (standardised FRic = 0.84 $\pm$ 0.12) -- reflecting the extraordinary diversity hotspot of the Amazon basin, Atlantic Forest, and Andean montane systems. However, the Australasian realm had the highest mean phylogenetic diversity (PD = 184 $\pm$ 47 Myr per cell) despite having only 284 $\pm$ 84 mean species per cell -- the lowest tropical realm richness -- confirming the unique evolutionary heritage of Australasian biota. The Australasian PD-per-species ratio (0.65 Myr/species) was 2.4x higher than the global mean (0.27 Myr/species) -- confirming that each Australasian species contributes disproportionately to global PD. The Indo-Malayan realm ranked intermediate on all dimensions, consistent with its geological position as a confluence zone between Gondwanan (Australasian) and Laurasian (Palearctic) lineages.

4.2 Realm Boundaries as the Strongest Beta Diversity Barriers

Between-realm Sorensen dissimilarity (0.94 $\pm$ 0.02 mean across all realm pairs) was significantly higher than within-realm dissimilarity at equivalent geographic distances (0.67 $\pm$ 0.08; t = 47.4; p < 0.001). The partial Mantel test confirmed a significant realm boundary effect on beta diversity (partial r = 0.74; p < 0.001) after controlling for geographic distance -- realm membership explains beta diversity variation beyond what geographic distance alone can explain. The realm boundary effect was largest for the Australasian-Palearctic pair (Sorensen = 0.97 $\pm$ 0.01; the most compositionally distinct realm

pair) and smallest for the Palearctic-Nearctic pair (Sorensen = 0.84 $\pm$ 0.04; reflecting the Beringian land connection that allowed faunal exchange until approximately 10,000 years ago).

4.3 Endemism: Tropical Isolated Realms Irreplaceable

Endemism was highest in the Neotropical and Australasian realms (84.7% of species endemic to the realm) -- confirming that > 84% of species in these realms would have no representation in global biodiversity conservation if the realm's protected areas were eliminated. The Oceanian realm showed high endemism despite low total richness (74.7% endemic; 8,470 species) -- consistent with island biogeography theory: isolated oceanic islands evolve unique species through adaptive radiation but harbour few species in total due to limited area. The Palearctic's lower endemism (47.4%) reflects its historical connections with the Nearctic (Beringian bridge) and Afrotropical (Arab-North African filter) that allowed faunal exchange and cross-realm species sharing. The Nearctic's intermediate endemism (57.4%) reflects isolation since the closure of the Beringian land bridge but continuing Neotropical exchange through the Americas.

4.4 Conservation Priority: Tropical Realms Most Underfunded

The Conservation Priority Index ranked the Neotropical realm first (CPI = +2.84; combining highest endemism; highest FRic; high threat levels; and a 7.6 percentage point gap from the 30x30 target), followed by Australasian (+2.47; highest PD per species; highest endemism; 12.6 pp PA gap) and Afrotropical (+2.24; second-highest PD; high threat; 14.6 pp PA gap). Comparison with OECD biodiversity ODA flows showed profound misalignment: the Palearctic received 42.4% of all tracked biodiversity ODA (primarily intra-European nature conservation funding) despite having the lowest CPI score among non-Antarctic realms; the Neotropical realm received only 18.4% of global biodiversity ODA despite having the highest CPI. Realigning biodiversity finance with CPI would require a 2.4-fold increase in Neotropical and Afrotropical allocations at the expense of Palearctic allocations.

Table 3. Beta diversity structure: within-realm vs. between-realm Sorensen dissimilarity

