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1 **ROBITT: a tool for assessing the risk-of-bias in studies of** 2 **temporal trends in ecology**

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20

21 **Abstract**

22 1. Aggregated species occurrence and abundance data from disparate sources are increasingly
23 accessible to ecologists for the analysis of temporal trends in biodiversity. However, sampling biases
24 relevant to any given research question are often poorly explored and infrequently reported; this has
25 the potential to undermine statistical inference. In other disciplines, it is common for researchers to
26 complete “risk-of-bias” assessments to expose and document the potential for biases to undermine
27 conclusions. The huge growth in available data, and recent controversies surrounding their use to infer
28 temporal trends, indicate that similar assessments are urgently needed in ecology.

29 2. We introduce ROBITT, a structured tool for assessing the “Risk-Of-Bias In studies of Temporal Trends
30 in ecology”. ROBITT has a similar format to its counterparts in other disciplines: it comprises signalling
31 questions designed to elicit information on the potential for bias in key study domains. In answering
32 these, users will define study inferential goal(s) and relevant statistical target populations. This
33 information is used to assess potential sampling biases across domains relevant to the research question
34 (e.g. geography, taxonomy, environment), and how these vary through time. If assessments indicate
35 biases, then users must clearly describe them and/or explain what mitigating action will be taken.

36 3. Everything that users need to complete a ROBITT assessment is provided: the tool, a guidance
37 document, and a worked example. Following other disciplines, the tool and guidance document were
38 developed through a consensus-forming process across experts working in relevant areas of ecology and
39 evidence synthesis.

40 4. We propose that researchers should be strongly encouraged to include a ROBITT assessment when
41 publishing studies of biodiversity trends, especially when using aggregated data. This will help
42 researchers to structure their thinking, clearly acknowledge potential sampling issues, highlight where
43 expert consultation is required, and provides an opportunity to describe data checks that might go
44 unreported. ROBITT will also enable reviewers, editors, and readers to establish how well research
45 conclusions are supported given a dataset combined with some analytical approach. It should also
46 strengthen evidence-based policy and practice, reduce differing interpretations of data, and provide a
47 clearer picture of the uncertainties associated with our understanding of ecological reality.

48 **Key words**

49 risk-of-bias; species occurrence data; temporal trends; Essential Biodiversity Variables; indicators;
50 uncertainty; insect declines

51 **Introduction**

52 Species occupancy and abundance are fundamental state variables in ecology. Understanding the rates
53 at which these variables are changing is required to monitor progress towards biodiversity targets and
54 the effects of conservation interventions. Ultimately, this information comes from data documenting
55 the detection of one or more individuals of some taxon; that is, species occurrence data, or, in some
56 countries, “biological records” (note that here we also use these terms to cover abundance data, as such
57 information may be considered an occurrence attribute). Species occurrence data from disparate
58 sources are often combined and analysed statistically to derive measures of biodiversity over large
59 taxonomic, spatial, and temporal extents (e.g. Gregory et al., 2005). Indeed, this is the premise of
60 species population “Essential Biodiversity Variables” (Jetz et al., 2019; Kissling et al., 2018; Pereira et al.,
61 2013). The temporal component of these data products may be averaged over spatial and taxonomic
62 domains to produce indicators (GEO BON, 2015); these have become a key source of information on
63 ecological change for policy makers (Navarro et al., 2017). Frequently then, evidence of temporal trends
64 in biodiversity is derived through the statistical analysis of species occurrence data.

65 Species occurrence data vary widely in terms of why and how they were recorded, and the information
66 that they provide. Presence-only data document the sighting of some species, with information on
67 where and when the sighting occurred. These data are derived from a variety of sources, including
68 natural history collections in museums and herbaria, surveys by professional biologists, and various
69 types of data collected by volunteer naturalists (Collen et al., 2013). Presence-absence data provide
70 additional information on sampling events which did not yield a detection of the focal taxon. These data
71 are most likely to be collected through structured monitoring schemes using specific protocols (but see
72 Sullivan et al., 2014). Abundance data can provide more information still: they document the number (or
73 other quantity) of individuals. All of these data can be used to provide information on trends in
74 biodiversity.

