1

No branch left behind: tracking terrestrial biodiversity from a phylogenetic completeness

perspective

Jesús N. Pinto-Ledezma[1]*, Sandra Díaz [2,3] , Benjamin S. Halpern[4,5], Colin Khoury[6,7],

Jeannine Cavender-Bares[1]*

*Equal contribution and shared first authorship

1 Department of Ecology, Evolution and Behavior, University of Minnesota, 1479 Gortner Ave,

Saint Paul, MN, 55108, USA

2 Consejo Nacional de Investigaciones Científicas y Técnicas, Instituto Multidisciplinario de

Biología Vegetal (IMBIV), CONICET, Universidad Nacional de Córdoba, Córdoba, Argentina

3 Facultad de Ciencias Exactas, Físicas y Naturales, Universidad Nacional de Córdoba, Córdoba,

Argentina

4 National Center for Ecological Analysis and Synthesis, University of California, Santa

Barbara, CA, 93101, USA

5 Bren School of Environmental Science and Management, University of California, Santa

Barbara, CA, 93106, USA

6 San Diego Botanic Garden, 230 Quail Gardens Dr., Encinitas, CA 92024, USA

7 International Center for Tropical Agriculture (CIAT), Km 17, Recta Cali-Palmira, Apartado

Aéreo 6713, 763537, Cali, Colombia

24   **Abstract**

25   Biodiversity, as we see it today, ultimately is the outcome of millions of years of evolution;

26   however, biodiversity in its multiple dimensions is changing rapidly due to increasing human

27   domination of Earth. Here, we present the "phylogenetic completeness" (PC) a concept and

28   methodology that intends to safeguard Earth's evolutionary assets that have arisen across the tree

29   of life. We performed a global evaluation of the PC approach using data from five major

30   terrestrial clades and compared the results to an approach in which species are conserved or lost

31   randomly. We demonstrate that under PC, it is possible to maximize the protection of greater

32   evolutionary assets of each clade for a given number of species extinctions. The PC approach is

33   flexible and can be used to assess biodiversity under different conservation scenarios. The PC

34   approach complements existing conservation efforts and is linked to the post-2020 Convention of

35   Biodiversity targets.

36

37

Introduction

39 Over more than 3.5 billion years of life on Earth, evolution has generated and honed a vast array

40 of innovations represented by the diversity of forms and genomes across the tree of life.

41 Contemporary species collectively represent the genetic assets that contribute to the functioning

42 of the current biosphere, and these functions in turn serve as the foundation of Nature's

43 Contributions to People (NCP) (Díaz *et al.* 2019). Put another way, species embody evolutionary

44 innovations that represent complex and unique approaches to life on Earth. These innovations

45 not only support current NCP, but are also necessary for future benefits to humanity, including

46 those not yet discovered.

47 Phylogenetic trees depict the hierarchy of life in which species are nested in larger and

48 larger clades, each descended from a more distant common ancestor (Figure 1). They provide

49 information on the breadth and variation of innovations evolution has generated and can be used

50 to inform approaches to species conservation with the goal of minimizing extinction of

51 evolutionary innovations (Faith 2002; Larkin *et al.* 2016). Close relatives typically have a high

52 proportion of shared genetics since they arose from a common ancestor at some point in the

53 comparatively recent past, and thus share many of the same innovations.

54 A wide range of phylogenetic metrics exist that capture diversity across the tree of life

55 (Tucker *et al.* 2017) and are relevant to discerning how much variation is captured under

56 different conservation scenarios. Most metrics of phylogenetic diversity are applied to

57 phylogenetic trees and represent a sum over phylogenetic branch lengths (possibly after

58 augmentation to account for other factors, such as probability of extinction). The canonical

59   example is phylogenetic diversity (PD, *sensu* (Faith 1992)), which, for a subset of species, is

60   defined as a sum of all branch lengths required to connect those species (Faith 1992, 2002).

61   In our era of rapid biodiversity loss (Tilman *et al.* 2017; Díaz *et al.* 2019) (Tilman *et al.*

62   2017; Díaz *et al.* 2019), keeping all species—the tips of the tree of life—is not realistic, and

63   indeed is impossible given recent extinction rates (Rounsevell *et al.* 2020). However, it may still

64   be possible to conserve all branches of the tree of life, depending on how deeply we define the

65   branches. This concept is the principle behind phylogenetic completeness, a concept and

66   methodology we propose here that aims to preserve Earth's evolutionary assets that have arisen

67   across the entire tree of life. Phylogenetic completeness (PC) and phylogenetic diversity (PD)

68   both aim to maintain as many branches as possible from the tree of life, recognizing it is not

69   possible to retain all species. But given the hierarchical nature of phylogenetic trees, how a

70   lineage is circumscribed—or what constitutes a "branch" that should be protected—can

71   influence the outcome. PC differs from PD in that it slices across the tree at a given point in

72   evolutionary history and defines a set of branches based on this cut off (Figure 1), using an

73   accounting framework, rather than merely maximizing phylogenetic breadth.

74   Here we conducted a series of analyses to explore the implications for conservation

75   depending on the depth in the tree of life where a "branch" is defined. The goal was to develop

76   and apply a framework for conservation of species that minimizes hemorrhaging of Earth's

77   evolutionary assets, given a fixed level of species loss that is assumed to be unavoidable. We

78   then compared the loss of PD under conservation scenarios in which the set of species targeted

79   for conservation was based on an "informed" phylogenetic completeness approach or in which

80   species conserved or lost to extinction occurred randomly.

