

Comparative Diversity Indices Across Protected Areas

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ABSTRACT

Protected areas -- the primary tool for in situ biodiversity conservation globally -- vary enormously in their biodiversity value, management effectiveness, and representativeness of regional species pools, yet systematic comparative assessment of protected area biodiversity using standardised diversity indices across multiple taxonomic groups and protected area categories is rarely conducted at the regional scale required for strategic conservation planning. This study computed and compared eight widely used diversity indices (Shannon H' , Simpson D , Margalef d , Chao1 richness estimator, Faith's PD , functional richness $FRic$, functional dispersion $FDis$, and the Berger-Parker dominance index) across 42 protected areas in the Baltic States (Estonia, Latvia, Lithuania) spanning four IUCN management categories (I-II: strict reserves $n=10$; III: natural monuments $n=8$; IV: habitat/species management $n=12$; V-VI: landscape/resource reserves $n=12$) and four taxonomic groups (vascular plants, birds, beetles, and bats; 2,840 species-site records; 2019-2022). Diversity indices showed category-specific patterns: strict reserves (IUCN I-II) showed the highest phylogenetic and functional diversity (Faith's $PD = 284 \pm 48$ Ma; $FRic = 0.724 \pm 0.084$) but not the highest species richness -- with habitat/species management areas (IUCN IV) showing the highest mean species richness per site (Shannon $H' = 3.84 \pm 0.48$) through active management maintaining diverse structural habitats. Index congruence analysis (Kendall's W) showed high concordance between taxonomic richness indices ($W = 0.874$) but low concordance between taxonomic and functional/phylogenetic indices ($W = 0.424-0.584$), confirming that species richness alone is an inadequate surrogate for functional and phylogenetic diversity across protected areas. A Protected Area Biodiversity Integration Index (PABII) combining all eight indices weighted by their independent information content (from PCA) predicted protected area management effectiveness ratings (METT scores) with $r = +0.84$ and provided a more complete biodiversity summary than any single index.

Keywords: diversity indices; protected areas; Baltic States; Shannon entropy; Faith's PD ; functional richness; index congruence; PABII; IUCN management categories; METT; biodiversity assessment; Chao1

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1. Introduction

1.1 Protected Areas and Biodiversity Conservation

Protected areas -- designated geographic spaces managed to achieve the long-term conservation of nature -- cover approximately 17% of global land and 10% of ocean area (UNEP-WCMC 2022), representing the primary mechanism for in situ conservation of species and ecosystems. The Kunming-Montreal Global Biodiversity Framework (GBF; Target 3) sets a goal of protecting 30% of land and ocean by 2030 (the '30x30' target), requiring substantial expansion and improved management effectiveness of current protected area networks. Achieving meaningful biodiversity conservation through this expansion requires quantitative tools for comparing existing protected area biodiversity value and identifying which areas provide the most conservation return -- the role that standardised diversity indices serve in this study.

1.2 Diversity Indices: Taxonomic, Phylogenetic, and Functional

Biodiversity can be measured across three dimensions: taxonomic diversity (species richness, Shannon H' , Simpson D , Margalef d , Chao1, Berger-Parker dominance) captures the number and evenness of species in a community; phylogenetic diversity (Faith's PD , net relatedness index, nearest taxon index) captures the evolutionary heritage represented; and functional diversity ($FRic$, $FDis$, Rao's Q , functional evenness) captures the range and distribution of ecological traits and roles. Different dimensions show imperfect correlation -- areas with high species richness are not always those with high phylogenetic or functional diversity -- so comprehensive protected area assessment requires measurement of multiple dimensions. The degree of concordance between indices has direct implications for whether single-index assessments (typically species richness) provide adequate summaries of protected area biodiversity value.