75 In recent years, species occurrence data have increased in volume and accessibility. This can be ascribed
76 to several initiatives: the digitization of historic biological records (Page et al., 2015); the proliferation
77 and growth of citizen science monitoring initiatives (Spear et al., 2017); the launch of online data
78 aggregators such as GBIF and similar regional portals (Nelson and Ellis, 2019); and the compilation of
79 more specialist databases focused on particular types of ecological community (Dengler et al.,

80 2011), monitoring data (Dornelas et al., 2018) or other evidence types (Hudson et al., 2017). Thanks to
81 these initiatives, it is now straightforward for ecologists to access large quantities of data, and to use
82 them for research. However, data quantity does not necessarily equal quality of scientific insight, and
83 there have been important questions raised concerning the suitability of some biodiversity data for
84 drawing reliable inferences about change over time (e.g. Ball-Damerow et al., 2019; Cardinale et al.,
85 2018; Pescott et al., 2019).

86 To appreciate the potential challenges associated with the analysis of heterogeneous data, it is useful to
87 define some key statistical concepts (see Box 1 in supplementary material 2 for a glossary of relevant
88 terms). Whilst there are many possible definitions of statistics (Barnett, 1982), one typical conception is
89 that of reasoning under uncertainty and inherent variability, with classical texts (e.g. Lehmann, 1959)
90 focusing on the use of observed data to make inferences concerning unobserved distributions. For
91 example, monitoring-type investigations can be appreciated as a sample-based approach to
92 understanding features of some broader environment; likewise, smaller-scale experiments are normally
93 conducted with generalisation in mind. In both these cases it is rarely feasible to census an entire
94 population of interest: researchers use samples. This leads to questions concerning the validity of
95 inferences. One assessment of a study's validity is to ask whether these inferences are well-supported
96 by the data in hand (internal validity). For sample-based results to be generalisable, however, they must
97 also be true of the wider population of interest (external validity). A study's external validity is likely to
98 be undermined if samples are not representative of the population with respect to important features
99 for the desired inferences (Meng, 2018); this is often known as "sampling bias", or sometimes "selection
100 bias".

101 To obtain a representative sample, researchers would ideally select individual units randomly from the
102 population (probability sampling). However, this is often impractical, in which case researchers might
103 make use of nonprobability samples, such as those found in aggregated biodiversity databases; these
104 are samples that were not necessarily collected to be representative of a clearly defined population.
105 Small samples may also be unrepresentative of important features by chance, even if they are
106 probability samples. Before researchers can understand a sample's representativeness, they must first
107 define their research question and statistical target population.

108 In studies of biodiversity trends, researchers tend to define their statistical populations along the axes of
109 space, time, and taxonomy (e.g. Dennis et al., 2019; Outhwaite et al., 2019; Powney et al., 2019; van
110 Strien et al., 2019). For example, one might be interested in trends in bird distributions in North America
111 over the period 1950 to the present day. It is also worth noting that, although they may not always be
112 defined explicitly, other axes may be important for inference. For example, researchers may be more
113 interested in whether samples represent all areas of some multi-dimensional environmental space (e.g.
114 as defined by a set of climatic variables), rather than just being considered representative of geographic
115 space. Likewise, for some purposes, representative coverage of species' traits may be desired along
116 with, or instead of, even phylogenetic coverage. To be representative of such populations, data should
117 be representative of all axes. To illustrate this point using the above example, data would need to be
118 sampled as close to randomly as possible across North America, across all relevant bird species, and
119 evenly between 1950 and the present day. Otherwise, it is possible that the data will be
120 unrepresentative of the populations of interest. For example, particular geographical areas may be over-

121 or under-sampled at particular times, leading to a confounding of time and space, and, ultimately,
122 conclusions that bear little resemblance to the true state of nature.

