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Plant demographic knowledge is biased towards short-term studies of temperate-region herbaceous perennials

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22 Summary

23 (1) Plant population dynamics research has a long history, and data collection rates have
24 increased through time. The inclusion of this information in databases enables
25 researchers to investigate the drivers of demographic patterns globally and study life
26 history evolution.

27 (2) Studies aiming to generalise demographic patterns rely on data being derived from a
28 representative sample of populations. However, the data are likely to be biased, both in
29 terms of the species and ecoregions investigated and in how the original studies were
30 conducted.

31 (3) Matrix population models (MPMs) are a widely-used tool in plant demography, so an
32 assessment of publications that have used MPMs is a convenient way to assess the
33 distribution of plant demographic knowledge. We assessed bias in this knowledge using
34 data from the COMPADRE Plant Matrix Database, which contains MPMs for almost
35 800 plant species.

36 (4) We show that tree species and tropical ecoregions are under-represented, while
37 herbaceous perennials and temperate ecoregions are over-represented. In addition, there
38 is a positive association between the number of studies per country and the wealth of
39 the country. Furthermore, we found a strong tendency towards low spatiotemporal
40 replication: More than 50% of the studies were conducted over fewer than 4 years, and only
41 17% of the studies have replication across >3 sites. This limited spatiotemporal coverage
42 means that the data may not be representative of the environmental conditions experienced
43 by the species.

44 (5) Synthesis: The biases and knowledge gaps we identify are a challenge for the progress
45 of theory and limit the usefulness of current data for determining patterns that would

46 be useful for conservation decisions, such as determining general responses to climate
47 change. We urge researchers to close these knowledge gaps with novel data collection.

48 **Keywords**

49 Biogeography, comparative biology, population growth rate, population projection matrix,
50 transient dynamics

51 Introduction

52 Population ecologists aim to understand and predict population dynamics using demographic
53 data that includes the vital rates of survival, reproduction, and development. Their efforts
54 include examining population responses to changes in climate, land use, and management
55 (Silva *et al.*, 1991; Buhler *et al.*, 1997; Eriksson *et al.*, 2002; Morris *et al.*, 2008; Colautti &
56 Barrett, 2013). Demographic data are also crucial for robust population viability analyses of
57 threatened and invasive species (Morris & Doak, 2002; Hansen & Wilson, 2006; Rueda-Cediel
58 *et al.*, 2019). Besides single-species studies, researchers have conducted comparative analyses
59 investigating broad demographic and life history patterns among species. These comparative
60 analyses have aided the development of general theories of life history variation, including r-
61 K selection theory (MacArthur & Wilson, 1967; Gunderson, 1980), Grime's C-S-R triangle
62 (Grime, 1974; Silvertown *et al.* 1992), Stearns' fast-slow continuum (Stearns, 1992; Franco &
63 Silvertown, 1996; Salguero-Gómez *et al.*, 2016) and reproductive strategies continuum
64 (Salguero-Gómez 2017). The empirical exploration of these themes requires large quantities of
65 data from diverse species experiencing a wide range of environmental conditions.

66 Comparative analyses often rely on the collation of published data to obtain sufficient sample
67 sizes. There are numerous recent examples of this (*e.g.*, Iriondo, 2009; Dalglish *et al.*, 2010;
68 Bullock *et al.*, 2012; Burns *et al.*, 2013), and large-scale collaborative efforts to collate global
69 demographic and life history and related data are increasingly common (*e.g.*, GBIF: The Global
70 Biodiversity Information Facility; Wright *et al.*, 2004; Loh *et al.*, 2005; NERC Centre for
71 Population Biology, 2010; Kattge *et al.*, 2011; Salguero-Gómez *et al.*, 2015). These databases
72 provide a rich resource for workers focussing on life history strategies and demographic
73 performance.

74 One of the most frequently used tools to describe a species' demography and life history are
75 matrix population models (MPMs, Crone *et al.*, 2011). MPMs depict a population's life cycle
76 in terms of survival, reproduction, and transitions among discrete life stages (Leslie, 1945;
77 Lefkovitch, 1965; Caswell, 2001). MPMs are particularly useful because they have well-
78 understood mathematical properties, and measures derived from MPMs are comparable across
79 diverse species (Silvertown *et al.*, 1993; Caswell, 2001; Salguero-Gómez & Kroon, 2010). The
80 COMPADRE Plant Matrix Database (Salguero-Gómez *et al.*, 2015) is the most comprehensive
81 database of plant studies using MPMs and thus reflects our collective knowledge of plant
82 demography. The contents of databases like COMPADRE were not explicitly collected for
83 inclusion in large databases but rather for the disparate purposes of the many original studies.
84 Although these large databases may be an unbiased (or even complete) sampling of the
85 literature, researchers likely focus on species or geographical areas of particular interest. The
86 resulting data collections are likely to be similarly taxonomically, geographically, or
87 methodologically biased.

88 Bias of this nature has far-reaching consequences for our understanding of plant demography
89 and could limit the usefulness of databases like COMPADRE for comparative analyses. To
90 identify potential biases in plant demographic data and discuss their implications, we used
91 COMPADRE to address the following questions: (1) When have the studies been published?
92 (2) Where is the research done? (3) For which species and populations do we have demographic
93 data? (4) How are the MPMs constructed? More precisely, we tested the following nine
94 hypotheses (H1-H9):

95

96 WHEN HAVE THE STUDIES BEEN PUBLISHED?

97 We expected (**H1**) to see that the proportion of published plant ecology articles that use MPMs
98 has increased through time, reflecting the growing importance of demographic research within
99 plant ecology.

100

101 WHERE IS THE RESEARCH DONE?

102 To assess the potential geographic bias of plant demographic studies, we focussed on
103 continental, ecoregion, and country-level biases. We also examined the relationship between
104 the number of studies and the country's wealth where the study was carried out (as indicated
105 by gross domestic product, GDP). We expected (**H2**) Europe and North America to be over-
106 represented and, likewise, that temperate ecoregions (which characterise these continents)
107 would dominate. Further, we expected (**H3**) wealthier countries would be over-represented
108 compared to their poorer counterparts since they have more funds for research.

109

110 FOR WHICH SPECIES AND POPULATIONS DO WE HAVE DEMOGRAPHIC DATA?

111 We expected (**H4**) the representation of growth forms would not be proportional to their natural
112 abundance, with herbaceous perennials being over-represented and some growth forms being
113 almost absent. This potential bias is important because, if true, it would limit opportunities to
114 make general inferences on the demography of poorly-represented growth forms. Furthermore,
115 we expected to find (**H5**) a tendency to preferentially study threatened species because they are
116 of particular interest in population ecology (Morris & Doak 2002). We also expected (**H6**) a
117 trend towards choosing flourishing populations (*i.e.*, those with $\lambda > 1$) for data collection,
118 reflecting the researchers' desire to ensure the long-term viability of their project.

119

120 HOW ARE THE MPMS CONSTRUCTED?

121 The usefulness of individual demographic studies for comparative analyses is sometimes
122 limited by the methods used to construct the MPMs. We explored this by examining within-
123 study spatio-temporal replication and MPM dimension, which can influence demographic
124 quantities calculated from MPMs, including asymptotic population growth rate (Salguero-
125 Gómez & Plotkin, 2010). We expected (**H7**) low rates of temporal and spatial replication,
126 meaning that the data may not represent adequately the environmental conditions experienced
127 by the population/species. We expected (**H8**) that matrix dimension would vary widely, with a
128 tendency for the MPMs of long-lived species such as trees to have a greater dimension.