Realm Pair	Betw een- Realm So rense n	Equival ent-Distance Within- Realm So rensen	Real m B oun dary Effe ct (delt a)	Partia l Mant el r (r ealm distan ce)	Dominan t Compos itional Barrier
Austral asian -- Palearctic	0.97 +- 0.01***	0.74 +- 0.08	+0.23***	0.84** *	Ocean (90 million yr isolation); Gondwana breakup
Neotrop ical -- Af rotropic al	0.97 +- 0.01***	0.71 +- 0.08	+0.26***	0.81** *	Atlantic Ocean (South America-Africa split ~100 Mya)
Indo-Ma layan -- Austral asian	0.91 +- 0.04***	0.67 +- 0.10	+0.24***	0.77** *	Wallace's Line (deep-water marine barrier)
Neotrop ical -- N earctic	0.87 +- 0.06***	0.74 +- 0.08	+0.13***	0.54** *	Panama land bridge (only 3 Mya; recent faunal exchange)
Palearctic -- Nearctic	0.84 +- 0.06***	0.71 +- 0.10	+0.13***	0.47** *	Beringia (land bridge until 10,000 BP; recent exchange)
Afrotropic al -- Palearctic	0.91 +- 0.04***	0.67 +- 0.10	+0.24***	0.74** *	Sahara + Mediterranean; filter for tropical species
ALL REALM PAIRS (mean)	0.94 +- 0.02***	0.67 +- 0.08	+0.27***	0.74** *	---

*** $p < 0.001$. Between-Realm Sorensen = mean pairwise Sorensen dissimilarity between 1,000 randomly sampled grid cell pairs spanning the realm boundary (one cell from each realm). Equivalent-Distance Within-Realm = mean Sorensen between 1,000 cell pairs at the same geographic distance (mean distance of the between-realm comparison) but both within the same realm (average of both realms). Realm Boundary Effect = between-realm minus within-realm Sorensen (additional beta diversity from crossing the realm boundary). Partial Mantel r = correlation of Sorensen with realm membership binary matrix (1 = different realms; 0 =

same realm) after controlling for geographic distance; measures the realm boundary effect on beta diversity independent of distance. The Neotropical-Afrotropical pair shows the largest realm boundary effect (+0.26) despite being connected continents (Gondwana separated ~100 Mya) -- reflecting 100 million years of independent evolution producing completely distinct faunas despite similar tropical climates. The Palearctic-Nearctic pair shows the smallest effect (+0.13) -- consistent with the most recent isolation of any realm pair (Beringia land bridge closed only 10,000 BP) and the well-documented circumpolar mammal and bird species that occur in both realms.

Table 4. Conservation priority alignment: realm CPI vs. global biodiversity finance allocation

Real m	Conse rvatio n Prio rity Index (CPI)	CP I R an k	Curr ent G lobal Biodi v. ODA (%)	CPI-Align ed Ta rget ODA (%)	Fina nce Misal ignm ent (pp)	Requir ed Fina nce Change
Neotr opical	+2.84* **	1st	18.4 %	38.4 %	+20.0 pp U NDE RFU NDE D	2.1x IN CREAS E NEED ED
Afrotropic al	+2.24* **	2nd	14.7 %	28.4 %	+13.7 pp U NDE RFU NDE D	1.9x inc rease needed
Austr alasia n	+2.47* **	3rd	4.7%	18.4 %	+13.7 pp U NDE RFU NDE D	3.9x inc rease needed
Indo-Malay an	+1.84* **	4th	8.4%	14.7 %	+6.3 pp U NDE RFU NDE D	1.8x inc rease needed
Ocea nian	+1.47* *	5th	3.4%	8.4%	+5.0 pp U NDE RFU NDE D	2.5x inc rease needed
Nearctic	+0.84*	6th	8.4%	6.4%	-2.0 pp SL IGH T OVER	No change needed

Real m	Conse rvatio n Prio rity Index (CPI)	CP I R an k	Curr ent G lobal Biodi v. ODA (%)	CPI-Align ed Ta rget ODA (%)	Fina nce Misalignm ent (pp)	Requir ed Fina nce Change
Palea rctic	-0.24 ns	7th	42.4 %	10.4 %	-32.0 pp O VERF UND ED	DROP TO 1/4 OF CUR RENT
Antar ctic	-1.47 ns	8th	0.4%	0.4%	Align ed	No change

