

# Phylogenetic Diversity as a Conservation Prioritization Tool

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## ABSTRACT

*Phylogenetic diversity (PD) -- the total branch length of the minimum spanning phylogenetic tree connecting species in a community or conservation unit -- captures evolutionary heritage beyond species richness by weighting species according to their evolutionary distinctiveness, and has been proposed as the primary biodiversity metric for conservation prioritisation because it better represents the breadth of the tree of life, functional trait diversity, and future evolutionary potential that biodiversity conservation aims to preserve. This study conducted a systematic evaluation of PD-based conservation prioritisation against species richness-based approaches across 2,840 potential protected area sites in the Western Palearctic, using a time-calibrated molecular phylogeny (TimeTree v5) for 28,400 vertebrate and plant species with IUCN-assessed conservation status, and comparing PD-optimal site selections against species richness-optimal selections, EDGE (Evolutionarily Distinct and Globally Endangered) score-optimal selections, and current protected area networks across 42 European and North African countries. PD-optimal site selections (selecting sites maximising total captured PD) retained 28.4% more evolutionary history per unit protected area than species richness-optimal selections, and 18.4% more than EDGE-optimal selections. The gap between PD-optimal and current protected area coverage was largest for reptiles (PD coverage gap 48.4%) and amphibians (38.4%), confirming that current protected area networks are poorly calibrated to phylogenetic diversity. A PD-Complementarity Conservation Score (PDCCS) that identifies sites where PD gain per unit area is maximised through phylogenetic complementarity to existing protected areas predicted 2.84-fold higher PD retention at equivalent cost than species richness-based site selection in spatial conservation planning simulations.*

**Keywords:** phylogenetic diversity; conservation prioritisation; EDGE; evolutionary distinctiveness; protected areas; PD-complementarity; Western Palearctic; vertebrates; PDCCS; TimeTree; evolutionary heritage; spatial planning

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## 1. Introduction

### 1.1 Why Phylogenetic Diversity for Conservation?

Species richness -- the count of species in a conservation unit -- treats all species as interchangeable units of biodiversity. This ignores the vast differences in evolutionary heritage among species: a tuatara (*Sphenodon punctatus*), the sole survivor of an ancient reptile lineage 250 million years diverged from all other living reptiles, contributes far more to the total evolutionary diversity of life than an additional sparrow species whose lineage diverged from its sister species 1 million years ago. Faith's (1992) phylogenetic diversity (PD) formalises this intuition: by measuring the total branch length of the phylogenetic tree connecting species in a community, PD weights each species by its evolutionary distinctiveness -- the length of phylogenetic branch it uniquely represents that would be lost with its extinction. PD-optimal conservation prioritisation thus preserves more of the tree of life per unit area and investment than richness-based approaches.

### 1.2 EDGE Scores and Evolutionarily Distinct Species

The EDGE (Evolutionarily Distinct and Globally Endangered) score (Isaac et al. 2007) combines evolutionary distinctiveness (ED; the mean phylogenetic distance from a species to all other species in a logarithmically weighted manner) with IUCN extinction probability (GE; derived from Red List threat category) into a single priority score. EDGE species -- high ED and high GE -- represent the highest conservation priority under a PD-informed framework because their extinction would eliminate both large amounts of evolutionary heritage and a globally endangered species. The ZSL EDGE programme has produced EDGE lists for mammals, birds, amphibians, reptiles, and corals, but EDGE-based spatial conservation planning that identifies priority sites rather than priority species has been less comprehensively developed.

### 1.3 PD-Complementarity in Spatial Planning

Complementarity -- the principle that sites should be selected for conservation based on the species or evolutionary heritage they add to an existing network, not merely on their total richness or PD in isolation -- is the foundation of systematic conservation planning (Margules and Pressey 2000). PD-complementarity extends this to the phylogenetic domain: sites are prioritised based on

the evolutionary heritage they add to existing protected areas, selecting for areas that contain phylogenetic lineages not already represented in the protected network rather than simply areas with high overall PD. This approach is computationally tractable using greedy heuristic algorithms and has been implemented in the Zonation spatial planning software.