129 Finally, we analysed the prevalence of a widespread simplification approach used in
130 parameterisation: the assumption of transition constancy in two or more consecutive stages.
131 This can occur, for example, when reproduction or survival in consecutive stages (*e.g.*, small,
132 medium, large plants) is assumed to be constant. Although researchers may justify this
133 simplifying assumption based on data limitations, estimates derived from such simplified
134 MPMs may be inaccurate, limiting their usefulness in comparative work. Studies featuring
135 analyses of life expectancy or generation time (Gaillard *et al.*, 2005; Staerk *et al.*, 2019), ageing
136 trajectories (Baudisch, 2011; Baudisch & Stott, 2019), and transient population dynamics (Stott
137 *et al.*, 2011) are all likely to be marred by the widespread use of this assumption. Despite this
138 problem, we expected (**H9**) a large proportion of studies to parameterise matrices using average
139 transition probabilities and fecundity estimates across stages in this way.

140 We discuss the implications of the biases we identify for several applications. Our results
141 highlight plant demographic knowledge gaps for assessing general patterns, and we encourage
142 researchers to close these taxonomic, biogeographic, and methodological gaps going forward.

143

144 Materials and methods

145 To quantify potential biases in our knowledge of plant demography, we used the COMPADRE
146 Plant Matrix Database version 5.0.0 (Salguero-Gómez *et al.*, 2015). Although COMPADRE
147 also contains data on red and brown algae, and lichens, we restrict our analysis to plants (*i.e.*,
148 land plants and green algae) (Cavalier-Smith, 1981). We analysed our data using R version
149 4.0.4 (R Core Team, 2021).

150 Data in COMPADRE are organised by research publication such that particular species can
151 appear multiple times in different articles, and a single publication can include several species.
152 We derived our sample from 641 articles on 746 species. Most articles (547) focussed on single
153 species while 94 focussed on multiple species (2-30 species). In some cases, the archived MPM
154 represents the element-by-element average across several transitions (*e.g.*, the average of 5
155 years of data). However, COMPADRE also often includes data for the individual transitions
156 (*e.g.*, annual transitions are most commonly used, and COMPADRE thus often includes data
157 on the transition from year 1 to 2, and another for year 2 to 3 and so on). Similarly, articles
158 often include several MPMs representing different experimental treatments and/or different
159 spatial areas for a given year or set of years. Our data set included 925 species-by-article
160 combinations and a total of 9,022 MPMs. In addition to the MPMs, we use COMPADRE
161 metadata on geolocation, ecoregion, growth form, taxonomy, and study timeframe, as well as
162 the MPM projection interval, to examine potential temporal, biogeographic and taxonomic
163 biases. We analyse this data in several ways. For most analyses, we use the entire data set but,
164 due to specific requirements for some analyses, we subset the data for some parts of our study.
165 For full transparency, we include the analysis code as supplementary information.

166

167 **WHEN HAVE THE STUDIES BEEN PUBLISHED?**

168 To assess temporal trends in the publication of demography-focussed articles in plant ecology
169 **(H1)**, we examined the estimated proportion of articles published in the *Journal of Ecology*
170 between 1991-2019 that used MPMs. We chose the *Journal of Ecology* as a proxy for the field
171 of plant ecology because it is among the leading and the oldest journals for this field and is thus
172 likely to reflect the temporal development of the discipline. To do this, we downloaded
173 metadata for all of the journal articles for 1991-2019 from the Web of Science. We queried this
174 dataset with the search terms [*projection model* OR *matrix model* OR *MPM*] to identify those
175 that used MPMs. We then compared graphically the estimated percentage of articles that
176 included MPMs.

177 To gauge the completeness of COMPADRE's data holdings, we compared COMPADRE's
178 currently available data (to February 2019) to the COMPADRE team's curated list of articles
179 targeted for eventual inclusion (data provided by Haydee Hernández-Yañez, pers. comm.,
180 2019).

181

182 **WHERE IS THE RESEARCH DONE?**

183 *Biogeography.*

184 We characterised biases in the distribution of studies among continents and ecoregions **(H2)**.
185 We first quantified the density of studied species (*i.e.*, number of studied species per unit area
186 (n/km^2) of each country). We then compared the distribution of species among ecoregions in
187 COMPADRE with the estimated actual species distribution in nature among those ecoregions
188 worldwide using Pearson's Chi-squared tests (hereafter, χ^2 -tests) and *post-hoc* proportion z-
189 tests (using `prop.test` in R). We could do this because COMPADRE assigns each studied
190 population to one or more of Olson's 14 ecoregions (Olson *et al.*, 2001). In some cases,
191 populations were assigned to multiple closely-related ecoregions (*e.g.*, different types of

192 temperate forests). To simplify the analysis, we collapsed Olson’s ecoregions into five broader
193 categories: tropical (Olson’s ecoregions TMB, TDB, TSC and TGV, see Table S1 for
194 explanation), temperate (TBM, TCF, TGS), Mediterranean/desert (MED, DES), tundra/boreal
195 (BOR, TUN, MON), and wetland (MAN, FGS). We extracted the estimated number of species
196 naturally occurring in each region from Kier (Kier *et al.*, 2005). Kier *et al.* (2005) did not
197 include bryophytes or algae, so we excluded them from this comparison.

198 *Country-specific wealth (GDP).*

199 We used country-level per-capita GDP for 2017 (World Bank, 2018) to examine whether
200 wealthy countries are overrepresented in COMPADRE (**H3**). To do this, we used a Poisson
201 generalised linear model (GLM) (log-link) with log-transformed GDP as the explanatory
202 variable and the number of demographic studies as the response variable. Log-transformation
203 of GDP was necessary to improve the fit of the model. We included only countries with at least
204 one demographic study on plants to avoid a zero-inflated model.

205

206 **FOR WHICH SPECIES AND POPULATIONS DO WE HAVE DEMOGRAPHIC** 207 **DATA?**

208 *Taxonomy.*

209 To characterise potential biases in taxonomy and growth form (**H4**), we first analysed the
210 distribution of taxa in COMPADRE among the taxonomic categories of angiosperm *vs.*
211 gymnosperm, monocot *vs.* eudicot (for the 849 angiosperms only), and Family. We then used
212 the COMPADRE database metadata variable `OrganismType` (hereafter, growth form),
213 which includes a range of paraphyletic growth form categories such as “tree”, “herbaceous
214 perennial”, and “shrub”. We compared the distribution of angiosperms *vs.* gymnosperms in
215 COMPADRE with estimates of their diversity across all plant species from Campbell *et al.*

216 (2018) and the numbers of eudicots and monocots with numbers derived from Evert *et al.*
217 (2013). We linked numbers of species within families extracted from COMPADRE with the
218 number of species per Family listed in The Plant List (2010) for the same families. FitzJohn *et*
219 *al.* (2014) and Willis (2017) estimate how many plant species in the world are woody, which
220 we compared with the number of trees and shrubs in COMPADRE. We compared the number
221 of epiphytes with estimates from (Zotz, 2013). As above, we used χ^2 -tests and post-hoc
222 proportion tests for these comparisons.

223 *Conservation status.*

224 To characterise potential bias in the conservation statuses of species studied (**H5**), we obtained
225 the IUCN Red List categories (IUCN 2019) for all species in our data set and in The Plant List,
226 using the R package `rredlist` v. 0.4.0 (Chamberlain, 2017). We compared the distribution
227 of COMPADRE species in each Red List category with the corresponding distribution of all
228 species in The Plant List using a χ^2 -test.