123 There are many situations in which occurrence data are unlikely to be representative of the statistical
124 populations implied by studies of biodiversity trends. Data collected opportunistically are highly likely to
125 be non-random along the key axes of space, time, and taxonomy (or other important dimensions).
126 Volunteer naturalists, for example, tend to preferentially sample accessible and attractive locations, and
127 interesting species (Barends et al., 2020; Prendergast et al., 1993). Structured data, collected according
128 to some sampling design, may well be representative of some set of domains; however, when multiple
129 datasets, with different aims, extents, and protocols, are aggregated (e.g. as on GBIF), then the target
130 population to which these data pertain becomes unclear. To illustrate this point, imagine several
131 datasets, each derived from structured monitoring of some taxon in some spatial unit at regular time
132 intervals. These data might be very informative about change in those units (but see Gonzalez et al.,
133 2016), but there is no reason to suppose that they can be combined and used to draw robust inferences
134 about some wider geographic domain, unless the samples happen to resemble a probability sample of
135 the broader population(s) of interest (Cardinale et al., 2018). The problem of a mismatch between
136 sample and population could be reduced or avoided if researchers first assessed their data to inform
137 readers of their choice of population and the scope of their inferences.

138 The frequent mismatch between sample and statistical target population in studies of biodiversity
139 trends has not gone unnoticed; indeed, it is a common subject for critical comments on studies in the
140 literature. For example, Sánchez-Bayo and Wyckhuys (2019) and van Klink et al. (2020) were criticised
141 for extrapolating their claims of insect declines beyond the taxonomic and geographical limits of their
142 data (Desquilbet et al., 2020; Jähnig et al., 2021; Saunders et al., 2020; Simmons et al., 2019). Vellend et
143 al. (2013) and Dornelas et al. (2014) were criticised for concluding that local species richness is not in
144 decline globally from meta-analyses of studies that were geographically biased in relation to human
145 disturbance and species richness itself (Cardinale et al., 2018; Gonzalez et al., 2016). Crossley et al.
146 (2020) and van Klink et al. (2020), on the other hand, were taxonomically selective when reporting their
147 conclusions: both sets of authors included non-insect groups in their analyses, but restricted their
148 conclusions (and paper titles) to insects (Desquilbet et al., 2021, 2020). Other studies of insect trends
149 have been criticised with regards to whether particular modelling approaches have appropriately dealt
150 with temporal biases in the data. For example, both Lister and Garcia (2018) and Soroye et al. (2020)
151 have been criticised in this regard (Anon., 2020; Guzman et al., 2021; Willig et al., 2019). This brief
152 overview of some recent disagreements highlights a fundamental problem: potential biases are rarely
153 communicated to the reader in sufficient detail; instead, they are often addressed with a passing
154 comment, if at all.

155 In other disciplines, strategies have developed to assist researchers in avoiding potentially inappropriate
156 inferential claims. In medicine and related areas, inclusion of a study in a systematic review often
157 requires that the original publication is subject to a “risk-of-bias” (RoB) assessment. Several tools have
158 been developed to conduct RoB assessments, each focusing on a particular type of study and data (see
159 **supplementary material 5**). Whilst many of these tools were designed for use in systematic reviews,
160 others were designed for use at the primary research stage, or both (**supplementary material 5**).
161 Regardless, the function of these tools is essentially the same: to clearly expose threats to the validity of
162 a study’s conclusions arising from potential biases in the underlying data. RoB tools in medicine have

163 been described as reflecting a “shift in focus from methodological quality to risk of bias” (Sterne et al.,
164 2016)—a shift that has yet to take place in ecology, despite efforts to provide structured approaches to
165 documenting methodological choices in some areas (e.g. Grimm et al., 2010). It is easy to appreciate
166 why this shift was needed in medicine: one would not want to approve some pharmaceutical product
167 which had only been demonstrated to be safe in some population subset, for example. We argue that
168 the increasing policy relevance of inferences about trends in biodiversity necessitates a similar transition
169 in ecology.