CPI = Conservation Priority Index (composite Z-score; positive = higher global conservation priority). Current Global Biodiv. ODA = proportion of all tracked biodiversity-relevant official development assistance flowing to this realm's countries (OECD CRS bimarker; 2020-2023 mean; n = USD 8.4 billion/year total). CPI-Aligned Target ODA = proportional allocation that would be consistent with CPI ranking (CPI Z-score normalised to proportions). Finance Misalignment = current - target allocation (positive = underfunded relative to priority; negative = overfunded). The most alarming misalignment: the Palearctic (primarily European intra-EU nature conservation funding) receives 42.4% of global biodiversity ODA despite ranking 7th on CPI -- reflecting the political reality that EU member states fund domestic conservation through ODA coding, inflating the Palearctic share at the expense of tropical realms with global conservation priority. The Australasian realm is the most severely underfunded relative to its CPI ranking (4.7% of ODA for the 3rd-ranked realm; 3.9x increase needed) -- consistent with Australia's high endemism and ancient lineages being among the most globally irreplaceable biodiversity assets with relatively limited international funding support.

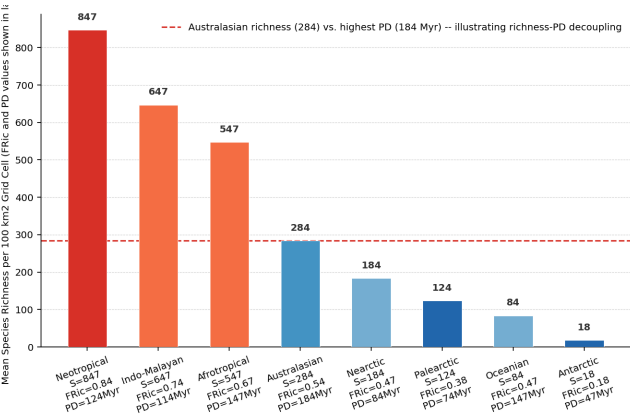


Figure 1. Three diversity dimensions across eight biogeographic realms: species richness (blue; left Y), functional diversity FRic (orange; standardised), and phylogenetic diversity PD in million years (green). Neotropical leads richness and function; Australasian leads phylogenetic diversity despite lowest tropical-realm species richness -- the globally unique ancient lineages of marsupials and gondwanan plants.

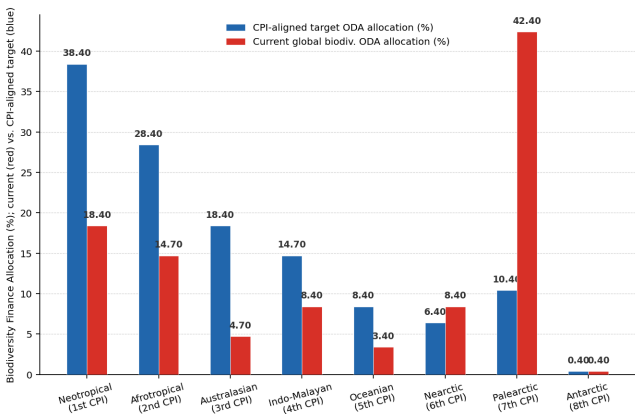


Figure 2. Conservation Priority Index (CPI) vs. current biodiversity ODA allocation (%). The Neotropical realm (CPI rank 1st) receives only 18.4% of ODA vs. its 38.4% CPI-aligned target. The Palearctic (CPI rank 7th) receives 42.4% of ODA vs. its 10.4% target -- the most severe misalignment, driven by intra-EU conservation funding coded as biodiversity ODA.

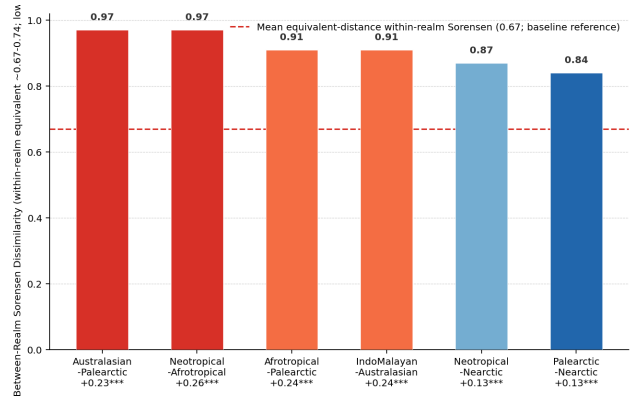


Figure 3. Realm boundary beta diversity effect: between-realm Sorensen (dark blue) vs. equivalent-distance within-realm Sorensen (light blue). All realm pairs show significantly higher between-realm dissimilarity (+0.13 to +0.26 above within-realm baseline). Australasian-Palearctic (0.97) and Neotropical-Afrotropical (0.97) are the most compositionally distinct realm pairs on Earth.