229 *Population growth rates.*

230 To assess whether researchers tend to collect demographic data on growing or declining
231 populations and whether researchers tend to study populations that are in a “boom phase” (**H6**),
232 we examined the asymptotic population growth rates (λ) calculated from each MPM. We first
233 filtered the data to include only studies that spanned at least five years, were experimentally
234 unmanipulated, and for which λ could be calculated (*i.e.*, the MPMs contained no missing
235 values and did not violate ergodicity and irreducibility assumptions (Stott *et al.*, 2010)). We
236 then fitted an ordinary least squares regression with λ as the response variable and year as the
237 explanatory variable. The slope of this model indicates the temporal trend in λ : a negative trend
238 supports our hypothesis that researchers preferentially work on initially flourishing sites where
239 population growth rates then decline over time.

240

241 **HOW ARE THE MPMS CONSTRUCTED?**

242 *Temporal and spatial replication.*

243 To explore potential biases in temporal and spatial replication (**H7**), we examined the
244 frequency distributions of study length (years) and the number of spatially distinct populations
245 (as defined by the original article authors) for all species-by-article combinations in
246 COMPADRE.

247 *Matrix model dimension.*

248 To examine how the MPM dimension chosen by modellers varies systematically among growth
249 form and ecoregion (**H8**), we compared the frequency distribution of the MPM dimension
250 across these variables. As above, we tested for an association statistically using Poisson GLMs.

251 *Averaging matrix model elements.*

252 In COMPADRE, MPMS (**A**) are defined as the sum of three submatrices, $\mathbf{A} = \mathbf{U} + \mathbf{F} + \mathbf{C}$,
253 where **U** represents survival-dependent transitions (*e.g.*, growth, stasis, shrinkage, ageing), **F**
254 describes sexual reproduction, and **C** represents clonal reproduction. We used these three
255 submatrices to address **H9** by characterising the prevalence of averaging across stage-/age-
256 classes. This approach was only possible for matrices without missing values. We assessed the
257 number of consecutive life cycle stages in each MPM that contained averaged rates of survival,
258 reproduction and clonality, using the following approaches:

259 To estimate the degree of survival averaging, we calculated stage-specific survival probability
260 as the column sums of the **U** matrix. When the survival probabilities across stages were all
261 different, we categorised the MPM as not containing averaged rates (“no averaging”). When
262 several survival probabilities were consecutively identical across up to 50% of stages, we
263 assumed they had been averaged over those stages (“≤50% averaging”). Finally, when more

264 than half of the stages have consecutively identical survival probabilities, we assumed that they
265 had been averaged (“> 50% averaging”).

266 To estimate the degree of averaging for sexual reproduction, we calculated stage-specific
267 sexual reproduction as the column sums of the **F** matrix. We classified the degree of averaging
268 into three categories in the same way as for survival. Whereas every survival column must sum
269 to >0, reproduction columns may include zero values. These may be before the stage of first
270 reproduction (pre-reproductive) or after (post-reproductive). Post-reproductive stages with
271 $F = 0$ are more likely to exist because researchers did not observe reproduction during
272 fieldwork, rather than due to the method of averaging over multiple life-stages. Our
273 assessments include only 'reproducing' stages (i.e., where reproduction >0). We estimated the
274 degree of clonality averaging in the same way, using the **C** matrix.

275 Results

276 WHEN HAVE THE STUDIES BEEN PUBLISHED?

277 The proportion of articles focussing on plant demography (**H1**) in the *Journal of Ecology* has
278 increased slightly in the past decades. However, the year-to-year variation is high, and the slope
279 is not significantly different from zero (linear model: slope = 0.034 ± 0.044 , $F_{1,21} = 0.601$,
280 $P = 0.447$; Fig. 1).

281

282 WHERE IS THE RESEARCH DONE?

283 *Biogeography*.

284 As expected (**H2**), geographical bias was obvious, with study density being greatest in Europe
285 (23.67 studies per million km²) and North America (17.56 studies per million km²), while
286 Oceania, South American, Asian, and African countries were relatively poorly-represented,
287 with 6.69, 5.10, 1.66, 1.02 studies per million km², respectively (see also Fig. 2B; Fig.S2).
288 Interestingly, a post-hoc analysis showed that the dominance of Europe and North America in
289 the COMPADRE database has increased since the year 2000: 75% of articles post-2000
290 focussed on these regions compared to 63% pre-2000 (Table S2).

291 As hypothesised (**H2**), there was a significant difference between the species distribution in
292 COMPADRE compared to in nature (χ^2 -test: $\chi^2 = 327.79$, d.f. = 4, $P < 0.001$). Indeed, species
293 from temperate ecoregions are significantly over-represented in COMPADRE (48% compared
294 to an estimated 24% of species inhabiting these regions in nature; proportion test: $\chi^2 = 267.71$,
295 d.f. = 1, $P < 0.001$; Fig. 2A). In contrast, tropical ecoregions are significantly under-represented
296 (27% vs. 42%; proportion test: $\chi^2 = 77.432$, d.f. = 1, $P < 0.001$). Similar results were apparent
297 for wetlands (1% vs. 5%; proportion test: $\chi^2 = 23.426$, d.f. = 1, $P < 0.001$) and tundra and boreal

298 ecoregions (6% vs. 13%; proportion test: $\chi^2 = 40.335$, d.f. = 1, $P < 0.001$). Species from
299 Mediterranean and desert ecoregions are represented in approximately the same proportion as
300 in nature (18% in COMPADRE vs. an estimated 17%: proportion test: $\chi^2 = 1.273$, d.f. = 1,
301 $P = 0.259$).

302 *Country-specific wealth (GDP).*

303 As expected (**H3**), the numbers of articles per country and per capita GDP are positively
304 correlated (Poisson GLM: Null Deviance = 1494.7, Residual Deviance = 1144.3, d.f. = 1, 54,
305 $P < 0.001$, Fig. 2C). Here, 73% of countries (161 out of 222) are not represented in
306 COMPADRE. The United States of America, with 202 research articles, dominates
307 COMPADRE, followed by Mexico with 88 articles, Sweden (33 articles), Australia and
308 Canada (both 26 articles), Spain (25 articles), Japan (22 articles), Czech Republic and the
309 United Kingdom (both 21 articles), and Brazil (19 articles). Interestingly, several of the
310 wealthiest countries are not represented in COMPADRE (*e.g.*, China, Iceland, and Ireland).
311 The positive correlation between the number of studies in COMPADRE and country GDP (Fig.
312 2C) remains statistically significant even when we remove the two outliers with most studies
313 (USA and Mexico).

314

315 **FOR WHICH SPECIES AND POPULATIONS DO WE HAVE DEMOGRAPHIC**
316 **DATA?**

317 *Taxonomy.*

318 As expected (**H4**), the representation of species in COMPADRE does not well-reflect natural
319 diversity. COMPADRE categorises species as angiosperm (91%), gymnosperm (6%), or “non-
320 seed plants” (3%) which includes ferns, mosses etc. (Fig. 2D). According to Campbell *et al.*
321 (2018), the corresponding figures in nature are 88% (angiosperm), 1% (gymnosperm) and 11%

322 (non-seed plants). Thus, COMPADRE's taxonomic representativity is different than that found
323 in nature (χ^2 test: $\chi^2 = 1282.7$, d.f. = 2, $P < 0.001$). In fact, COMPADRE over-represents
324 gymnosperms (proportion test: $\chi^2 = 1127.1$, d.f. = 1, $P < 0.001$) and under-represents the non-
325 seed plants (proportion test: $\chi^2 = 64.39$, d.f. = 1, $P < 0.001$).

326 Of COMPADRE's angiosperms, 74% are eudicots and 26% monocots (Fig 2E), which
327 approximately reflects Evert *et al.*'s (2013) estimate of their natural diversity distribution (69%
328 eudicot, 31% monocot). Our χ^2 test nevertheless indicated the COMPADRE distribution was
329 significantly different to the natural distribution (χ^2 test: $\chi^2 = 9.79$, d.f. = 1, $P = 0.002$).