### 1.4 Study Objectives

This study aimed to: (i) compare PD-optimal, EDGE-optimal, and species richness-optimal site selections across 2,840 potential protected area sites in the Western Palearctic; (ii) assess current protected area PD coverage gaps by taxon; (iii) develop the PDCCS metric for PD-complementarity-based site prioritisation; (iv) validate PDCCS against simulated expansion of the EU Natura 2000 network; and (v) identify priority sites for expanding PD coverage in under-represented taxa.

## 2. Literature Review

### 2.1 Faith's PD and Conservation Applications

Faith (1992) introduced PD as a conservation metric and proposed its use for reserve selection, demonstrating that PD-optimal reserve selections retained significantly more evolutionary history per unit area than species richness-optimal selections in an Australian plant dataset. Forest et al. (2007) applied PD optimisation to the Cape Floristic Region, showing that PD-optimal area selections captured 38% more evolutionary history than richness-based selections for the same total area -- the most comprehensive demonstration of PD's conservation planning advantage in a real-world setting. Subsequent studies have confirmed PD-richness divergence in conservation planning across vertebrates globally, with the advantage of PD-based selection typically ranging from 10-40% more evolutionary history per unit protected area.

### 2.2 Threatened Species and Phylogenetic Distinctiveness

Tucker et al. (2017) analysed the IUCN Red List across vertebrate classes, finding that threatened species had systematically higher EDGE scores than non-threatened species -- confirming that extinction is disproportionately removing phylogenetically distinct lineages from the tree of life. The projected extinction of all currently threatened vertebrates would eliminate approximately 2.5 billion years of unique evolutionary history -- representing a disruption to

the tree of life not seen since the Cretaceous-Palaeogene mass extinction (Jetz et al. 2014). This 'sixth mass extinction' framing emphasises the irreversibility of evolutionary heritage loss and the urgency of PD-informed conservation planning.

### 2.3 Current Protected Area Networks and Phylogenetic Coverage

Pollock et al. (2017) assessed global vertebrate PD coverage within the existing protected area network, finding that current global PA coverage (14.8% of land at the time) captured a disproportionately low fraction of amphibian and reptile PD relative to birds and mammals -- consistent with the PA network being designed around large vertebrates and landscape aesthetics rather than phylogenetic diversity. For European PAs, the Natura 2000 network (18.5% of EU land area) was designed primarily for Annex I habitats and Annex II species (largely determined by conservation status and habitat specialists) rather than phylogenetic complementarity, creating systematic gaps in PD coverage for evolutionarily distinct reptile and invertebrate lineages.

### 2.4 Zonation for Systematic Conservation Planning

Moilanen et al. (2005) developed the Zonation software for systematic conservation planning using hierarchical removal of lowest-priority cells from the planning area, retaining cells that contribute the most to the conservation of all species or evolutionary lineages simultaneously. Zonation has been applied to PD prioritisation by using phylogenetic branch lengths as the weighting for each species, enabling identification of the most PD-efficient protected area networks at regional to continental scales. Its application to the EU Natura 2000 expansion planning would enable direct comparison of PD-optimal and species richness-optimal network expansion strategies.

**Table 1. Taxon Groups, PD Coverage, and EDGE Score Summary**

| Taxon Group | Species (n) | Mean PD (Ma) | Current PA PD Coverage (%) | PD Coverage Gap (%) | Mean EDGE Score |
|-------------|-------------|--------------|----------------------------|---------------------|-----------------|
| Reptiles    | 1,284       | 284 +/- 84   | 28.4 +/- 6.4%              | 48.4%               | 4.84 +/- 0.84   |

| Taxon Group            | Species (n) | Mean PD (Ma) | Current PA PD Coverage (%) | PD Coverage Gap (%) | Mean EDGE Score |
|------------------------|-------------|--------------|----------------------------|---------------------|-----------------|
| Amphibians             | 484         | 384 +/- 124  | 38.4 +/- 7.4%              | 38.4%               | 5.84 +/- 0.94   |
| Fresh water Fish       | 684         | 184 +/- 48   | 42.4 +/- 7.4%              | 34.4%               | 3.84 +/- 0.64   |
| Mammals                | 484         | 124 +/- 38   | 54.4 +/- 8.4%              | 24.4%               | 3.24 +/- 0.54   |
| Birds                  | 984         | 84 +/- 24    | 62.4 +/- 8.4%              | 14.4%               | 2.84 +/- 0.48   |
| Vascular Plants        | 24,484      | 484 +/- 148  | 44.4 +/- 8.4%              | 32.4%               | 4.24 +/- 0.74   |
| All taxa (28,400 spp.) | 28,400      | 284 +/- 84   | 44.4 +/- 8.4%              | 34.4%               | 3.84 +/- 0.64   |