81

82 **Methods**

83 *Phylogenetic completeness (PC) approach*

84 We developed an approach in which a phylogeny is iteratively sliced at different periods of time

85 (T_N) until a specified finish time (T_F). For example, if a phylogeny is sliced every $T_N = 2$ million

86 years until $T_F = 50$ million years, a total of 25 slice points is obtained (see also Figure 1). These

87 slice points are then used to drop all but one terminal tips—or operational taxonomic units

88 (OTU)—from the phylogeny; with this approach, we ensure that at least one OTU of each

89 lineage at a specific time (T_N) is kept. In other words, by keeping at least one OTU from each

90 lineage in the tree of life, we aim to maximize the preservation of the deepest evolutionary

91 history. At each slice point (T_N) we additionally calculated the number of species (T_{SP}) and

92 phylogenetic diversity (T_{PD}) as the simple sum of branch lengths at the specific slice point (T_N).

93

94 *Empirical assessment*

95 The empirical assessment was focused on five major terrestrial clades (seed plants, amphibians,

96 squamates, birds, and mammals). Description of the data can be found in the WebPanel 1.

97 We tested the reliability of the PC approach by slicing each phylogeny every $T_N = 100$

98 Ky until $T_F = 100$ My and calculated the T_{SP} and T_{PD} at every slice point. These metrics were

99 then used to identify change points in the phylogenetic diversity over the 100 My time period.

100 Change points were evaluated using Bayesian Multiple Changing Points (MCP) regressions. The

101 first changing point plus its credible intervals (CIs) identified by the MCP analysis were used as

102 cutoff thresholds to estimate the number and identities of OTUs to be kept. This procedure

103 allowed us to identify different change points or cutoff thresholds in the phylogenetic diversity

104   over 100 My for each clade separately and consequently prevent us establishing a fixed arbitrary

105   cutoff threshold (e.g., setting a changing point at 2 My as cutoff threshold) for all clades.

106   We compared the diversity in each clade for a PC conservation scenario, in which species

107   were managed to maintain all phylogenetic branches to random losses (RDM). In other words,

108   we removed OTUs at random until the identified cutoff threshold for each clade separately. This

109   procedure was repeated 1000 times, and at each step the T_{SP} and T_{PD} were estimated.

110   Finally, using the OTUs identities from both the PC and the random loss scenarios we

111   mapped the phylogenetic diversity of seed plants and terrestrial vertebrates globally. These maps

112   were used to estimate the difference (ΔPD) between the observed PD (PD_{OBS}) and the expected

113   PD (PD_{EXP}) under either the phylogenetic completeness (PD_{PC}) and the random loss approach

114   (PD_{RDM}).

$$\Delta PD = \frac{PD_{EXP} - PD_{OBS}}{PD_{OBS}} \; x \; 100$$

115

116   These maps represent the proportional difference between the observed (PD_{OBS}) and

117   expected (PD_{PC} or PD_{RDM}) phylogenetic diversity, where negative values suggest that a grid cell

118   will lose a proportion of its PD according to a specific conservation scenario, e.g., under the PC

119   scenario. Note that the lower CI from the Bayesian MCP regressions were used as variable cutoff

120   thresholds for each clade for mapping purposes.

121

122   *Protected areas assessment*

123   We were also interested in evaluating the role of protected areas (PAs) in protecting the

124   evolutionary history of terrestrial biodiversity. To do so, we overlayed the PAs with the

125   vertebrate and seed plants PAMs to obtain the presence-absence of species within the PAs

126   (PAM_{PA}) globally (WebPanel 1). These PAM_{PA} were then used to estimate the number of

127   species and phylogenetic diversity within each PA. Using this information, we estimate and map

128   the ΔPD between the observed PD (PD_{OBS}) and the PD within PAs (PD_{PA}). The resulting maps

129   show how much evolutionary history are currently protected within the PAs.

130

131   **Results**

132   *Phylogenetic completeness*

133   Bayesian MCP models revealed variable cutoff thresholds for each clade (Figure 2; WebTable

134   1). Based on these thresholds, losses of species ranging from 1.34% to 18.11% are estimated to

135   occur in each of the major clades (seed plants, amphibians, squamates, birds, and mammals)

136   (WebTable 1) while still safeguarding between 97.27% to 99.97% of the phylogenetic

137   diversity—i.e., of the evolutionary history of each clade (WebTable 1; Figure 2). If the lower

138   credible interval (LCI) of our Bayesian model estimates were used to define the phylogenetic

139   branches to be conserved (Figure 2; WebTable 1), a higher number of species and branches in

140   the tree of life would be safeguarded (Table 1).

141   These analyses demonstrate that if conservation efforts are focused on maintaining

142   defined branches of the tree of life it is possible to maximize the accumulated evolutionary

143   innovations that are safeguarded across all clades even when individual species go extinct.

144   Figure 3 shows the comparison between the estimates of PD under both phylogenetic

145   completeness (PC) and random loss (RDM) scenarios. Under PC, a higher number of branches

146   (Table 1) and greater evolutionary history in each clade is preserved for a given number of

147   species extinctions (Figure 3).

148   Spatial patterns of ΔPD under PC and RDM scenarios (Figure 4; WebFigure 1), show

149   how conservation informed by PC safeguards a greater proportion of evolutionary history even

150   with the same number of species extinctions. For example, for seed plants in tropical regions

151   across the world, conservation informed by PC resulted in PD loss below 10%, whereas the

152   RDM scenario resulted in 10-20 % of PD loss. Extinction patterns of terrestrial biodiversity

153   under PC and RDM scenarios at the biome level (WebFigure 2) also show greater preservation

154   of accumulated evolutionary innovations when conservation is targeted to maintain branches of

155   the tree of life. Nevertheless, we find that Tundra and Taiga biomes are susceptible to high losses

156   in PD, especially for seed plants, birds, and mammals, even under PC scenarios. In contrast,

157   tropical biomes (for both forest and grasslands) show limited losses in PD for the same threshold

158   values used to define branches, as in Tundra and Taiga biomes (WebFigure 2). These results

159   indicate that for the a given number of species extinctions, tropical biomes will lose fewer

160   branches of the tree of life and are thus less susceptible to loss of evolutionary history.