330 To better understand the distribution of COMPADRE species across plant families, we
331 examined the five largest eudicot families (according to The Plant List, 2010): Compositae
332 (Asteraceae), Leguminosae (Fabaceae), Orchidaceae, Rosaceae, and Rubiaceae (Fig. 2F). The
333 χ^2 test showed that the distributions differed between COMPADRE and in nature patterns
334 (χ^2 test: $\chi^2 = 24.161$, d.f. = 4, $P < 0.001$). However, this difference is driven by the Rubiaceae
335 and Orchidaceae, which are significantly under-represented (Rubiaceae: proportion test:
336 $\chi^2 = 13.616$, d.f. = 1, $P < 0.001$; Orchidaceae: proportion test: $\chi^2 = 7.0719$, d.f. = 1, $P = 0.008$).
337 The other families are fairly proportionately represented in COMPADRE (all $P > 0.05$).

338 Half of the species in COMPADRE are herbaceous perennials (462 of 932 species), and only
339 26% are woody plants. This figure contrasts with current estimates that 45-48% of the world's
340 vascular plant species are woody (FitzJohn *et al.*, 2014; Willis, 2017).

341 *Conservation status.*

342 The IUCN has assessed only 29% (n = 220) of the species in COMPADRE. Of these, contrary
343 to our expectations (**H5**), COMPADRE's content with respect to the Red List status reflects
344 current Red List assessments (χ^2 test: $\chi^2 = 4.054$, d.f. = 4, $P = 0.399$). Most of COMPADRE's

345 species are assessed as Least Concern (62%), with the rest falling into one of the threatened
346 categories (Vulnerable, Endangered, or Critically Endangered) (Fig. 3A).

347 *Population growth rates.*

348 As predicted (**H6**), there is a slight but statistically significant tendency to study growing
349 populations (*i.e.*, $\lambda > 1$), the effect size is small and driven by the skewed nature of the data
350 (Fig. 3B; two-sided t-test on $\lambda = 1$: $t = 10.941$, d.f. = 2312, $P = 0.001$). The overall mean value
351 for $\log \lambda$ was 0.013 (standard deviation = 0.45). Our analysis of ordinary least-squares
352 regression slopes from the subset of populations with at least a 5-year time-series shows no
353 tendency for researchers to select populations where λ is initially high but then decreases,
354 leading to negative slope values (Fig. 3C; t-test: $t = -0.020$, d.f. = 192, $P = 0.984$).

355

356 **HOW ARE THE MPMS CONSTRUCTED?**

357 *Temporal and spatial replication.*

358 As expected (**H7**), most studies in COMPADRE are short-term (Fig. 4A). The modal study
359 duration is three years, while the median is four years. The mean is slightly longer (5.48 years),
360 reflecting the skewed nature of the distribution. Some long-term exceptions include studies of
361 the shrub *Cassia nemophila* (Silander, 1983) and the tree *Acer saccharum* (Lin & Augspurger,
362 2008), which both span 51-years. The study duration varies by ecoregion, with tropical and
363 marine studies tending to be shorter than those from other ecoregions (Fig. S3A). There was
364 minimal variation in study duration among growth forms and, contrary to expectation, trees (a
365 typically long-lived growth form) are not studied for longer periods than typically shorter-lived
366 growth forms (Fig. S4A).

367 As expected, most studies have a low degree of spatial replication (Fig 4B). Most studies are
368 carried out at a single site, though the distribution is skewed (mean = 2.82, median = 2,

369 range = 1-60). Interestingly, species studied at four or more sites are mainly herbaceous
370 perennials (57%).

371 Each MPM is obtained from a different study site or year. Therefore, the number of MPMs
372 present in a study may be an indicator of the range of environmental conditions captured by
373 the study. However, the number of MPMs per study does not vary much among ecoregions
374 (Fig S3A and S3B) or growth form (Fig S4A and B).

375 *Matrix model dimension.*

376 We expected (**H8**) that the MPM dimension would vary widely and would be greater for long-
377 lived groups like trees. MPM dimension ranges between two and 60 (for *Rhododendron*
378 *ponticum*, (Travis *et al.*, 2011) but is left-skewed (mean = 6.51, median = 5; Fig. 4C).
379 Furthermore, typical matrix dimension varied significantly among ecoregions (ANOVA on log
380 matrix dimension: $F = 17.967$, d.f. = 5 and 884, $P < 0.001$) (Fig. S3C), with tropical species
381 tending to have slightly larger matrices than temperate or Mediterranean ones (t-test on log
382 matrix dimension: $t = 6.855$, d.f. = 375.36, $P < 0.001$; though this effect is likely driven by large
383 tropical tree matrices). Finally, MPM dimension varies systematically across growth forms
384 (ANOVA on log matrix dimension: $F = 22.718$, d.f. = 6 and 730, $P < 0.001$) with tree MPMs
385 tending to be larger (mean = 9.48, median = 8, range = 2-60) than other growth forms (Fig.
386 S4C), thus supporting our initial hypothesis (**H8**).

387 *Averaging matrix model elements.*

388 Contrary to our expectation (**H9**), researchers do not often appear to average survival rates
389 across life cycle stages when parameterising MPMs. In COMPADRE, 77% of MPMs have no
390 averaging of survival across consecutive stages at all, and only 4% have more than half of their
391 stage-specific survival rates averaged across consecutive stages (Fig. 4D). A similar pattern
392 follows for fecundity: 79% have no averaging and a smaller proportion (5.1%) have over half

393 of their stage/age-specific fecundity rates averaged (Fig. 4E). Fewer than 1% of the MPMs
394 showed averaging in clonality rates (Fig. 4F).

395

396 Discussion

397 Before analysing large heterogeneous databases, it is essential to understand their potential
398 biases and inconsistencies. Under-representation of particular ecoregions or taxonomic groups
399 may lead to incorrect generalisations if those under-represented regions or groups have distinct
400 demographic behaviour. Improved knowledge of systematic biases in databases like
401 COMPADRE, and a recognition of their impact on inferences, will improve our understanding
402 of the natural world. Researchers should carefully consider potential systematic biases in these
403 large-scale datasets, especially when conducting comparative studies that seek to generalise
404 across disparate taxa and geographic regions.

405 COMPADRE v.5.0.0. contains data for 746 species, representing 0.002% of the ~370,000
406 extant plant species (not including green algae) (The Plant List, 2010). Although COMPADRE
407 covers only a fraction of plant diversity, we show that it contains the majority of published
408 MPM-based plant demographic work (Fig. 1B). Thus, this database is a valid indicator of our
409 knowledge of MPM-based plant demography and reveals demographic knowledge gaps for
410 most species. We note, however, that the vast majority of these studies are published in the
411 English language literature. Amano *et al.* (2016) found that a third of the literature in
412 biodiversity conservation was non-English, and that half provide neither the title nor the
413 abstract in English. About 16% of this corpus is unsearchable using English keywords, thus
414 remaining hidden. Assuming that there is a similar pattern for plant demography literature,
415 some knowledge gaps in the English-speaking research community could undoubtedly be

416 closed by engaging researchers familiar with non-English language literature to assist with
417 contributions to COMPADRE.

418

419 **WHEN HAVE THE STUDIES BEEN PUBLISHED?**

420 The number of articles that focus on plant demography has steadily accumulated since the
421 1970s (Fig. 1B). Our hypothesis that an increasing proportion of plant ecology research would
422 be demography-focussed (**H1**) was supported, based on our survey of articles published in the
423 *Journal of Ecology* (Fig 1A), although the relationship was rather noisy. The downturn in the
424 rate of increase in MPM-related publication in recent years (since about 2015) may be due to
425 the increasingly important role that integral projection models (IPMs, Easterling *et al.*, 2000)
426 play in plant demographic research.