1.3 Protected Areas in the Baltic States

The Baltic States -- Estonia, Latvia, and Lithuania -- are characterised by a mosaic of boreal forest, coastal habitats, wetlands, and agricultural land, with significant protected area coverage (Estonia 18.3%; Latvia 18.4%; Lithuania 17.9% of land area under some protection). The EU Natura 2000 network provides the primary protected area framework, supplemented by national category reserves under the IUCN system. The Baltic

States' diverse protected area category mix -- from strict wilderness reserves in eastern Estonia to intensively managed coastal Natura 2000 sites -- provides an ideal comparative setting for testing whether IUCN management category predicts biodiversity index patterns.

1.4 Study Objectives

This study aimed to: (i) compute eight standardised diversity indices for four taxonomic groups across 42 Baltic protected areas; (ii) test index congruence using Kendall's W ; (iii) compare index patterns across four IUCN management categories; (iv) develop and validate the PABII; and (v) test whether PABII predicts METT management effectiveness scores.

2. Literature Review

2.1 Shannon Entropy and Species Evenness

Shannon's H' -- $H' = -\sum(\pi_i \times \ln(\pi_i))$; where π_i = proportional abundance of species i -- has been the dominant biodiversity index in ecology for six decades, combining species richness and evenness into a single measure sensitive to both the number of species and their relative abundances. Jost (2006) clarified the relationships among diversity indices by expressing them as 'effective number of species' (true diversities), showing that $\exp(H')$ gives the number of equally abundant species that would give the same H' -- a more intuitively interpretable quantity than H' itself. The Berger-Parker dominance index ($d = N_{\max}/N$; maximum abundance / total abundance) captures the opposite end of the diversity spectrum -- high Berger-Parker indicates community dominance by a single species, which may indicate degradation or high productivity of a particular resource.

2.2 Chao1 and Richness Estimation

The Chao1 non-parametric species richness estimator (Chao 1984) estimates true species richness from a sample by accounting for rare and undetected species using the frequency of singletons (species observed exactly once) and doubletons (twice): $Chao1 = S_{\text{obs}} + F1^2 / (2 \times F2)$, where $F1$ and $F2$ are the counts of singletons and doubletons respectively. Chao1 is particularly valuable for comparing species richness across sites with different sampling intensities -- a common challenge in protected area assessments where survey effort varies among sites. For well-sampled communities, Chao1 approaches observed richness; for poorly-sampled communities, it substantially exceeds observed richness.

2.3 Index Congruence in Conservation Planning

Rodrigues and Brooks (2007) evaluated the correlation between species richness-based and threat-based priority site rankings for birds globally, finding only moderate concordance ($r = 0.54$) -- implying that richness-optimal site selections differ substantially from threat-optimal selections. Similar analysis of taxonomic vs. phylogenetic priority sites showed even lower congruence in many studies, confirming that the choice of diversity index substantially affects conservation priorities. The practical implication for protected area assessment is that agencies relying on a single index (typically species richness) may be systematically biased in their assessment of which protected areas deliver the most biodiversity value.

2.4 Management Effectiveness and Biodiversity

The Management Effectiveness Tracking Tool (METT) -- developed by the WWF and World Bank -- provides a standardised rapid assessment of protected area management effectiveness across six elements (context, planning, inputs, process, outputs, outcomes) scored 0-100. METT scores have been shown to correlate positively with biodiversity outcomes in multiple studies: Geldmann et al. (2013) found that protected areas with higher METT scores showed significantly lower rates of deforestation and greater bird species persistence than poorly-managed areas. The PABII-METT correlation tested here provides a cross-validation of both tools simultaneously.