161

162   *Protected areas assessment*

163   The currently implemented PAs across the world cover an area of approximately 26,775,820

164   km—~18% of the land surface. Collectively, ~97% of the species in our dataset overlap their

165   ranges with the system of PAs globally (Table 2). Although the proportion of likely protected

166   species is high, a large proportion of the Earth's land surface, and thus most of the ranges of

167   most of these species, is not protected (Figure 4; WebFigure 3) and is threatened by land use

168   change and other human activities.

169

170   **Discussion**

171   Our "phylogenetic completeness" framework for informing biodiversity conservation focuses on

172   maintaining the accumulated evolutionary innovations across the tree of life with the intent of

173   leaving no branch behind. We introduce a rigorous approach for defining branches across clades

174   of terrestrial organisms to ascertain where in the tree of life there is high evolutionary

175   redundancy and where a single species may represent an entire branch. In doing so, we establish

176   phylogenetic branches as units of conservation priority. By defining these branches and the

177   species contained within them, the phylogenetic completeness approach provides critical

178   information on branches at risk of extinction where there is low redundancy as well as flexibility

179   in which species can targeted for conservation in cases of high redundancy. The approach is

180   particularly useful in developing conservation priorities in relation to protected areas by tracking

181   which branches of the tree of life are currently safeguarded and by identifying the branches that

182   are at highest risk—those not currently protected or with the least amount of their range

183   protected. This approach is consistent with the Convention on Biodiversity draft Milestone A.2,

184   that *the increase in the extinction rate is halted or reversed, and the extinction risk is reduced by*

185   *at least 10 per cent, with a decrease in the proportion of species that are threatened, and the*

186   *abundance and distribution of populations of species is enhanced or at least maintained.* Yet it

187   also captures elements of diversity not delineated by the CBD by accounting for the breadth of

188   evolved variation in plant and vertebrate-animal life.

189   Increasing human domination of Earth and its ecosystems is rapidly changing

190   biodiversity patterns and negatively impacting the capacity of ecosystems to provide goods and

191   services to humanity (Tilman *et al.* 2017; Díaz *et al.* 2019). Safeguarding all remaining

192   biodiversity, although desirable, is unrealistic on the basis of virtually all projections (Pimm *et*

193   *al.* 2014; Urban 2015; Tilman *et al.* 2017); the footprint of humanity is currently too large to

194   completely avoid further extinctions. Scientists have recognized the challenge of developing

195   logical conservation solutions given the complexity of stakeholders, managers, and indirect

196   actors as a 'wicked problem' that has no straightforward solution (Vane-Wright *et al.* 1991;

197   DeFries and Nagendra 2017). Focusing on the conservation of evolutionary history has been

198   hailed as an integrative way to safeguard most of the biodiversity and its functions (Faith 1992;

199   Mooers 2007). For example, a recent study by Molina-Venegas and collaborators (Molina-

200   Venegas *et al.* 2021) (Molina-Venegas *et al.* 2021) found strong evidence that plant evolutionary

201   history is tightly linked to multiple plant use categories and therefore to human well-being

202   (Molina-Venegas *et al.* 2021). These findings, among others, support the idea that conserving

203   evolutionary history is critical for future human well-being (Forest *et al.* 2007; Molina-Venegas

204   *et al.* 2021).

205   Multiple approaches have been proposed to assess changes in biodiversity focusing on

206   "hotspot" areas (spatial prioritization), or taxa (taxonomic prioritization) for conservation

207   purposes (Margules and Sarkar 2007). These approaches rely on the use of metrics that capture

208   different dimensions of biodiversity, e.g., metrics that capture evolutionary changes among a set

209   of taxa (Margules and Sarkar 2007) or the variation in form and function of taxa within

210   communities (Díaz and Cabido 2001; Petchey and Gaston 2006). Despite their usefulness for

211   assessing the state and the fate of biodiversity, most of these metrics, if not all, are sensitive to

212   information completeness. Missing information can result in misleading metric calculations and

213   inappropriate interpretations of spatial or taxonomic comparisons (e.g., Weedop *et al.* 2019). The

214   PC framework introduced here represents a complementary approach to counting numbers of

215   species or comparing levels of phylogenetic diversity to assess biodiversity under alternative

216   conservation scenarios. It provides an accounting framework that prioritizes conservation of

217   branches of the tree of life rather than individual species (Table 1; Figure 2). It also allows the

218   identification of areas susceptible to high losses of evolutionary assets (Figure 4; WebFigure 1),

219   which can be used as baseline information for spatial prioritization, providing a broader context

220   for local decision making (Chaplin-Kramer *et al.* 2022). Moreover, in the context of spatial

221   prioritization, the PC framework may be less susceptible to missing data given that it focuses on

222   the branches of the tree of life. To illustrate this point, if we consider protecting at least one

223   descendant taxon from a specific node in the phylogeny, this taxon contains genetic information

224   that captures most of the evolutionary history of the entire branch (see Figure 1). If species

225   within the branch have not yet been identified or are not readily observed, the branch itself is still

226   preserved, with the caveat that phylogenetic information remains imperfect.

227   Substantial efforts have been invested to prevent the extinction of biodiversity. In

228   particular, the establishment, expansion, and enhancement of protected areas (PAs) have

229   received considerable attention due to their critical role in protecting Earth's biodiversity and

230   preventing the erosion of its benefits to humans (Naughton-Treves *et al.* 2005; Watson *et al.*

231   2014). Despite important progress in establishing terrestrial PAs around the world (Table 2),

232   several critical areas are still unprotected, leaving many branches of the tree of life vulnerable to

233   extinction (Figure 4; WebFigure 3). Note that in our evaluation we used the species presence

234   within current PAs to estimate which species are less vulnerable to extinction for the purposes of

235   deciphering which branches of the tree of life are most at risk. We thus assume that species not

236   present in PAs are the most vulnerable to extinction and in greatest need of conservation or

237   assistance.