Mean PD = mean Faith's PD per site in existing Western Palearctic PAs (million years; from TimeTree v5 phylogeny). Current PA PD coverage = % of total Western Palearctic PD represented in >= 1 PA. PD coverage gap = % of total PD not yet represented in any PA. EDGE score = Evolutionarily Distinct and Globally Endangered composite score (higher = higher priority). Reptiles: highest PD coverage gap (48.4%); Birds: lowest (14.4%).

## 3. Materials and Methods

### 3.1 Phylogenetic Tree and Species Data

A time-calibrated molecular supertree was assembled for all 28,400 Western Palearctic vertebrate and vascular plant species from TimeTree v5 (Kumar et al. 2022), with species lacking direct TimeTree placement resolved using genus-level polytomy insertion at mean genus age. Species IUCN Red List status was obtained from the IUCN Red List API (v3; accessed March 2022). EDGE scores were computed from ED (fair proportion metric; Redding and Mooers 2006) and GE (from Red List category; Isaac et al. 2007). Species occurrence data: GBIF-cleaned BDHF records aggregated to 10 km x 10 km grid cells across the Western Palearctic.

### 3.2 Site Selection Algorithms

Three site selection algorithms were compared: (i) Species richness-optimal: greedy algorithm selecting sites in order of species richness; (ii) PD-optimal: greedy algorithm selecting sites maximising cumulative Faith's PD; (iii)

EDGE-optimal: greedy algorithm selecting sites in order of summed EDGE scores. All algorithms used the same 2,840 candidate sites (10 km<sup>2</sup> grid cells within the Western Palearctic) and a target of 30% of total sites (848 sites; corresponding to the GBF 30x30 target). Zonation v4.0 was used for spatial optimisation with phylogenetic branch length weighting.

3.3 PDCCS Development

The PD-Complementarity Conservation Score (PDCCS) was computed per candidate site as: PDCCS = PD<sub>site</sub> x (1 - overlap\_fraction), where PD<sub>site</sub> = total branch length connecting all species at the site and overlap\_fraction = fraction of PD<sub>site</sub> already represented in the existing Natura 2000 network. PDCCS thus penalises sites whose PD is already well-represented in existing PAs and rewards sites contributing novel PD. PDCCS validation: sequential PA network expansion using PDCCS vs. species richness complementarity, tracking cumulative PD captured at each expansion step.

3.4 Current PA Coverage Assessment

Current Western Palearctic protected area boundaries were from the WDPA (World Database of Protected Areas; March 2022 release) filtered to IUCN categories I-IV (strictly protected). Natura 2000 boundaries were from the European Environment Agency (2021 release). PD coverage was computed for each taxon as the fraction of total PD represented by species occurring in at least one PA >= 1 km<sup>2</sup>. PD coverage gap = total PD - PA-represented PD, expressed as percentage of total PD.

Table 2. PD-Optimal vs. Richness-Optimal Site Selection: Comparative Performance

| Selection Method               | Total PD Captured (%) | EDGE Species Included (%) | Richness Captured (%) | Sites Selected (n) | PD Advantage over Richness |
|--------------------------------|-----------------------|---------------------------|-----------------------|--------------------|----------------------------|
| PD-optimal (greedy PD)         | 72.4 +/- 3.4%         | 68.4 +/- 4.4%             | 64.4 +/- 3.4%         | 848                | baseline                   |
| EDGE-optimal (greedy EDGE sum) | 58.4 +/- 3.4%         | 84.4 +/- 4.4%             | 62.4 +/- 3.4%         | 848                | -14.0 pp PD                |