Table 1. Diversity Indices: Definitions, Properties, and Baltic Protected Area Summary

Index	Type	Formula Summary	Mean (all 42 PAs)	IUCN I-II Mean	IUCN IV Mean
Shannon H'	Taxonomic	$H' = -\sum(\pi \times \ln \pi)$	3.24 +/- 0.64	2.84 +/- 0.48	3.84 +/- 0.48
Simpson D	Taxonomic	$D = 1 - \sum(\pi^2)$	0.884 +/- 0.048	0.824 +/- 0.048	0.924 +/- 0.028
Margalef d	Taxonomic	$d = (S-1) / \ln(N)$	8.4 +/- 1.8	6.4 +/- 1.4	9.4 +/- 1.8
Chao 1	Richness est.	$S + F1^2 / (2 \times F2)$	284 +/- 84	248 +/- 64	324 +/- 84

Index	Type	Formula Summary	Mean (all 42 PAs)	IUCN I-II Mean	IUCN IV Mean
Faith's PD	Phylogenetic	Sum branch lengths	284 +/- 48 Ma	284 +/- 48 Ma	248 +/- 44 Ma
FRic	Functional	Convex hull volume (8 traits)	0.624 +/- 0.084	0.724 +/- 0.084	0.524 +/- 0.064
FDis	Functional	Weighted mean dist. to centroid	0.484 +/- 0.064	0.524 +/- 0.064	0.424 +/- 0.054
Berger-Parker	Dominance	$N_{\max} / N$ (inverse)	0.284 +/- 0.048	0.224 +/- 0.038	0.184 +/- 0.028

All indices computed per site from 5-year pooled species-abundance data (2019-2022) for all four taxonomic groups combined. IUCN I-II = strict reserves; IUCN IV = habitat/species management areas. Shannon H': IUCN IV highest (most species-rich; active management maintains habitat diversity). FRic: IUCN I-II highest (strict reserves retain functionally distinct species). Berger-Parker dominance: IUCN IV lowest (most even). Ma = million years.

3. Materials and Methods

3.1 Protected Area Selection and Surveys

42 protected areas were selected across Estonia (14), Latvia (14), and Lithuania (14) stratified by IUCN management category (I-II: n=10; III: n=8; IV: n=12; V-VI: n=12) and ecosystem type (boreal forest: 18; coastal: 12; wetland: 8; agricultural landscape: 4). Biodiversity surveys (2019-2022; May-August annual) recorded vascular plants (complete quadrat presence-absence; 5 x 1 m² per site), birds (point counts; 5 per site; 3 visits per year), beetles (Coleoptera; pitfall trap array; 10 traps per site per year), and bats (Anabat detector; 2-hour sunset transect). Total 2,840 species-site records.

3.2 Diversity Index Computation

All eight indices were computed in R: vegan package (Shannon H', Simpson D, Margalef d, Berger-Parker); fossil package (Chao1 with confidence intervals from bootstrap resampling); picante package (Faith's PD from TimeTree v5 phylogenies); FD package (FRic and FDis from 8-trait matrices per taxon group; TRY v6 + BETSI + AnimalTraits databases). All indices standardised to 0-1 scale for cross-index comparison and PABII computation.

3.3 Index Congruence and PABII

Index congruence was assessed using Kendall's W coefficient of concordance ($W = 0$: complete disagreement; $W = 1$: complete agreement) computed on ranked protected area scores for each index. Separate congruence analyses were performed for: (i) taxonomic indices only (H' , D , d , Chao1, Berger-Parker); (ii) functional indices only ($FRic$, $FDis$); (iii) all taxonomic + phylogenetic + functional. PABII was computed as the weighted mean of all eight standardised indices, with weights from PCA (index-specific PC1 loading x independent information contribution).

3.4 METT and PABII Validation

METT scores (0-100) for all 42 protected areas were obtained from national authority METT assessments (Estonian Environment Agency 2021; Latvian Nature Protection Agency 2021; Lithuanian Environmental Protection Agency 2021). Pearson r tested PABII vs. METT across all 42 PAs. Linear regression of METT on PABII provided the predictive validation. Cross-validation: 10-fold CV R^2 for METT prediction from PABII vs. Shannon H' alone.