238   At high latitudes (tundra) an individual species frequently represents an entire

239   phylogenetic branch while at low latitudes (tropics), a branch is likely to contain many species.

240   This pattern is largely the consequence of more recent divergence times and higher speciation

241   rates in the tropics. However, the spatial scale (grain size) must also be considered, for example,

242   one hectare in a tropical forest can hold ~650 tree species more than all tree species that occur at

243   high latitudes (Coley and Kursar 2014). Despite this high diversity, tropical forests are usually

244   hyperdominated by a fraction of species (~1.4% of about 16,000 tree species estimated for the

245   Amazonian Forest are considered as hyperdominant) that are specialists to their habitats and

246   have large geographical ranges (ter Steege *et al.* 2013). The less abundant species or poorly

247   known species with small geographical ranges are potentially threatened. Although it is beyond

248   the scope of this article, PC evaluations at local and regional scales could help to identify which

249   species may be prioritized to prevent losing branches of the tree of life at local and regional

250   scales.

251   Furthermore, the combined effects of climate and land-use changes are likely to limit the

252   role of PAs in safeguarding biodiversity (Hoffmann *et al.* 2019; Asamoah *et al.* 2021). About

253   one-quarter of the PAs globally are projected to suffer rapid climate change, with small PAs

254   being the most impacted (Hoffmann *et al.* 2019; Asamoah *et al.* 2021). Advancing projections of

255   combined limits to species tolerance to climate change and migration capability without

256   assistance could be oriented towards understanding which branches of the tree of life currently

257   protected are most likely to be lost. Doing so, could help inform costly efforts to establish

258   corridors for movement within human-dominated landscapes (Gibson *et al.* 2011; Wintle *et al.*

259   2019) and assisted migration plans to target the protection of species that maintain all the

260   branches of the tree of life.

261

262   **Conclusion**

263   In our era of rapid global change and rapid biodiversity loss, conservation efforts must reckon

264   with the reality that we will not succeed in saving all species on Earth. We outline an approach

265   for conservation, which we call phylogenetic completeness, that focuses on saving the

266   accumulated innovations that have evolved in Earth's biota by counting individual branches in

267   the tree of life as units of conservation priority. The approach benefits from detailed information

268   of the tree of life that is only now sufficiently resolved to be applicable to all of life on Earth.

269   The approach complements other conservation efforts and is directly relevant to the targets of the

270   post-2020 Convention of Biodiversity.

271

Acknowledgements

272

277

Statement of Authorship

278

279   All authors contributed intellectually to the manuscript. J.C.-B. and J.N.P.-L. conceived of and

280   framed the manuscript. J.N.P.-L. performed all the statistical and spatial analyses with input from

281   J.C.-B. All authors edited the manuscript.

282

Open Research

283

Data Availability Statement

284

285   All data used in this manuscript are publicly available. Main sources are provided in the

286   WebPanel 1. R functions and examples for data analyses are publicly available at

287   https://github.com/jesusNPL/FITBITs.

288

References

290

291   Asamoah EF, Beaumont LJ, and Maina JM. 2021. Climate and land-use changes reduce the

292   benefits of terrestrial protected areas. *Nat Clim Chang* **11**: 1105–10.

293   Chaplin-Kramer R, Brauman KA, Cavender-Bares J, *et al.* 2022. Conservation needs to integrate

294   knowledge across scales. *Nat Ecol Evol* **6**: 118–9.

295   Coley PD and Kursar TA. 2014. On Tropical Forests and Their Pests. *Science* **343**: 35–6.

296   DeFries R and Nagendra H. 2017. Ecosystem management as a wicked problem. *Science* **356**:

297   265–70.

298   Díaz S, Settele J, Brondízio ES, *et al.* 2019. Pervasive human-driven decline of life on Earth

299   points to the need for transformative change. *Science* **366**: eaax3100.

300   Díaz S and Cabido M. 2001. Vive la différence: plant functional diversity matters to ecosystem

301   processes. *Trends in Ecology & Evolution* **16**: 646–55.

302   Faith DP. 1992. Conservation evaluation and phylogenetic diversity. *Biological Conservation*

303   **61**: 1–10.

304   Faith DP. 2002. Quantifying Biodiversity: a Phylogenetic Perspective. *Conservation Biology* **16**:

305   248–52.

306   Forest F, Grenyer R, Rouget M, *et al.* 2007. Preserving the evolutionary potential of floras in

307   biodiversity hotspots. *Nature* **445**: 757–60.

308   Gibson L, Lee TM, Koh LP, *et al.* 2011. Primary forests are irreplaceable for sustaining tropical

309   biodiversity. *Nature* **478**: 378–81.

310   Hoffmann S, Irl SDH, and Beierkuhnlein C. 2019. Predicted climate shifts within terrestrial

311   protected areas worldwide. *Nat Commun* **10**: 4787.

312   Larkin DJ, Jacobi SK, Hipp AL, and Kramer AT. 2016. Keeping All the PIECES:

313   Phylogenetically Informed Ex Situ Conservation of Endangered Species (N Cellinese,

314   Ed). *PLoS ONE* **11**: e0156973.

315   Margules CR and Sarkar S. 2007. Systematic conservation planning. Cambridge ; New York:

316   Cambridge University Press.

317   Molina-Venegas R, Rodríguez MÁ, Pardo-de-Santayana M, *et al.* 2021. Maximum levels of

318   global phylogenetic diversity efficiently capture plant services for humankind. *Nat Ecol*

319   *Evol* **5**: 583–8.