427

428 **WHERE IS THE RESEARCH DONE?**

429 *Biogeography*.

430 Plant biodiversity is unevenly distributed. Equatorial regions are usually relatively species-
431 rich, with declining biodiversity towards the poles for most plant groups (Gaston, 2000).
432 Biodiversity and endemism hotspots are concentrated in the tropics, on equatorial islands, and
433 in the southern hemisphere (Myers *et al.*, 2000; Kier *et al.*, 2009). Our finding that ~73% of
434 demographic studies are carried out in the mainly temperate regions of the western northern
435 hemisphere (Fig. 2A & B) contrasts with those hotspots, thus supporting **H2**. This result is not
436 surprising given similar findings for population dynamics (Amano & Sutherland, 2013; McRae
437 *et al.*, 2017), biodiversity time-series (Dornelas *et al.*, 2018), and the distribution of ecological
438 study sites (Martin *et al.*, 2012). Collectively, these patterns highlight important knowledge
439 gaps for some of the planet's most threatened ecosystems. For example, sub-Saharan Africa

440 and Southeast Asia have among the least ecological data yet show the most rapid decline of
441 terrestrial ecosystems (MEA, 2005). Given that demographic data is important for assessing
442 extinction risk, *e.g.*, by assessing population trends and population viability analyses (IUCN
443 2019; Rodrigues, *et al.*, 2006), the lack of demographic data is a concerning impediment to
444 species-level conservation. Beyond conservation, this biogeographic bias limits our
445 understanding of global ecological trends and drivers of population dynamics and life history
446 evolution.

447 *Country-specific wealth (GDP).*

448 As anticipated (**H3**), the number of demographic articles was positively associated with the
449 per-capita GDP of the country where the work was carried out (Fig. 2C). We expected this
450 because high-GDP countries can invest more in research (van Noorden & Butler, 2019; World
451 Bank, 2019), and researchers tend to conduct research near their home institution for logistical
452 reasons (Coutts *et al.*, 2016). The fact that the relationship is relatively loose reflects the
453 international networks and mobility of some researchers who carry out research away from
454 their home institution. Nevertheless, one way to correct this bias is for funding bodies to
455 encourage plant demographic research, and collaboration with researchers, in understudied and
456 threatened regions.

457

458 **FOR WHICH SPECIES AND POPULATIONS DO WE HAVE DEMOGRAPHIC**
459 **DATA?**

460 *Taxonomy.*

461 As expected (**H4**), most of COMPADRE's species are angiosperms, reflecting the high
462 diversity of this group. However, COMPADRE over-represents gymnosperms and under-
463 represents the non-seed plants. Within the angiosperms, most of COMPADRE's species are

464 eudicots. Although this reflects the natural distribution of eudicot *vs.* monocot species, we did
465 detect a statistically significant bias towards the study of eudicots. COMPADRE's species
466 distribution among the major eudicot plant Families approximated the natural distribution,
467 except for Rubiaceae and Orchidaceae, which were under-represented. The pattern for
468 Rubiaceae may be explained by geographical bias since it mainly occurs in the (sub)tropics,
469 which are not well-represented in COMPADRE. As expected (**H4**), we know more about the
470 demography of herbaceous perennials than any other growth form. Trees, which are important
471 both economically (Poore, 2013) and ecologically (Chambers *et al.*, 2001), are under-
472 represented, probably due to the logistical difficulties of studying large, long-lived organisms,
473 but perhaps also due to the relatively low tree species diversity in temperate regions.

474 Although some of these biases may be overcome statistically (*e.g.*, by resampling or
475 rarefaction), the scarcity of demographic data on several growth forms, including ferns, lianas,
476 and bryophytes, drastically reduces our ability to draw general patterns for these growth forms
477 and set them in context with more commonly-studied forms. This issue is particularly
478 troublesome for comparative studies of the evolution of plant life history.

479 *Conservation status.*

480 Demographic models are an indispensable tool to guide management decisions for threatened
481 species (Norris, 2004). Contrary to our expectation (**H5**) that researchers may collectively
482 focus on threatened species, the distribution of demographic studies in COMPADRE well-
483 approximates the distribution of Red List statuses of plants in general: There is no tendency to
484 favour studies of threatened species. However, we should regard this result with caution
485 because it is based on the subset of ~25% of COMPADRE species that have been assessed for
486 the IUCN Red List. The true distribution of species among IUCN Red List categories may be
487 quite different, especially since species endemic to biodiversity hotspots are less likely to have
488 been assessed.

489 *Population growth rates.*

490 There was a slight tendency for researchers to preferentially study growing populations
491 (supporting **H6**) but there was no evidence for a “regression to the mean” effect whereby
492 population growth rates decline along the time-series (contrary to Buckley *et al.*, 2010). We
493 initially expected this tendency because we expected researchers to select obviously flourishing
494 populations to avoid the risk and logistical cost of local extinction. The differences between
495 our results and those of Buckley *et al.* (2010) could be due to differences in data or methods.
496 This effect warrants further investigation because biased sampling (*e.g.*, towards growing
497 populations) could lead to incorrect conclusions about population dynamics in comparative
498 research.

499

500 **HOW ARE THE MPMS CONSTRUCTED?**

501 *Temporal and spatial replication.*

502 The fact that demographic studies tend to have low spatial and temporal replication supports
503 our original hypothesis (**H7**) and confirms previous findings (Crone *et al.*, 2011; Ehrlén *et al.*,
504 2016). Limited spatial replication may affect confidence in inferences made from those models.
505 The geographic distribution of plants varies widely, with some only occurring in specific small
506 areas (*e.g.*, *Iliamna remota* is endemic to the ~8 hectare Langham Island, Illinois, USA;
507 Swinehart & Jacobs, 1998) and others even spanning continents (*e.g.*, *Plantago major*, Sagar
508 & Harper, 1964). Widely distributed species are likely to experience a greater range of
509 environmental conditions than those with small ranges, and demographic data should ideally
510 be collected in representative parts of this range to understand the species’ demography more
511 fully. Work by Doak & Morris (2010), Wardle *et al.* (2014), and Römer *et al.* (2021) are good
512 examples of such efforts.

513 The limited temporal extent in most studies is also a concern. Researchers have argued that
514 accurate forecasting of population dynamics typically requires time-series extending well
515 beyond three years, especially because of the demographic impacts of rare extreme weather
516 events (Doak & Morris, 2010; Ehrlén *et al.*, 2016; Teller *et al.*, 2016; Pérez-Llorca, *et al.*,
517 2018). Given the cost and effort required for long-term research, it is not surprising that the
518 temporal extent of studies in COMPADRE is short. In some settings, researchers could use an
519 alternative space-for-time substitution approach to resolve this problem. The approach enables
520 a rapid accumulation of data representing a large range of environmental conditions allowing
521 the modelling of responses to future climate scenarios without the need for long time-series
522 (Blois *et al.*, 2013; Teller *et al.*, 2016; Damgaard, 2019; Römer *et al.*, 2021). However, the
523 approach assumes that drivers of demographic variation across space are equivalent to those
524 that drive temporal variation, which may not be the case (Pickett, 1989). In any case, the low
525 spatial replication in COMPADRE may currently limit the application of this approach.