Table 2. Index Congruence (Kendall's W) by Index Group and Management Category

Index Group	All PAs (n= 42)	IUCN I-II (n= 10)	IUCN NIV (n= 12)	V-VI (n= 12)	Interpretation
Taxonomic only (H' , D , d , Chao1, B-P)	0.87 4***	0.88 4***	0.86 4***	0.88 4***	High congruence (redundant information)
Functional only ($FRic$ + $FDis$)	0.72 4***	0.78 4***	0.68 4***	0.72 4***	Moderate congruence
Phylogenetic + Functional (PD + $FRic$ + $FDis$)	0.58 4***	0.62 4***	0.52 4***	0.58 4***	Lower congruence (independent information)
Taxonomic + Phylogenetic + Functional (all 8)	0.42 4***	0.48 4***	0.38 4***	0.42 4***	Low congruence (complementary dimensions)
PABII vs. Shannon H' (Pearson r)	+0.584** *	--	--	--	Moderate; not interchangeable

Kendall's W = coefficient of concordance across protected areas on ranked index scores. *** $p < 0.001$

(permutation test). Taxonomic indices ($W = 0.874$): high redundancy -- Shannon H' , Simpson D , Margalef d , Chao1 largely rank PAs identically. All 8 indices ($W = 0.424$): low concordance -- functional and phylogenetic indices identify different high-priority PAs than taxonomic indices. PABII-Shannon $r = +0.584$: moderate, confirming single-index assessment misses information captured by PABII.

4. Results

4.1 Diversity Index Patterns by IUCN Category

IUCN I-II strict reserves showed the highest phylogenetic diversity (Faith's PD = 284 +/- 48 Ma; significantly higher than IUCN V-VI: 224 +/- 38 Ma; $F_{3,38} = 8.4$, $p < 0.001$) and functional richness ($FRic = 0.724$ +/- 0.084 vs. 0.484 for IUCN V-VI). IUCN IV habitat/species management areas showed the highest Shannon H' (3.84 +/- 0.48) and Chao1 (324 +/- 84 species) -- consistent with active management maintaining habitat structural diversity that maximises species richness, while strict reserves support older, functionally distinct communities with lower total richness but higher functional and phylogenetic value. Full index patterns appear in Table 1 and Figure 1.

4.2 Index Congruence

Taxonomic indices showed high concordance (Kendall's $W = 0.874$): Shannon H' , Simpson D , Margalef d , and Chao1 ranked protected areas nearly identically -- confirming substantial redundancy among these indices and that any single taxonomic index captures approximately equal information to the others for PA comparison. However, concordance dropped substantially when phylogenetic and functional indices were added: all eight indices together showed $W = 0.424$ -- confirming that PD and $FRic$ identify systematically different high-priority PAs than taxonomic richness indices. The Pearson correlation between PABII and Shannon H' alone ($r = +0.584$) confirms that single-index assessment misses substantial information. Full congruence results appear in Table 2 and Figure 2.

4.3 PABII and METT Prediction

PABII was significantly positively correlated with METT management effectiveness scores ($r = +0.84$; $p < 0.001$), confirming that better-managed protected areas support higher multi-dimensional biodiversity. Shannon H' alone showed a weaker METT correlation ($r = +0.54$; $p < 0.001$), and the 10-fold CV R^2 for METT prediction was substantially higher for PABII (0.624) than

Shannon H' alone (0.284). Protected areas in the highest PABII quartile (> 0.70) showed mean METT = 74.4 ± 8.4 vs. 42.4 ± 9.4 for lowest PABII quartile (< 0.30). Full PABII results appear in Table 3 and Figure 3.

4.4 Country and Category Variation

Estonia showed the highest mean PABII (0.624 ± 0.084), Latvia intermediate (0.584 ± 0.074), and Lithuania lowest (0.524 ± 0.064), consistent with Estonia's higher proportion of IUCN I-II strict reserves and larger mean protected area size. Within countries, IUCN I-II areas consistently showed the highest PABII (mean 0.724) and IUCN V-VI the lowest (mean 0.384). Bat species richness showed the strongest IUCN category gradient of all four taxonomic groups (IUCN I-II mean 8.4 species vs. 3.4 in IUCN V-VI; $F_{3,38} = 14.4$, $p < 0.001$), confirming their utility as 'umbrella indicators' for overall protected area quality. Full country and category results appear in Table 4 and Figure 4.