320   Mooers AØ. 2007. The diversity of biodiversity. *Nature* **445**: 717–8.

321   Naughton-Treves L, Holland MB, and Brandon K. 2005. THE ROLE OF PROTECTED AREAS

322   IN CONSERVING BIODIVERSITY AND SUSTAINING LOCAL LIVELIHOODS.

323   *Annu Rev Environ Resour* **30**: 219–52.

324   Petchey OL and Gaston KJ. 2006. Functional diversity: back to basics and looking forward. *Ecol*

325   *Letters* **9**: 741–58.

326   Pimm SL, Jenkins CN, Abell R, *et al.* 2014. The biodiversity of species and their rates of

327   extinction, distribution, and protection. *Science* **344**: 1246752.

328   Rounsevell MDA, Harfoot M, Harrison PA, *et al.* 2020. A biodiversity target based on species

329   extinctions. *Science* **368**: 1193–5.

330   Steege H ter, Pitman NCA, Sabatier D, *et al.* 2013. Hyperdominance in the Amazonian Tree

331   Flora. *Science* **342**: 1243092.

332   Tilman D, Clark M, Williams DR, *et al.* 2017. Future threats to biodiversity and pathways to

333   their prevention. *Nature* **546**: 73–81.

334   Tucker CM, Cadotte MW, Carvalho SB, *et al.* 2017. A guide to phylogenetic metrics for

335   conservation, community ecology and macroecology: A guide to phylogenetic metrics for

336   ecology. *Biol Rev* **92**: 698–715.

337   Urban MC. 2015. Accelerating extinction risk from climate change. *Science* **348**: 571–3.

338   Vane-Wright RI, Humphries CJ, and Williams PH. 1991. What to protect?—Systematics and the

339   agony of choice. *Biological Conservation* **55**: 235–54.

340   Watson JEM, Dudley N, Segan DB, and Hockings M. 2014. The performance and potential of

341   protected areas. *Nature* **515**: 67–73.

342   Weedop KB, Mooers AØ, Tucker CM, and Pearse WD. 2019. The effect of phylogenetic

343   uncertainty and imputation on EDGE Scores. *Anim Conserv* **22**: 527–36.

344   Wintle BA, Kujala H, Whitehead A, *et al.* 2019. Global synthesis of conservation studies reveals

345   the importance of small habitat patches for biodiversity. *Proc Natl Acad Sci USA* **116**:

346   909–14.

347

348   **Tables**

349

350   Table 1. Number of branches (NB) conserved under the scenarios of phylogenetic completeness

351   (PC) and random loss (RDM) conservation scenarios. The number of branches conserved under

352   the phylogenetic completeness approach is higher than the random loss scenario for the same

353   number of species except for birds and mammals. Percentages of NB under PC and RDM

354   scenarios are displayed within brackets. Number of branches for all species within a clade

355   assuming no extinction is displayed for reference. The number of species under PC/RDM

356   correspond to the number of species at the minimum threshold (lower credible interval)

357   identified using the Bayesian MCP regressions. Note that the observed number of species

358   (second column) corresponds to the number of species sampled in each phylogenetic tree and

359   might not represent each clade's true number of species.

360

Clade	Observed N species	PC/RDM N species	Threshold (My)	NB all species	NB-PC	NB-RDM
Seed plants	353185	312540	1.76	438863	397974 [90.68%]	391851 [89.29%]
Amphibians	7238	5927	4.43	14474	12614 [87.15%]	11852 [81.88%]
Squamata	9755	8141	2.61	19508	17186 [88.10%]	16280 [83.45%]
Birds	9993	9859	0.33	19984	19716 [98.66%]	19716 [98.66%]
Mammals	5911	5802	0.31	11820	11602 [98.16%]	11602 [98.16%]

361

362

363

364 Table 2. Summary of terrestrial biodiversity within protected areas. Table summarizes the

365 number and percentage of species currently protected in protected areas. Our estimations of

366 %protected and % of loss are based on the number of species available in the geographical

367 ranges and phylogenetic datasets (see methods). Note that the number of seed plant species with

368 available geographic ranges is 207,146, so the estimations of %protected and % of loss may be

369 underestimated. The observed number of species (second column) corresponds to the number of

370 species sampled in each phylogenetic tree and might not represent each clade's true number of

371 species.

372

Clade	Observed N species	WPA N species	%Protected	%Loss
Seed plants	353,185	191,830	92.61	7.39
Amphibians	7,238	6,630	91.60	8.40
Squamata	9,755	8,872	90.95	9.05
Birds	9,993	9,710	97.17	2.83
Mammals	5,911	5,661	95.77	4.23

373

374

375

376   **Figure legends**

377   Figure 1. Schematic diagram of the phylogenetic relationships of species within a lineage of

378   organisms, showing the hierarchical nesting of hypothetical species. The number of species that

379   need to be conserved in order to prevent the extinction of any branches in the tree depends on the

380   depth in the phylogeny we define the branch. Dashed lines represent different ages (T_N) or

381   depths in the phylogeny used to define branches—the corresponding number of species

382   preserved (T_{SP}), if one species per branch is conserved, is colored the same as the dashed line.

383   For example, purple circles (fewer branches and species with a deep slice at T_{N3}) to red ones

384   (more branches and species with a more recent slice at T_{N1}). The deeper we "slice" the

385   phylogeny, the fewer the species need to be saved in order to preserve all branches of the

386   phylogeny at that slice. Black circles represent species at T_{N0}, i.e., the current species, assuming

387   no extinction. Open circles filled with "x" indicate species that went extinct at a specific T_N.