170 In this paper we introduce ROBITT, a tool for assessing the “Risk-Of-Bias In studies of Temporal Trends in
171 ecology”. The tool has a similar format to its counterparts in other fields: it comprises a number of
172 “signalling” questions (Sterne et al., 2016) designed to elicit information on the potential for bias in a
173 study. Users are first asked to define the statistical target population about which they intend to make
174 inferences, and then to assess whether their data are likely to be representative of this population in the
175 geographic, temporal, environmental, and taxonomic domains as relevant (the latter defined broadly as
176 covering any organismal space that might be important for inference). If the data are found to be
177 potentially biased, then the user is asked to explain how they will mitigate those biases, or how they will
178 be clearly and appropriately communicated. Below we describe the development of the tool, provide an
179 overview, describe its sections, and refer the reader to the supplementary material for the tool itself, a
180 guidance document, and worked example. Finally, we discuss the potential value of ROBITT for ecology,
181 and propose its inclusion as supplementary information for all studies of biodiversity trends based on
182 species occurrence data—particularly where those data are obtained from aggregated databases.

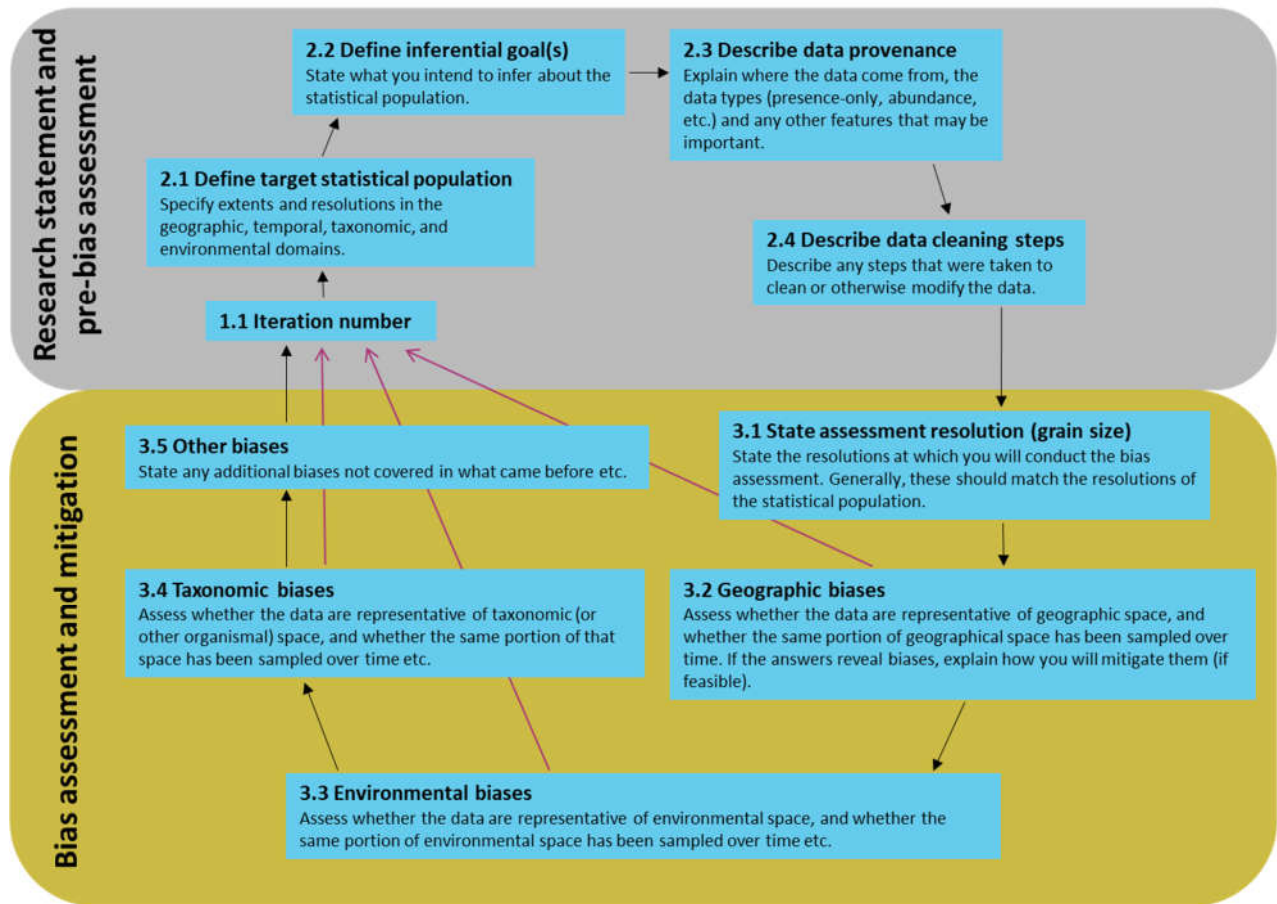
183 **ROBITT tool**

184 **Development**

185 ROBITT was developed through a consensus-forming process involving experts across relevant areas of
186 ecology and evidence synthesis (the authors). See supplementary material **3** for details.

187 **Overview**

188 ROBITT comprises 17 questions designed to elicit information on a study’s potential for bias. The user
189 may answer the questions using text and/or figures. The first section, the “research statement and pre-
190 bias assessment”, comprises four questions concerning the scope of the research and related issues; the
191 remainder constitutes the bias assessment itself. See Figure 1 for an overview of the tool. The ROBITT
192 tool and supporting guidance document can be found in supplementary materials **1 and 2**. The guidance
193 follows the PRISMA model (Page et al., 2021b): i.e., an explanation of the rationale for each question is
194 given, followed by a summary of the expected response. Worked examples of ROBITT are provided in