526 *Matrix model dimension.*

527 Researchers constructing MPMs decide an appropriate dimension for their model, based on
528 factors including species life-history (including longevity or life cycle complexity), the study's
529 purpose, and the amount of data available to parameterise each stage. As expected (**H8**), matrix
530 dimension varies hugely, with a substantial proportion (~20%) having a low dimension of 3 or
531 less. This low dimension could limit utility in some cases. For example, this is likely to be too
532 low for the derivation of measurements relying on the calculation of age trajectories from stage-
533 based MPMs (Cochran & Ellner, 1992; Caswell, 2001) such as Keyfitz's entropy (Keyfitz,
534 1968). Furthermore, other derived metrics, including elasticities (Salguero-Gómez & Plotkin,
535 2010) and some transient measures (Stott *et al.*, 2010), are sensitive to the MPM dimension.
536 Besides influencing individual metrics, the systematic bias in model dimension among growth

537 forms and ecoregion could lead to spurious inferences in multi-species comparative studies if
538 not taken into account.

539 *Averaging matrix model elements.*

540 MPM-derived metrics of population dynamics such as transient dynamics metrics (Stott *et al.*,
541 2010) and measures of life-history (*e.g.*, survival inequality or entropy) are sensitive to
542 homogeneity among the vital rates of stages because peaks and troughs of survival or mortality
543 in certain life stages might be undetected. Despite this, researchers sometimes have no option
544 but to parameterise MPMs with average vital rates across consecutive stages. We expected this
545 would be common (**H9**), but our results show that plant ecology researchers seldom take this
546 approach. This finding is good news because averaging of reproduction or survival could lead
547 to an underestimation of the effects of temporal variation in the environment underlying the
548 vital rates (Stott *et al.*, 2010). This underestimation would be a challenge for applications that
549 are not based on asymptotic properties of the MPM, such as calculations of extinction risk, the
550 stochastic growth rate in population viability analyses, and short-term predictions of population
551 fate (transient dynamics; Stott *et al.*, 2011). Thus, inference from MPMs that have been
552 parameterised in this way could lead to misguided management strategies that miss
553 opportunities to influence the population dynamics in the desired way by manipulating vital
554 rates with strong influences on short-term or stochastic population growth. This averaging of
555 vital rates would also be problematic for comparative life-history research, and in particular, work
556 that relies on age-from-stage methods (Cochran & Ellner, 1992; Caswell, 2001) to calculate
557 demographic trajectories and derived measures. We, therefore, encourage researchers to,
558 wherever possible, avoid parameterisation using averaging over consecutive stages.

559

560 **Conclusions**

561 Our current knowledge of global plant demography is based on geographically biased data
562 heavily focused on herbaceous perennials, leaving important knowledge gaps. Demographic
563 studies are constrained by funding, with the temporal length reflecting the typical grant and
564 PhD tenure, with most work concentrated in wealthy countries. We did not find significant bias
565 in conservation status or population growth rate, which indicates that researchers do not focus
566 on species of conservation concern nor growing or shrinking populations. To close the
567 aforementioned knowledge gaps and better understand generalities in life-history strategy and
568 population dynamics, research targeting neglected growth forms and ecoregions is desirable,
569 as is increased spatial and temporal replication within species. Furthermore, an improved
570 understanding of the impact of these biases on model predictions and methodological
571 developments to account for known biases would be helpful.

572

573 Acknowledgements

574 We thank the researchers that have contributed data to the COMPADRE Plant Matrix
575 Database. We also thank T. Knight and attendees of the German Centre for Integrative
576 Biodiversity Research (iDiv) sApropos (Analysis of PROjections of POpulationS) workshops
577 in Leipzig led by RS-G, for valuable discussions on this topic. GR was supported to attend the
578 sAPROPOS workshops by German Centre for Integrative Biodiversity Research (iDiv), ORJ
579 was supported by the Danish Council for Independent Research (grant number DFF - 6108-
580 00467). RS-G was also supported by NERC-IRF NE/M018458/1.

581

582 Author's contributions

583 GR, RS-G and ORJ conceived the ideas and designed methodology; ORJ and RS-G provided
584 additional data; GR, ORJ and IS analysed the data; GR led the writing of the manuscript. All
585 authors contributed to manuscript writing and gave final approval for publication.

586 Data availability

587 Most of the used data is open access and can be downloaded on the following webpages: The
588 COMPADRE Plant Matrix Database: <http://www.compadre-db.org> (Salguero-Gómez *et al.*,
589 2015); IUCN Red List data: <http://www.iucnredlist.org> (IUCN, 2019); The Plant List:
590 <http://www.theplantlist.org> (The Plant List, 2010); GDP data was obtained from the World
591 Bank: <https://data.worldbank.org/indicator/NY.GDP.PCAP.CD> (World Bank, 2018). Code for
592 the analyses is included in the supplementary information.

593

594 Figure captions

595 Figure 1: Publication trajectories in plant demography. **(A)** The percentage of articles in a
596 sample of plant ecology literature that use matrix population models (MPMs). Note that the
597 time-series starts in 1993 before which abstracts have been not digitised. **(B)** The cumulative
598 number of MPM-based studies by year, archived in the COMPADRE Plant Matrix Database
599 (at February 2019) (blue line) compared to the estimated cumulative number of all published
600 studies containing plant MPMs (black line).

601

602 Figure 2. Geographic and taxonomic biases in the COMPADRE Plant Matrix Database. **(A)**
603 The species distribution among ecoregions in COMPADRE compared to the natural
604 distribution (Trop = tropical; temp = temperate; Med/Des = Mediterranean and deserts;
605 Tund/Bor = tundra and boreal regions; Wetl = Wetlands). **(B)** The distribution of plant
606 demography study density across continents. **(C)** The relationship between country per-capita
607 GDP and the number of plant demography studies. The regression line represents a gamma-
608 error GLM, conditioned on countries having at least one plant demography study. **(D)**
609 Comparison of the species distribution among broad categories of angiosperms, gymnosperms
610 and non-seed plants, in COMPADRE and in nature. **(E)** Comparison of the distribution of
611 angiosperm species among monocot and eudicot categories, in COMPADRE and in nature. **(F)**
612 Comparison of the distribution of species among the five largest dicot families, in
613 COMPADRE and in nature (Comp = Compositae; Legum = Leguminosae;
614 Orchid = Orchidaceae; Rosa = Rosaceae; Rubia = Rubiaceae). **(G)** The distribution of species
615 among growth form categories (Herb = herbaceous perennials; Tree = trees; Shrub = shrubs;
616 Suc = succulents; Palm = palms; An = annuals; Epi = epiphytes; Other = includes mosses and
617 ferns).