388

389   Figure 2. Changes in the phylogenetic diversity and number of species over 100 million years for

390   terrestrial biodiversity, including seed plants (A), woody plants (B), amphibians (C), squamates

391   (D), birds (E), and mammals (F). Black dashed vertical lines represent the first changing point

392   identified by the Bayesian Multiple Changing Points (MCP) regressions. Black dotted vertical

393   lines represent the 95 credible intervals. Red long-dashed horizontal lines represent the observed

394   number of species for each clade. Red dashed horizontal lines are the number of species expected

395   under the first changing point. Red dotted horizontal lines represent the expected number of

396   species under the lower bound (or credible interval) of the first changing point. See WebTable 1

397   for a comprehensive numerical summary of the changing points. Silhouettes obtained from

398   Phylopic (http://phylopic.org).

399

400   Figure 3. Difference between the remaining phylogenetic diversity under phylogenetic

401   completeness (red) and random loss (green) scenarios. X-axis was log-transformed for plotting

402   purposes. In all cases, the phylogenetic diversity is higher for the phylogenetic completeness

403   approach.

404

405   Figure 4. Mapped phylogenetic diversity for seed plants (A-B) and birds (D-E) globally under

406   scenarios of phylogenetic completeness and random loss. Legends indicate the proportional loss

407   of phylogenetic diversity (ΔPD). Blue tones indicate that more branches of the tree of life have

408   been preserved and red tones that more branches have been lost. Comparing the two scenarios,

409   globally more branches of the tree of life are conserved in the phylogenetic completeness

410   scenario for the same number of vertebrate species extinctions. Bottom panels (C and F) show

411   the differences in phylogenetic diversity (ΔPD) in 1° grid cells between the species currently

412   estimated to occur in those cells and the fraction of those estimated to occur in protected areas

413   globally. Red colors represent greater ΔPD, meaning more branches of the tree of life are not

414   currently protected. Continental China is shaded gray given that protected area information is

415   currently unavailable in the WDPA for this country. Maps for amphibians, squamates, and

416   mammals can be found in the supplementary material.