195 supplementary material **4**.



196

197 **Figure 1.** A conceptual overview of ROBITT with brief details about what is required at each stage. Black
 198 arrows indicate the order in which users should proceed through a ROBITT assessment. Purple arrows
 199 are used to indicate that completing a ROBITT form can be an iterative process: if the data are found to
 200 be unrepresentative of any domain, then it may be necessary to return to step 1.1 and redefine the
 201 extent and/or resolution of the statistical population accordingly.

202 **Tool sections**

203 ***Research statement and pre-bias assessment***

204 The purpose of this section is to assemble the information needed to assess a study's risk of bias. The
 205 first step is to define the target population about which inferences are desired. This must include a
 206 specification of the extents of any relevant domains (e.g. geographic, temporal, taxonomic,
 207 environmental). It must also include a statement of the resolutions at which analyses will be conducted
 208 (e.g., 1 km grid cells, annual increments etc.). This is important because the scale at which a research
 209 question is formulated can influence data availability and the nature of, and potential for, biases (e.g.
 210 Pescott et al., 2019). The next step is to state the inferential goal; for example, "to estimate temporal
 211 trends in species' occupancy". In the remainder of this section, the user must document data
 212 provenances, and explain and justify any steps that were taken to modify or clean data.

213 ***Bias assessment***

214 The main section of ROBITT is the bias assessment. This begins with a specification of the geographic,
215 temporal, and taxonomic resolutions (grain sizes) at which the assessment will be conducted. Generally,
216 these should match the resolutions at which inferences are desired (as specified in the research
217 statement section). It would likely be inappropriate, for example, to assess data in decadal time periods
218 and 100 km grid cells, and then conclude that they were unbiased for making yearly inferences at the 1
219 km resolution. We note that there may be limited exceptions to this: for example, it is not possible to
220 assess sampling biases at the species level using presence-only data because these say nothing about
221 sampling effort where the focal species was not observed.