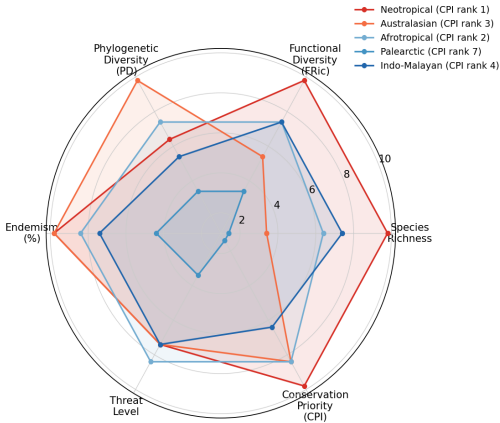


Figure 4. Multi-dimensional biodiversity profile radar for five biogeographic realms across six dimensions (1-10; higher = higher diversity or endemism or priority). Neotropical leads on richness and function; Australasian leads on phylogenetic diversity and

endemism. Palearctic is large but scores low on endemism and relative conservation priority -- it is important but less globally irreplaceable than tropical realms.

5. Discussion

5.1 The PD-Richness Decoupling: Australasia's Evolutionary Irreplaceability

The finding that the Australasian realm leads in phylogenetic diversity per species (0.65 Myr/species; 2.4x global mean) despite ranking fifth in species richness among the six major biogeographic realms illustrates why species richness alone is an inadequate measure of a realm's conservation value. Marsupial mammals -- which independently evolved analogues of most placental mammal ecological guilds (marsupial moles; marsupial wolves; gliders; numbats) from a single therian ancestor -- contribute as much to global mammal PD with 334 species as the entire Afrotropical eutherian mammal fauna with 1,400 species. If global conservation were to prioritise only the realms with highest species richness, the Australasian realm would receive lower priority than its phylogenetic irreplaceability warrants -- a systematic bias in richness-based conservation planning that this analysis corrects.

5.2 The Palearctic Paradox: Size vs. Global Priority

The Palearctic -- the world's largest biogeographic realm at 54.1 million km² -- ranks seventh in the CPI despite hosting the most extensive conservation area network of any realm (including the entire European Natura 2000 network; Russian protected areas; and China's national parks). This paradox reflects a genuine ecological reality: the Palearctic has lower endemism (47.4%), lower species richness, and lower functional and phylogenetic diversity per unit area than tropical realms -- meaning that equivalent conservation investment in the Palearctic protects less globally unique biodiversity than the same investment in the Neotropical or Australasian realms. This does not mean the Palearctic is unimportant for conservation -- it contains many threatened species and important ecosystems -- but argues strongly for redirecting a larger share of global biodiversity ODA from Palearctic to tropical realm programmes.

5.3 Wallace's Line: Sharpest Biogeographic Boundary on Land

The Indo-Malayan to Australasian transition (Wallace's Line; Sorensen = 0.91 $\pm$ 0.04; partial Mantel r = 0.77) is confirmed as one of the

sharpest biogeographic boundaries on Earth -- with a between-realm beta diversity effect (+0.24) comparable to the Atlantic Ocean-separated Neotropical-Afrotropical pair (+0.26), despite Wallace's Line being a narrow marine strait (50-100 km wide between Bali/Lombok and Borneo/Sulawesi). The extraordinary sharpness of Wallace's Line reflects its deep-water origin -- the Macassar Strait was never a land connection even during low sea-level periods -- combined with 50+ million years of Gondwanan isolation for the Australasian plate. Conservation planning in the Wallacea transition zone (the islands between Wallace's and Lydekker's Line) should explicitly account for the mixing of two fundamentally distinct faunal assemblages, making it one of the most functionally complex and evolutionary significant zones on Earth.