417

418 **Figures**

419 Figure 1
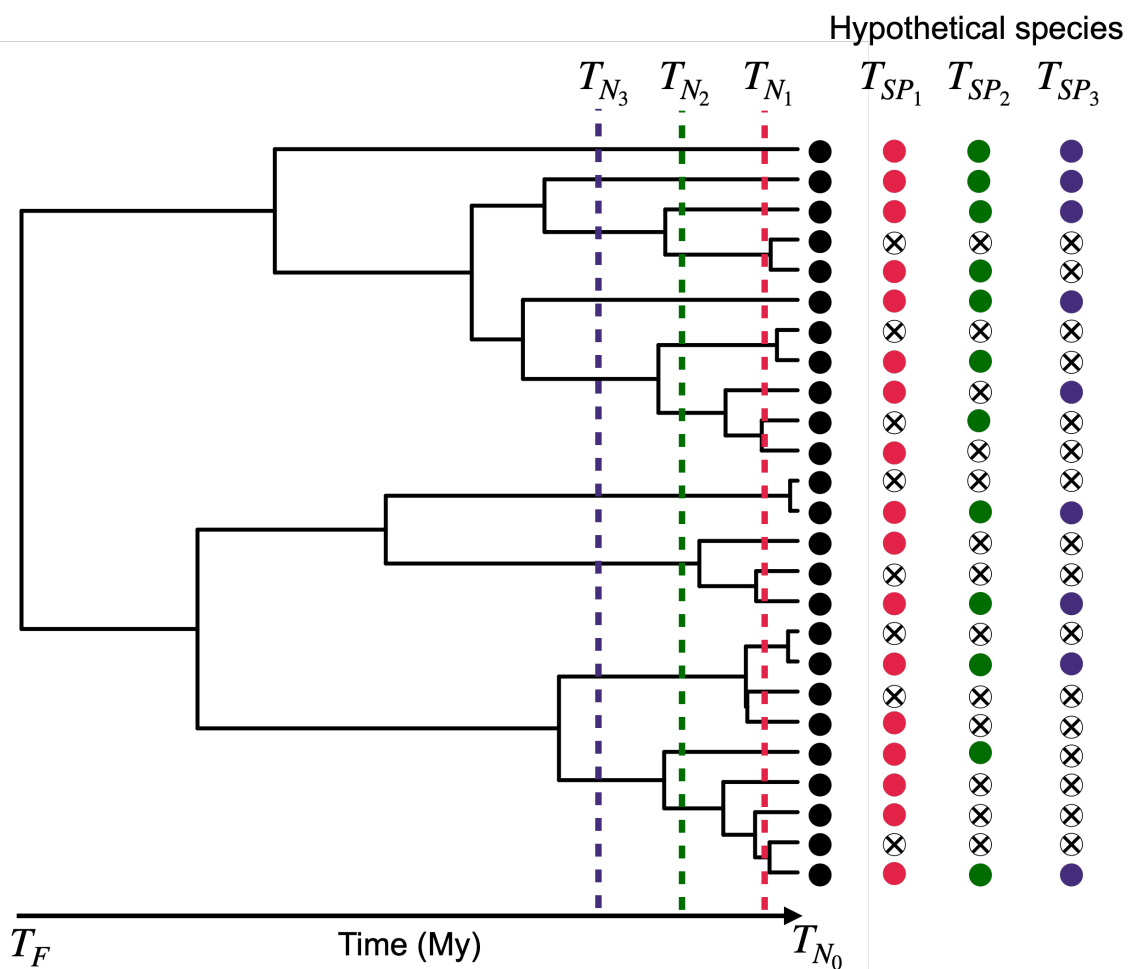
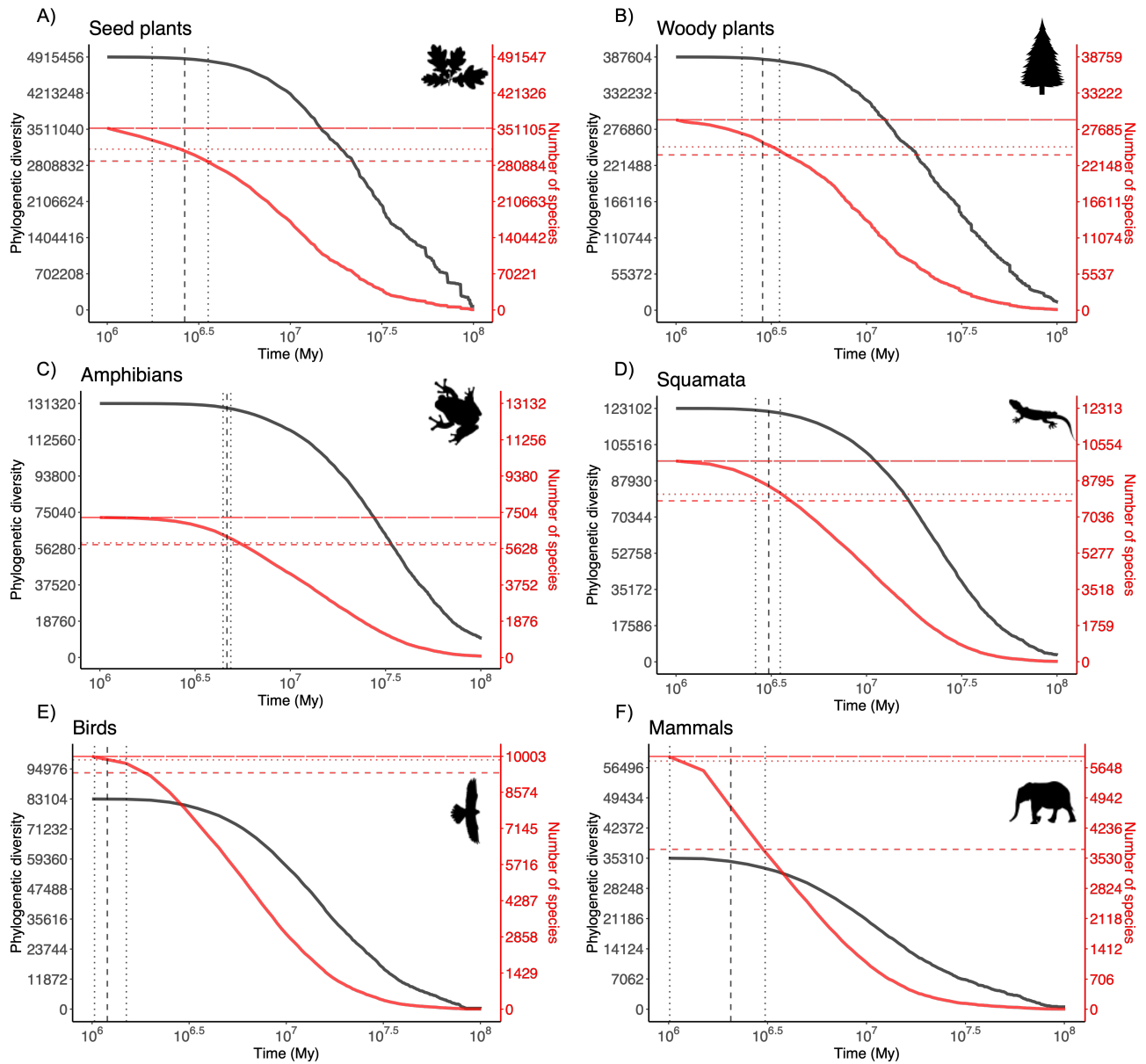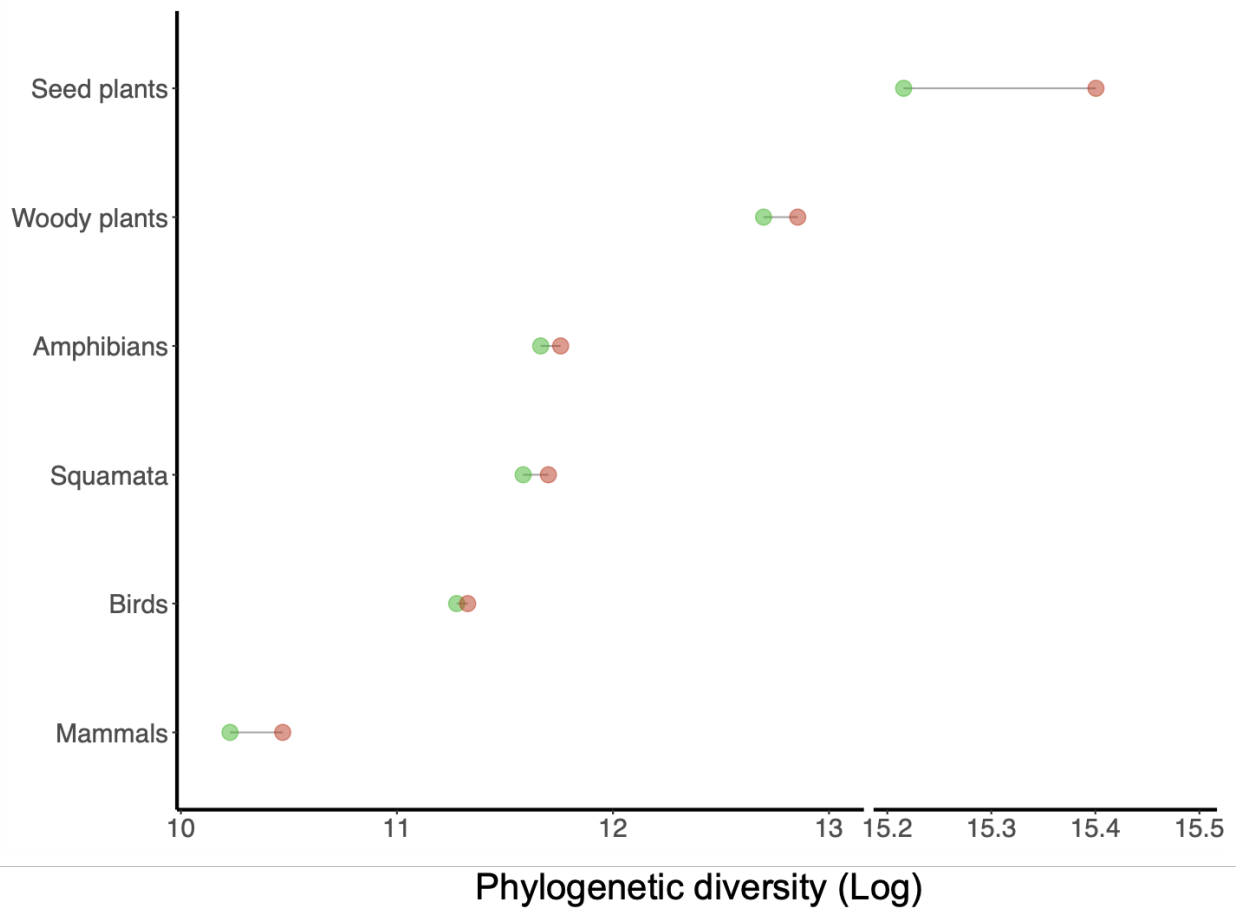