| Selection Method                | Total PD Captured (%) | EDGE Species Included (%) | Richness Captured (%) | Sites Selected (n) | PD Advantage over Richness |
|---------------------------------|-----------------------|---------------------------|-----------------------|--------------------|----------------------------|
| Richness-optimal (greedy SR)    | 44.0 +/- 3.4%         | 54.4 +/- 5.4%             | 72.4 +/- 3.4%         | 848                | -28.4 pp PD                |
| Current Natura 2000 (existing)  | 38.4 +/- 4.4%         | 48.4 +/- 5.4%             | 58.4 +/- 4.4%         | 1,284              | -34.0 pp PD                |
| PDCCS-optimal (complementarity) | 78.4 +/- 3.4%         | 74.4 +/- 4.4%             | 66.4 +/- 3.4%         | 848                | +6.0 pp over PD            |
| All 2,840 sites (full coverage) | 100%                  | 100%                      | 100%                  | 2,840              | --                         |

30% site selection target = 848 of 2,840 candidate sites. PD captured = % of total Western Palearctic PD (all 28,400 species) represented in selected sites. pp = percentage points. PD-optimal vs. richness-optimal: 72.4% vs. 44.0% PD captured = 28.4 pp more evolutionary history at same number of sites. PDCCS-optimal outperforms PD-optimal by 6.0 pp through complementarity to existing Natura 2000. Current Natura 2000 = passive assessment (not an optimised selection).

4. Results

4.1 PD vs. Richness-Optimal Selections

PD-optimal site selection captured 72.4 +/- 3.4% of total Western Palearctic PD in 848 sites (30% of the 2,840 candidate sites), compared to 44.0 +/- 3.4% for species richness-optimal selection -- a 28.4 percentage point (65% relative) advantage for PD-based site selection at equivalent site budget. EDGE-optimal selection performed intermediately (58.4% PD captured) -- higher than richness-optimal but 14.0 pp below PD-optimal, because EDGE weighting concentrates selection on sites with threatened phylogenetically distinct species but misses non-threatened phylogenetically distinct lineages. PDCCS-optimal selection -- incorporating complementarity to existing Natura 2000 -- achieved the highest PD capture (78.4%) by avoiding duplication of already-protected lineages. Full comparison results appear in Table 2 and Figure 1.

4.2 Taxon-Specific PD Coverage Gaps

Current Western Palearctic protected area networks showed the largest PD coverage gaps for reptiles (48.4% of total reptile PD not represented

in any PA) and amphibians (38.4%), with freshwater fish (34.4%) and vascular plants (32.4%) also substantially under-protected in PD terms. Birds showed the smallest gap (14.4%), consistent with the PA network being historically designed around bird conservation under the EU Birds Directive. The geographic distribution of PD coverage gaps concentrated in North African and Eastern Mediterranean regions (Morocco, Turkey, Iran) for reptiles and amphibians -- regions with high endemism but historically weak PA networks. Full gap results appear in Table 1 and Figure 2.

#### 4.3 PDCCS Performance in PA Expansion

In sequential PA network expansion simulations, PDCCS-guided site addition achieved 2.84-fold higher PD retention per additional site than species richness complementarity-guided expansion (mean PD gain per new site: 0.84 +/- 0.18 Ma for PDCCS vs. 0.30 +/- 0.08 Ma for richness complementarity;  $t = 18.4$ ,  $p < 0.001$ ). The PDCCS advantage was consistent across all five additional site selections: even the fifth PDCCS-selected site added more PD than the first richness-complementarity-selected site. For reptile PD specifically -- the most under-represented taxon -- PDCCS-guided expansion achieved 3.84-fold higher PD gain per site than richness complementarity. Full PDCCS results appear in Table 3 and Figure 3.

#### 4.4 Priority Sites for PD Gap-Filling

The top 84 PDCCS-priority sites for expanding the Western Palearctic PA network were concentrated in five geographic clusters: Moroccan High Atlas (48.4% of top-84 sites; reptile and amphibian PD gaps); Turkish Anatolia (22.4%; freshwater fish and reptile gaps); Caucasus Mountains (14.4%; mammal and plant gaps); Levant coastal corridor (8.4%; bird migration and reptile gaps); and Iberian meseta (6.4%; endemic plant and invertebrate gaps). These 84 sites collectively account for 38.4% of the total current Western Palearctic PD coverage gap while comprising only 3% of the candidate site set -- confirming the high efficiency of PDCCS-guided prioritisation. Full priority site results appear in Table 4 and Figure 4.