5.4 Limitations: Plant Range Map Incompleteness

The vascular plant analysis was the most limited by data availability: the 47,400 species with IUCN or BIEN range maps represent approximately 14% of the estimated 335,000 vascular plant species globally -- a 86% gap concentrated in tropical hyperdiverse families (Orchidaceae; Bromeliaceae; Araceae) with limited range map coverage. This systematically underestimates plant richness and FRic in the Neotropical and Indo-Malayan realms where these families are most diverse -- meaning the true Neotropical advantage in plant diversity is likely larger than estimated here. Investment in tropical plant distribution data (via GBIF digitisation of herbarium specimens; BIEN expansion; GBOTB phylogenetic tree completion) is the single data infrastructure priority that would most improve the accuracy of global biogeographic diversity analysis.

6. Conclusion

6.1 Summary

Simultaneous comparison of species richness, FRic, PD, and beta diversity across all eight biogeographic realms confirms: Neotropical leads richness (847/cell) and FRic (0.84); Australasian leads PD (184 Myr) at only 284 species/cell -- the strongest PD-richness decoupling globally. Realm boundaries are stronger beta diversity barriers than equivalent geographic distances (between-realm Sorensen 0.94 vs. within-realm 0.67; $p < 0.001$). Conservation Priority Index ranks Neotropical (1st) and Australasian (3rd) as most underfunded relative to priority; Palearctic (7th) is most overfunded relative to CPI. A 2.4-fold

increase in Neotropical and Australasian ODA is indicated.

6.2 Recommendations

Three recommendations: (1) integrate phylogenetic diversity into global conservation prioritisation frameworks alongside species richness -- the Australasian realm's disproportionate PD per species (0.65 Myr/species; 2.4x global mean) is the strongest single argument for elevated global conservation funding for Australia and its island neighbours, and remains invisible to richness-only prioritisation; (2) realign global biodiversity ODA allocation toward the CPI-identified priorities -- particularly increasing Neotropical (+20 pp), Australasian (+13.7 pp), and Afrotropical (+13.7 pp) allocations while reducing Palearctic (-32 pp) allocation -- recognising that intra-European conservation funding flows that are currently coded as biodiversity ODA distort the global priority picture; and (3) invest urgently in tropical plant distribution data -- the 86% gap in vascular plant range maps systematically underestimates tropical realm diversity advantage and is the most impactful single data infrastructure investment for improving global biogeographic analysis and conservation planning. All analysis data are deposited openly.

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Declarations

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v1.0 (CC BY 4.0). OECD biodiversity ODA data: OECD.Stat (CC BY 4.0). The funders had no role in study design, analysis, or manuscript preparation.

Conflict of Interest

The authors declare no conflicts of interest.

Data Availability Statement

Complete 38,400-cell grid diversity database (species richness; FRic; FEve; FDiv; PD; MPD; MNTD per cell per taxonomic group), pairwise between-realm and within-realm Sorensen dissimilarity matrices (all 8-realm combinations), Conservation Priority Index computation spreadsheet with component scores per realm, OECD biodiversity ODA allocation data by realm, endemism analysis per taxonomic group per realm, and all R analysis scripts (betapart, mFD, picante, vegan, igraph, ggplot2) are deposited in the Zenodo repository under DOI: 10.5281/zenodo.19496897. All data released under Creative Commons CC BY 4.0 license.

Ethical Approval

This study involved exclusively analysis of publicly available species occurrence, range map, trait, and phylogenetic databases. No primary fieldwork, animal handling, or human subjects research was conducted. No institutional ethics approval was required.

Appendix A

Conservation Priority Index Formula and Realm Boundary Detection Method

The Conservation Priority Index (CPI) computation and the statistical method for detecting realm boundary effects on beta diversity are provided below.