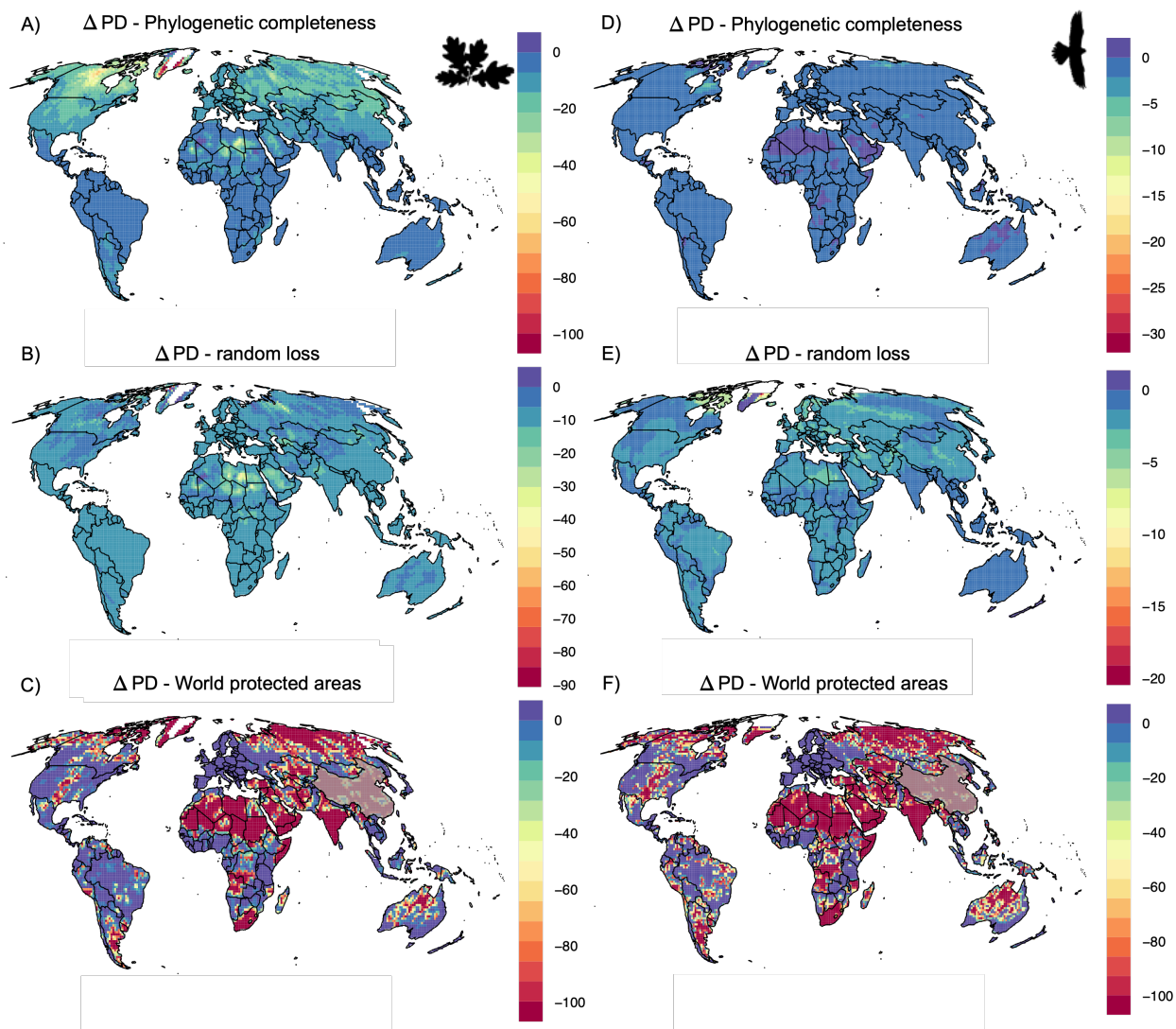

420

421

422

423   Figure 2

424

425

426

427

428

429   Figure 3

430

431

432

433   Figure 4

434

435

436

437