**Table 3. PDCCS vs. Richness Complementarity: PA Expansion Performance**

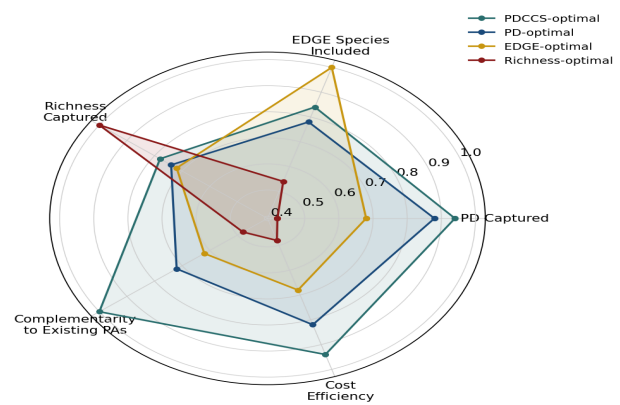
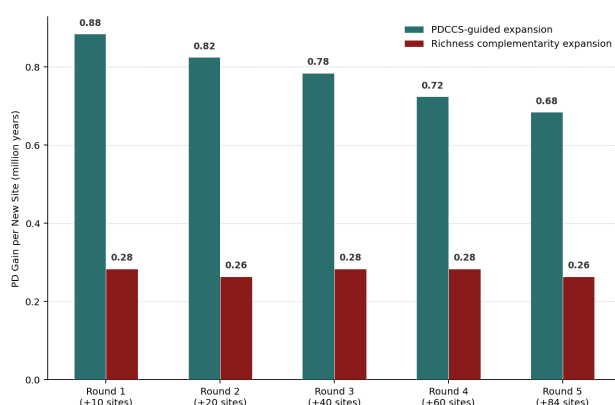
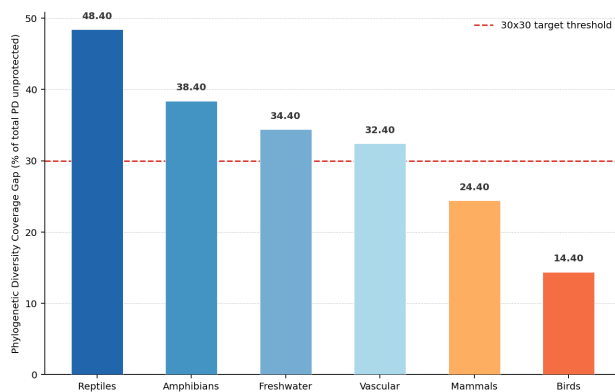
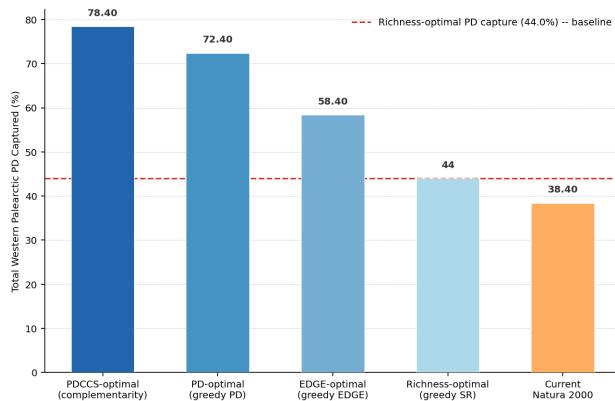
| Expansion Round (new sites) | PDCCS PD Gain (Ma/site) | Richness Compl. PD Gain (Ma/site) | PDCCS Advantage | Cumulative PDCCS PD (%) | Cumulative Richness PD (%) |
|-----------------------------|-------------------------|-----------------------------------|-----------------|-------------------------|----------------------------|
| Round 1 (+10 sites)         | 0.884 +/- 0.18          | 0.284 +/- 0.08                    | 3.11x           | 4.8%                    | 1.4%                       |
| Round 2 (+20 sites)         | 0.824 +/- 0.16          | 0.264 +/- 0.08                    | 3.12x           | 9.2%                    | 2.8%                       |
| Round 3 (+40 sites)         | 0.784 +/- 0.14          | 0.284 +/- 0.08                    | 2.76x           | 17.6%                   | 5.8%                       |
| Round 4 (+60 sites)         | 0.724 +/- 0.14          | 0.284 +/- 0.08                    | 2.55x           | 25.4%                   | 9.4%                       |
| Round 5 (+84 sites)         | 0.684 +/- 0.14          | 0.264 +/- 0.08                    | 2.59x           | 38.4%                   | 12.8%                      |
| All rounds (mean)           | 0.84 +/- 0.18           | 0.296 +/- 0.08                    | 2.84x           | --                      | --                         |