618

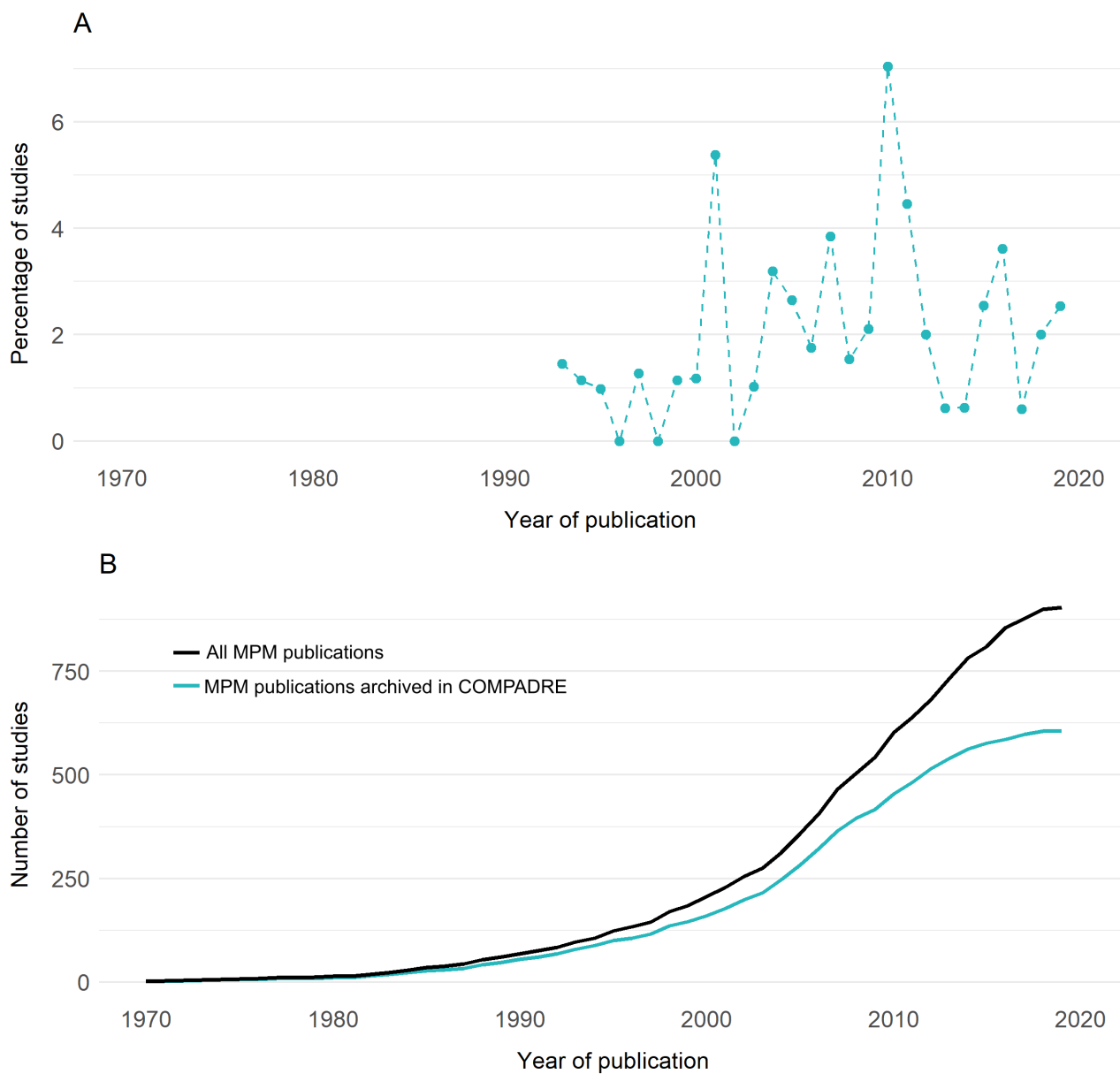
619 Figure 3. Conservation status and population trend biases in the COMPADRE Plant Matrix
620 Database. **(A)** Comparison of the distribution of species among IUCN Red List conservation
621 status in COMPADRE (blue) and in nature (black) (LC = Least Concern, NT = Near
622 Threatened, VU = Vulnerable, EN = Endangered, CR = Critically Endangered). **(B)** The
623 distribution of population growth rates (λ) for MPMs in COMPADRE. The graph is limited to
624 λ -values between 0 and 4 to show the interesting area around $\lambda = 1$ (and $\lambda > 4$ seems
625 biologically unreasonable and may represent errors). **(C)** The density distribution of the slope
626 of the linear $\lambda \sim \text{year}$ relationship for studies with >5 years of data.

627

628 Figure 4: Spatiotemporal replication and MPM construction. **(A)** The distribution of study
629 duration in COMPADRE. **(B)** The distribution of the number of study sites (spatial replication)
630 in COMPADRE. **(C)** The distribution of matrix dimension across MPMs in COMPADRE. The
631 magenta and yellow lines show the mean and median, respectively. **(D, E, F)** Summaries of
632 element averaging in MPM submatrices of **(D)** survival, **(E)** fecundity and **(F)** clonality.
633 *none* = all stages have different survival / fertility / clonality estimates; $\leq 50\%$ = apparent
634 averaging with two or more consecutive values are the same, but the number of stages apparent
635 averaging does not exceed 50%; $>50\%$ = more than half of the stages have the same value.