222 The next three subsections denote our three main domains of potential bias: geographic, environmental
223 and taxonomic (or other organismal axis, such as functional group). Temporal biases are dealt with
224 within each of these three sections (see below). In each subsection, the user must answer three
225 questions: the first two are designed to reveal potential biases relative to the research question (i.e. the
226 inferential goal). The first asks whether the data are representative of that domain; that is to say, do the
227 data cover the whole domain evenly (ideally randomly)? The second question asks whether the same
228 portion of the focal domain has been sampled over time; that is, is there any indication of temporal
229 changes in coverage? The answers to this second question are crucial for assessing the suitability of the
230 data for estimating temporal trends. To illustrate this, imagine that species data are collected from one
231 location in one time period, and then from another in the next. Using these data to estimate changes in
232 species' distributions or abundances between time periods will likely be problematic, because shifts in
233 space are confounded with shifts in time. In one sense, the distinction between the first and second
234 question can be considered equivalent to the distinction between external and internal validity: a study
235 might have low external validity if it is not representative of some domain overall; however, for a subset
236 of that domain (e.g. a well-sampled portion of geographic space), the data might be very informative
237 about change (i.e. high internal validity). The answers to these first two questions in each domain have
238 important implications for how one answers the third.

239 The third question in each domain subsection asks the user to state how they will mitigate potential
240 biases indicated by the preceding two questions. There are several ways in which one might go about
241 mitigating biases, which we review in the Discussion. There will be cases in which it is unnecessary to
242 mitigate for a lack of coverage or inconsistent sampling over time, because these are not relevant to the
243 inferential goal. For example, even coverage in environmental space may be inappropriate if
244 environmental change is expected over time for the geographic extent of the analysis. Users are not
245 required to explain poor coverage in any domain if it is irrelevant to their inferences. There could also be
246 situations in which a bias is deemed relevant but mitigation is not feasible. In this case the resultant
247 trends should be appropriately and clearly caveated.

248 The final subsection is "Other potential biases". This is different to the previous three in that it does not
249 relate to a single domain; rather, it provides an opportunity for the user to consider additional biases
250 that might affect their research. The first question asks whether there are any temporal biases that do
251 not relate to the ecological states of interest. Often these biases will relate to observation error or the
252 estimation of some parameter in a model related to this. For example, site-occupancy models are
253 sometimes used to estimate trends in species' occupancies (Kéry and Royle, 2016). These models
254 normally require data from replicate visits to sites within short spaces of time to estimate detection
255 probabilities (thus correcting for imperfect detection). Where these models are used, analysts should

256 consider whether there is variation in the quantity and type of repeat visits that could result in biased
257 estimates of these parameters (Royle, 2006).

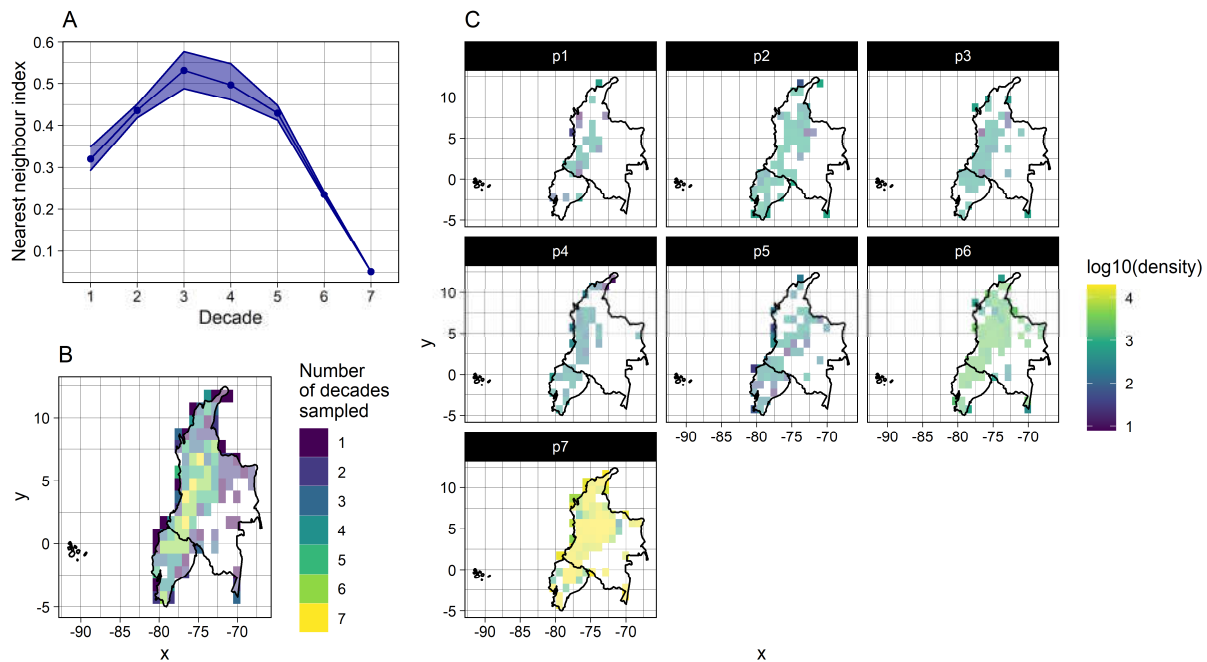
258 The second question in the “other biases” section asks the user to consider whether there are any other
259 biases not covered by the preceding questions. Examples include biases relating to phenology, such as a
260 mismatch between sampling dates and a species’ flight period; temporal baselines; and changes in the
261 portion of one domain that has been sampled over some other domain, such as geographic variation in
262 taxonomic coverage. Like earlier sections, the final question asks users to explain how they plan to
263 mitigate biases revealed in their answers to the two preceding questions. See the guidance document in
264 supplementary material 2 for detail on the expected content of responses to the ROBITT questions and
265 other background information.