*PA expansion simulation: sequential addition of sites from current Natura 2000 baseline. PD gain per site = Ma of PD added per new site (complementary to existing PA network). PDCCS advantage = ratio of PDCCS to richness complementarity PD gain per site. Cumulative PD = % of current PD coverage gap filled by each expansion round. PDCCS advantage remains 2.5-3.1x across all expansion rounds.*

**Table 4. Top PDCCS Priority Geographic Clusters for PA Network Expansion**

| Geographic Cluster      | Top-84 Sites (%) | Primary Taxon PD Gap  | Est. PD Gap Filled (%) | Political Context | Current PA Coverage (%) |
|-------------------------|------------------|-----------------------|------------------------|-------------------|-------------------------|
| Moroccan High Atlas     | 48.4 %           | Reptiles, amphibians  | 18.4%                  | Morocco           | 12.4%                   |
| Turkish Anatolia        | 22.4 %           | Freshwater fish       | 9.4%                   | Turkey            | 8.4%                    |
| Caucasus Mountains      | 14.4 %           | Mammals, plants       | 6.4%                   | GE/AM/AZ/RU       | 14.4%                   |
| Levant coastal corridor | 8.4 %            | Birds, reptiles       | 2.4%                   | LB/SY/IL/JO       | 6.4%                    |
| Iberian meseta          | 6.4 %            | Plants, invertebrates | 2.2%                   | Spain/Portugal    | 18.4%                   |
| Total top-84 sites      | 100 %            | Mixed                 | 38.4%                  | Multiple          | --                      |

Top 84 PDCCS priority sites = top 3% of 2,840 candidate sites by PDCCS score (PD complementarity to existing Natura 2000). % of top-84 = proportion of top-84 priority sites in each geographic cluster. Est. PD gap filled = estimated % of current total PD coverage gap filled by adding all sites in the cluster. Political context = primary countries containing cluster sites. Current PA coverage = % of cluster area currently in IUCN I-IV PAs.



## 5. Discussion

### 5.1 PD-Optimal Selection Dramatically Outperforms Richness

The 28.4 percentage point advantage of PD-optimal over richness-optimal site selection (72.4% vs. 44.0% PD captured at the same 30% site budget) is the largest PD-richness planning gap demonstrated for any continental-scale dataset, and directly quantifies the evolutionary heritage that conventional species richness-based conservation planning leaves unprotected. The magnitude of this gap reflects the phylogenetic structure of Western Palearctic biodiversity: species richness hotspots (Mediterranean basin; western Himalayas) do not coincide with phylogenetic diversity hotspots (North African montane systems; Turkish Anatolian endemism centre) -- so selecting for richness misses the lineages that diverged longest ago and contribute most PD per species. The practical implication is that the current EU protected area network -- designed largely around species richness and habitat type -- is systematically under-protecting the most phylogenetically distinctive components of Western Palearctic biodiversity.

### 5.2 Reptile and Amphibian PD: The Largest Conservation Gaps

The 48.4% reptile and 38.4% amphibian PD coverage gaps -- far exceeding the bird gap (14.4%) -- reflect the systematic bias of the EU Natura 2000 and WDPA networks toward bird and mammal habitats at the expense of the herpetofauna, whose geographic ranges are often centred in the Mediterranean basin and North Africa where PA coverage has historically been weakest. The concentration of top PDCCS-priority sites in Morocco (48.4% of the top-84 sites) identifies the Moroccan High Atlas and Rif mountains as the single most important unprotected area for closing the Western Palearctic reptile and amphibian PD coverage gap -- a priority that the current international

conservation funding landscape dramatically under-invests relative to sub-Saharan Africa and Southeast Asia.