636

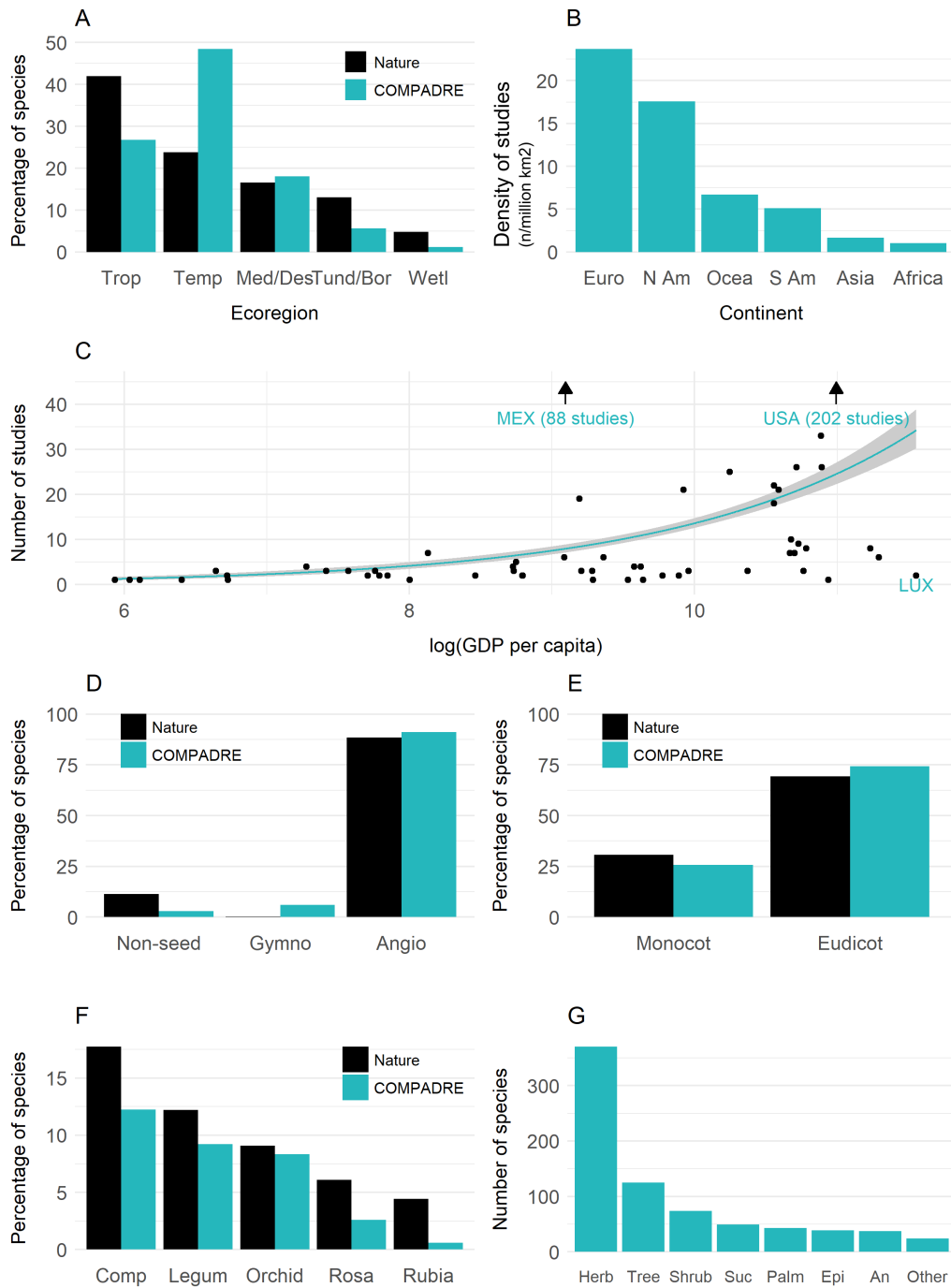
637 Figures and Tables



638

639 Figure 1.

640



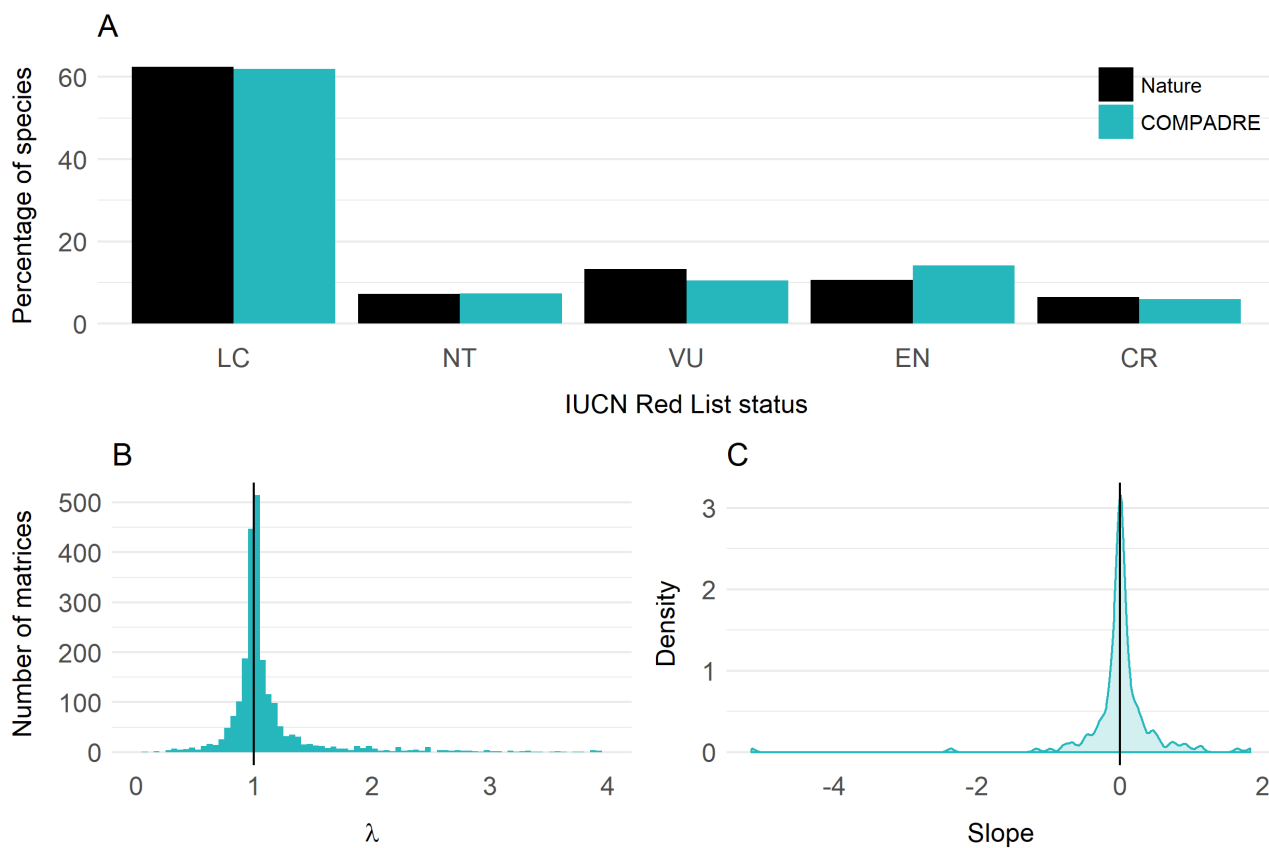
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643 Figure 2.

644

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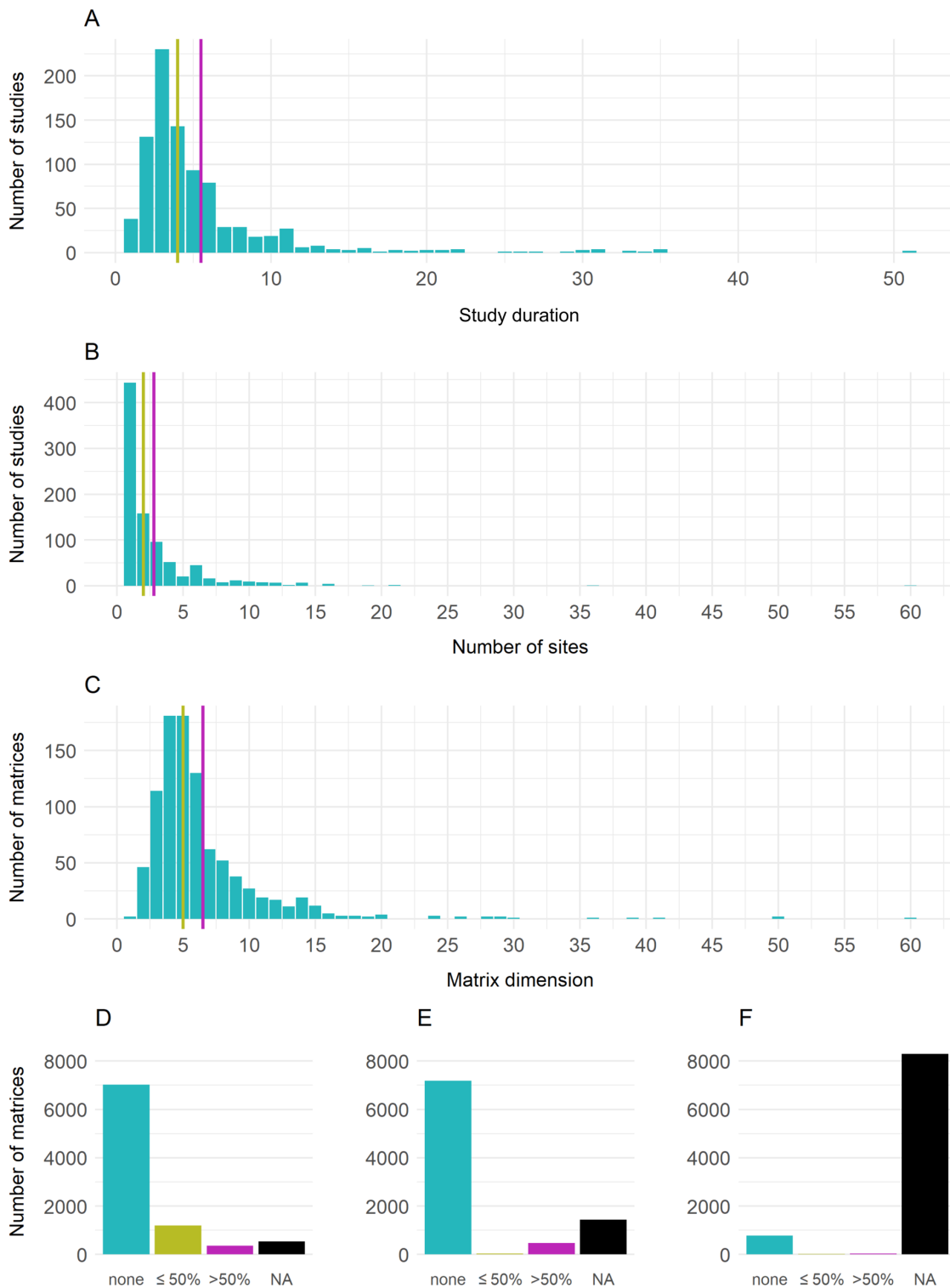


646

647 Figure 3.

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649



650

651 Figure 4.

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903 Supporting information

904 Appendix S1: Supplementary figures and tables

905 Appendix S2: Analysis code

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