266 **Completing the assessment**

267 Whilst the assessment questions require individual answers, it may be that researchers prefer to provide
268 responses in the main text of a report. As a point of comparison, PRISMA (Page et al., 2021a) provides a
269 checklist format that allows researchers to direct the reader to the answer to any given question. This
270 could also be the case here; for example, paper subheadings could be provided in response to a
271 question, provided the text referenced was a complete answer to it.

272

273 Users may go about answering the questions in the bias assessment section in the best ways they see fit.
274 However, we have found the use of “heuristics” that indicate the potential for bias to be of value. We
275 use the term “heuristic” to acknowledge that it is generally not possible to determine the exact extent of
276 bias without a probability sample for comparison. Many heuristics have been used to screen biodiversity
277 data for biases in the literature; we briefly review these in Table 1 in supplementary material 2. The
278 most common example is a map of the density of records across geographic space; such maps could
279 provide evidence of geographic representativeness (or lack thereof). Taking this further, one could
280 produce several maps, each pertaining to some time period; these could be used to assess temporal
281 variation in geographic coverage. To obtain a more formal, quasi-statistical measure of geographic
282 representativeness, one could compare the nearest neighbor distances of their data to those of a
283 simulated random distribution (Clark and Evans, 1954). This gives an index indicating the extent to which
284 the data depart from a random distribution geographically. In Figure 2 we present three example
285 heuristics that could be used to screen data for geographic biases. In these examples, the heuristics are
286 applied to hummingbird (Trochilidae) records collected between 1950 and 2019 in Ecuador and
287 Colombia. Whilst heuristics of this type will be useful, it is important to remember that a ROBITT
288 assessment is not intended to be a contextless set of numbers or figures: bias can strictly only be
289 defined in relation to some inferential goal. The central point of ROBITT is that assessments of bias are
290 clearly linked to a research question, and assessed in the context of this and any analytical tools being
291 used to answer that question.



292

293 Figure 2. Three “heuristics” indicating the potential for geographic biases in data on hummingbird
 294 occurrences collected in Ecuador and Colombia from 1950-2019. These data were downloaded from
 295 GBIF (see supplementary material 3 for full details of the provenance of these data). In these examples,
 296 the data are assessed in seven decadal time periods (p1 = 1950-1959, p2 = 1960-1969, etc.) and in 1°
 297 grid cells. Panel A shows the nearest neighbor index for each decade; values further from one indicate a
 298 greater departure from a simulated random distribution. The shaded band denotes uncertainty derived
 299 by bootstrapping. Panel B is a map showing the number of decades in which records are available for
 300 each grid cell. This is a simple measure of how the spatial distribution of sampling has changed over
 301 time. Panel C shows the density of records in each grid cell for each decade on a log10 scale.