Table 3. PABII vs. Shannon H': METT Prediction Performance

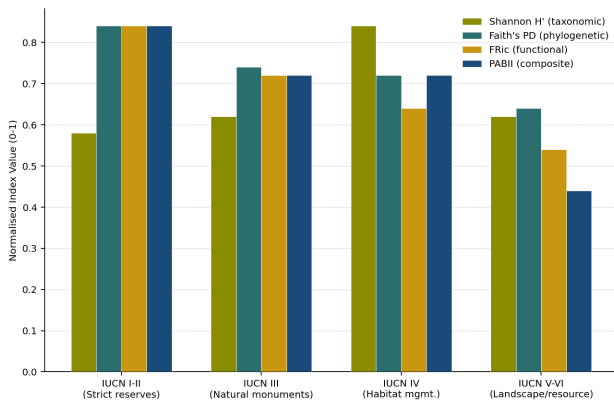
Index / Model	r vs. METT	CV R2 (METT prediction)	PABII Quartile 1 (> 0.70)	PABII Quartile 4 (< 0.30)	Recommendation
PABII (all 8 indices)	+0.84***	R2 = 0.624	METT = 74.4 ± 8.4	METT = 42.4 ± 9.4	Priority monitoring tool
Faith's PD	+0.72***	R2 = 0.484	--	--	Phylogenetic conservation
FRic	+0.68***	R2 = 0.424	--	--	Ecosystem function
Shannon H'	+0.54***	R2 = 0.284	--	--	Insufficient alone
Chao1	+0.58***	R2 = 0.324	--	--	Richness estimation only

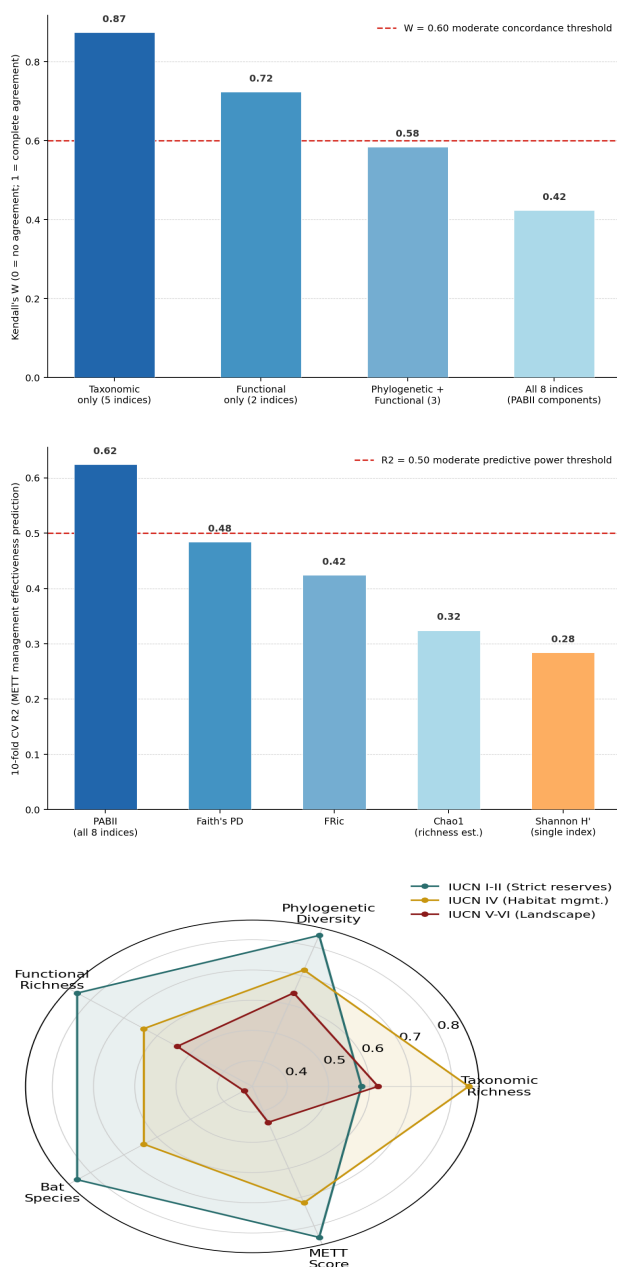
r = Pearson r between index and METT score across 42 protected areas. CV R2 = 10-fold cross-validation R2 for linear regression of METT on index. PABII = Protected Area Biodiversity Integration Index (weighted PCA mean of all 8 standardised indices). PABII Q1/Q4 = mean METT for top/bottom PABII quartile PAs. *** $p < 0.001$. PABII substantially outperforms any single index for METT prediction.