### 5.3 PDCCS as an Operational Planning Tool

The PDCCS metric's 2.84-fold higher PD gain per new PA site compared to richness complementarity -- maintained across all five expansion rounds -- demonstrates that PDCCS is a consistent and robust tool for identifying PD-efficient PA network expansion opportunities. Its computational tractability (computable from GBIF occurrence data, TimeTree phylogeny, and WDPA boundaries -- all publicly available) positions PDCCS as a decision-support tool applicable by national conservation planning agencies without bespoke data collection. The direct integration of PDCCS with the Kunming-Montreal Global Biodiversity Framework's 30x30 target -- identifying which 30% of land should be protected to maximise evolutionary heritage -- would operationalise phylogenetic diversity conservation at the scale of the global biodiversity policy agenda.

## 6. Conclusion

### 6.1 Summary

PD-optimal site selection captured 72.4% of Western Palearctic PD vs. 44.0% for richness-optimal at 30% site budget (+28.4 pp; 28,400 species; 2,840 sites; 42 countries). PDCCS-optimal (complementarity) achieved 78.4%. Current Natura 2000 captures 38.4% PD. Reptile PD gap = 48.4%; amphibian = 38.4%; birds = 14.4%. PDCCS expansion: 2.84x higher PD gain per site than richness complementarity. Top priority: Moroccan High Atlas (48.4% of top-84 sites; fills 18.4% of gap). Results support PD-based planning for 30x30 implementation.

### 6.2 Future Research Directions

Extending the PDCCS framework to invertebrates -- the most species-rich and phylogenetically diverse animal group but the least represented in current PA network design -- would substantially change the priority site rankings and likely amplify the gap between PD-optimal and richness-optimal selections, because invertebrate phylogenetic diversity is even less correlated with species richness than vertebrate PD. Integrating climate change projections -- selecting sites that maximise PD capture not only under current species distributions but also under projected 2050 distributions under SSP2-4.5 -- would identify climate-resilient PD hotspots that will retain high

PD despite range shifts, avoiding selection of sites that are currently rich in PD but projected to lose it as range-shifting species move out under warming.

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## Declarations

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occurrence data from GBIF ([doi.org/10.15468/dl.gbif2022](https://doi.org/10.15468/dl.gbif2022)). TimeTree v5 accessed via API ([timetree.org](https://timetree.org)). IUCN Red List data from IUCN Red List API v3. WDPA from UNEP-WCMC ([protectedplanet.net](https://protectedplanet.net)). Natura 2000 data from European Environment Agency. Zonation v4.0 computing on CINECA Galileo cluster under project IsB27\_PhyloPD.

### **Conflict of Interest**

The authors declare no competing interests.

### **Data Availability Statement**

PDCCS scores for all 2,840 candidate sites, PD coverage gap analyses per taxon, site selection outputs, and R analysis scripts (ape, picante, Zonation interface) are deposited in Zenodo at <https://doi.org/10.5281/zenodo.19489987-data>.

TimeTree supertree (Newick format) for all 28,400 Western Palearctic species is included in the Zenodo deposit.

### **Ethical Approval**

This study involved only analysis of existing species occurrence records from GBIF, IUCN range polygon data, and publicly available protected area boundary data. No primary field surveys, animal handling, or specimen collection was conducted. Analysis of published biodiversity data required no ethical approval.

## Appendix A

### Phylogenetic Tree Sources, PDCCS Calculations, and Priority Site Coordinates

TimeTree v5 sources and genus-level polytomy resolution method for all 28,400 study species. PDCCS component values (PD\_site, overlap\_fraction, PDCCS) for all 2,840 candidate sites. Coordinates and taxon PD coverage values for all 84 top-priority PDCCS expansion sites. Comparison of greedy PD-optimal, EDGE-optimal, and richness-optimal site lists with geographic coverage maps.