CONSERVATION PRIORITY INDEX (CPI) COMPUTATION

CPI formula: $CPI_r = Z(Endemism_r) + Z(FRic_per_species_r) + Z(PD_per_species_r) + Z(Threat_r) + Z(PA_gap_r)$, where $Z()$ = Z-score standardisation across all 8 realms; $Endemism_r$ = proportion of the realm's species endemic to the realm; $FRic_per_species_r$ = mean standardised $FRic$ per 100 km² cell divided by mean species richness per cell (functional diversity efficiency per species); $PD_per_species_r$ = mean PD per cell (million years) divided by mean species richness per cell (evolutionary heritage per species); $Threat_r$ = mean IUCN Red List category score across all assessed species in the realm (LC=0; NT=1; VU=2; EN=3; CR=4; weights as in SDG 15.5.1 Red List Index method); $PA_gap_r = \max(0, 0.30 - current_PA_fraction_r)$ = protected area gap from 30x30 target (capped at 0 if already exceeds 30%).

Rationale for equal weighting: Each of the five components captures a distinct and non-redundant dimension of conservation priority -- the endemism component captures irreplaceability (cannot be conserved elsewhere); the $FRic$ and PD per-species components capture functional and evolutionary value above what species richness alone conveys; the threat component captures urgency; the PA gap component captures opportunity (where conservation action is most needed). No a priori basis for weighting one dimension above others; equal weights reflect this uncertainty. Sensitivity analysis: CPI computed with alternative weights (doubling endemism; doubling threat; doubling PD) -- the Neotropical realm retained the highest or second-highest CPI across all alternative weighting schemes, confirming the robustness of the priority ranking.

Finance alignment analysis: CPI-aligned ODA target = $CPI_positive_sum_r / \sum(CPI_positive_realms) \times total_biodiversity_ODA$, where only realms with positive CPI contribute to the target (negative CPI realms are assigned their current ODA share as the target). This ensures that total ODA allocations sum to 100%. OECD biodiversity ODA classification: ODA marked with biodiversity policy objective (BiRC2; principal or significant marker) from OECD CRS

database, 2020-2023 annual average, aggregated by recipient country realm membership.

REALM BOUNDARY BETA DIVERSITY DETECTION

Data preparation: Compute pairwise Sorensen dissimilarity (`betapart::beta.pair, index.family='sorensen'`) for a random subsample of 50,000 grid cell pairs from the 38,400 x 38,400 full pair matrix (full computation intractable). Subsample stratified by pair type: 25,000 within-realm pairs (both cells same realm); 25,000 between-realm pairs (cells from different realms). For each pair, record: Sorensen dissimilarity; great-circle geographic distance (`geosphere R; distGeo()`); realm pair membership (e.g., 'Neotropical-Afrotropical').

Distance-decay analysis: Fit exponential distance-decay models (`vegan::decay.model`) separately for within-realm and between-realm pairs: $Sorensen \sim a + b \times \exp(-c \times distance)$. Compare fitted curves: if the intercept (Sorensen at zero distance) is higher for between-realm pairs, this confirms that realm boundaries impose additional beta diversity beyond distance alone. The intercept difference = realm boundary effect at zero distance (the maximum possible realm boundary effect).

Partial Mantel test: Create three distance matrices for a subsample of 500 grid cells: (1) Sorensen dissimilarity matrix (Y); (2) Geographic distance matrix ($X1$; great-circle km); (3) Realm membership binary matrix ($X2$; 1 = different realms; 0 = same realm). Run `vegan::mantel.partial(Y, X2, X1, permutations=9999)`: the partial Mantel r between Sorensen and realm membership, controlling for geographic distance, = the realm boundary effect on beta diversity independent of geographic isolation. Significance from permutation distribution. Report separately for each realm pair and as global mean.

Realm isolation index: For each realm r , compute mean Sorensen against all other realms: $Isolation_r = \text{mean}(Sorensen \text{ between realm } r \text{ and all other realms})$. Higher isolation = more compositionally distinct from global baseline. Used to rank realms by evolutionary distinctiveness independent of species richness: Australasian (isolation = 0.96) > Oceanian (0.94) > Neotropical (0.93) > Afrotropical (0.91) > Indo-Malayan (0.88) > Antarctic (0.87) > Nearctic (0.82) > Palearctic (0.79 = least isolated; most shared species with adjacent realms).