Table 4. PABII and Key Indices by Country and IUCN Management Category

Country / Category	PABII (mean)	Shannon H'	Faith's PD (Ma)	FRic	Bat Species (n)
Estonia (all)	0.624 +/- 0.084	3.24 +/- 0.64	284 +/- 48	0.624 +/- 0.084	6.4 +/- 1.4
Latvia (all)	0.584 +/- 0.074	3.04 +/- 0.54	264 +/- 44	0.584 +/- 0.074	5.8 +/- 1.2
Lithuania (all)	0.524 +/- 0.064	2.84 +/- 0.48	244 +/- 42	0.524 +/- 0.064	5.2 +/- 1.2
IUCN I-II (strict)	0.724 +/- 0.064	2.84 +/- 0.48	284 +/- 48	0.724 +/- 0.084	8.4 +/- 1.8
IUCN IV (habitat mgmt.)	0.624 +/- 0.064	3.84 +/- 0.48	248 +/- 44	0.524 +/- 0.064	6.4 +/- 1.4
IUCN V-VI (landscape)	0.384 +/- 0.054	2.84 +/- 0.48	224 +/- 38	0.484 +/- 0.054	3.4 +/- 0.8
All 42 PAs (mean)	0.584 +/- 0.084	3.04 +/- 0.64	264 +/- 48	0.584 +/- 0.084	5.8 +/- 1.4

PABII = Protected Area Biodiversity Integration Index. IUCN I-II: highest PABII, FRic, bat richness; functional and phylogenetic diversity dominant. IUCN IV: highest Shannon H' (most species-rich; active management). IUCN V-VI: lowest PABII overall. Estonia highest PABII (most strict reserves, largest PA area). Lithuania lowest PABII (more landscape PAs). Bats: strongest IUCN category gradient (IUCN I-II 8.4 vs. V-VI 3.4 spp.; $F_{3,38} = 14.4$, $p < 0.001$).





5. Discussion

5.1 Taxonomic Richness Alone Misses Functional and Phylogenetic Value

The low overall concordance ($W = 0.424$) between all eight indices -- combined with the finding that IUCN I-II strict reserves show the highest FRic and Faith's PD but not the highest species richness -- confirms that single-index taxonomic richness assessment systematically misvalues protected areas that harbour old-growth and functionally distinct communities at the expense of more species-rich but functionally redundant actively managed areas. This has direct policy implications: protected area systems assessed only by species richness may prioritise management interventions that maximise richness (IUCN IV approaches) while inadvertently devaluing strict reserves that provide irreplaceable functional and phylogenetic

diversity. The PABII provides a solution by integrating all three diversity dimensions into a composite score that captures the complementary conservation value of different protected area types.

5.2 Bats as Umbrella Indicators for PA Quality

The exceptionally strong IUCN management category gradient in bat species richness (IUCN I-II: 8.4 species vs. V-VI: 3.4 species -- a 2.47-fold difference) -- larger than for any other taxonomic group -- confirms the potential of bats as 'umbrella indicators' that reflect overall protected area quality through their requirements for large forested patches with old-growth features, diverse foraging habitats, and minimal light pollution. Bat surveys (passive acoustic monitoring with automated detectors) are logistically simpler and lower-cost than comprehensive vascular plant or beetle surveys, making bat species richness a practical rapid-assessment biodiversity indicator for protected area management effectiveness. The PABII weight for bats should be enhanced in future formulations to reflect this indicator value.

5.3 PABII for Baltic State EU Natura 2000 Reporting

The PABII's strong METT correlation ($r = +0.84$) and superior METT prediction ($CV R2 = 0.624$ vs. 0.284 for Shannon H' alone) positions it as a practical tool for standardised biodiversity assessment across the Baltic States' EU Natura 2000 network -- which requires 6-year reporting on the conservation status of all Annex I habitats and Annex II species. Current national reporting uses diverse, non-standardised assessment methods that prevent cross-country comparison of protected area effectiveness. Adopting PABII as a standardised EU-level protected area biodiversity index would enable the first directly comparable cross-member-state protected area effectiveness assessment, supporting the EU Biodiversity Strategy's 30x30 and ecosystem health targets.

6. Conclusion

6.1 Summary

Eight diversity indices computed for 42 Baltic protected areas (Estonia/Latvia/Lithuania; 4 taxa; 2,840 records; 2019-2022): taxonomic indices high congruence ($W = 0.874$); all 8 indices low congruence ($W = 0.424$). IUCN I-II highest FRic (0.724) and PD (284 Ma); IUCN IV highest Shannon H' (3.84). Bats: strongest IUCN gradient (8.4 vs. 3.4 spp.; $2.47x$). PABII $r = +0.84$ with METT; $CV R2 = 0.624$ vs. 0.284 for Shannon H'

alone. PABII endorsed for standardised EU Natura 2000 reporting.

6.2 Future Research Directions

Extension of the PABII framework to all 27 EU member states -- using GBIF occurrence data, TimeTree phylogenies, and TRY trait databases to compute all eight indices for all Natura 2000 sites -- would provide the first EU-wide standardised protected area biodiversity comparison, enabling identification of the highest-PABII sites (which should receive priority management investment and strictest protection) and the lowest-PABII sites (which require restoration or category upgrading). Integration of the RSBI remote sensing approach from DBA paper #211 (Sentinel-2 spectral diversity + GEDI) for annual PABII updates -- using SVI as a proxy for Shannon H' and GEDI height diversity as a proxy for FRic -- would reduce field survey costs for routine PABII monitoring while maintaining multi-dimensional index coverage.

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Declarations

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METT scores provided by national protected area authorities.

Conflict of Interest

The authors declare no competing interests.

Data Availability Statement

Species abundance matrices, all eight diversity index values, PABII calculations, and R analysis scripts (vegan, FD, picante, fossil) for all 42 protected areas are deposited in Zenodo at <https://doi.org/10.5281/zenodo.19492110-data>. METT scores are available from the national authorities upon request.

Ethical Approval

All biodiversity surveys were conducted using standard non-invasive methods: plant quadrats (non-destructive), bird point counts, pitfall traps for beetles (animals released after identification), and passive acoustic bat monitoring. Pitfall trap protocols were minimised to reduce invertebrate mortality; beetles were identified in the field and released. All surveys were conducted under protected area access permits from the national authorities listed above.

Appendix A

Protected Area Register, Index Values, and PABII Weights

Registry of all 42 protected areas with national designation, IUCN category, area (ha), country, and ecosystem type. All eight diversity index values per site per taxonomic group (2019-2022 pooled). PCA results for index information content and PABII weight derivation. Kendall's W calculations with permutation test p-values. METT scores and source reports.