302 In some cases completing a ROBITT assessment will be an iterative process. For example, researchers
 303 might complete a first iteration of the tool and find that data coverage is not sufficient in portions of
 304 their geographic domain of interest. In this case, they might decide to redefine this domain to exclude
 305 poorly sampled regions; this would mean completing a second iteration of ROBITT using an appropriate
 306 subset (Fig. 1, see supplementary material 4). Where a ROBITT assessment is iterative, the user should
 307 clearly version control (i.e. track and record changes over time) their documents and provide this history
 308 as supporting information to their work.

309 Discussion

310 Sampling biases have long been recognised as a challenge for inference in ecology (e.g. Peters, 1991),
 311 however, unlike in other disciplines, no formal tools for assessing these have been produced. We have
 312 designed and introduced ROBITT, a tool for assessing the potential “Risk-Of-Bias in studies of Temporal
 313 Trends in ecology”. The tool comprises a number of questions, each designed to clearly elicit the
 314 potential for bias in the study under assessment. In answering these, users will define their research

315 question and target population across relevant domains, and then assess the degree to which their data
316 are likely to be representative of these. We propose that researchers be strongly encouraged to include
317 a ROBITT assessment as supporting information when publishing studies of temporal trends in
318 biodiversity, especially when using aggregated data. We expect that this will support scientists in writing
319 clear methods sections, strengthen evidence-based policy and practice, help resolve scientific
320 controversies around biodiversity trends, assist editors, reviewers, and readers, and, ultimately,
321 highlight the uncertainty associated with our understanding of ecological reality. Accumulated over
322 studies, ROBITT assessments will also highlight where data are required to address pressing questions
323 concerning biodiversity change.

324 We hope that the completion of ROBITT will become a standard requirement where researchers
325 estimate trends from aggregated species occurrence data. The tools listed in **supplementary material 5**
326 have set similar precedents in other disciplines; many are endorsed by journals and uptake is generally
327 high. Whilst some reporting tools for various subdisciplines of ecology already exist, they do not focus
328 on risk-of-bias. These include the ODD (Grimm et al., 2010, 2006) and TRACE (Schmolke et al., 2010)
329 protocols for describing and documenting individual-based models, and the ODMAP (Zurell et al., 2020)
330 protocol for documenting the use of species distribution models. In medicine, some reporting tools have
331 evolved from a general focus on methodology to a more specific, and arguably more in-depth, focus on
332 the impacts of bias on inference (Sterne et al., 2016). There is no doubt a place for both in ecology
333 (indeed, some tools in medicine combine these aspects, e.g. Page et al., 2021a), however, we agree with
334 Sterne et al. (2016) that in-depth, qualitative, assessments of risk-of-bias across relevant domains are
335 more useful and revealing than simply checking methodological items off a list.

336 We suggest that researchers will get the greatest benefit from our tool if they use it to structure their
337 research. ROBITT contains questions that researchers should be asking themselves already; indeed, it
338 provides an opportunity to demonstrate the large amount of work that goes into studies of temporal
339 trends in biodiversity, but which may go unreported. An interesting possibility is that ROBITT
340 assessments could be supplied as part of the preregistration process, which is becoming increasingly
341 common in ecology (e.g.,
342 [https://besjournals.onlinelibrary.wiley.com/hub/journal/26888319/registered-reports-author-](https://besjournals.onlinelibrary.wiley.com/hub/journal/26888319/registered-reports-author-guidelines)
343 [guidelines](https://besjournals.onlinelibrary.wiley.com/hub/journal/26888319/registered-reports-author-guidelines)). If, on the other hand, a ROBITT form is completed just before the submission of an article
344 for publication, then it may reveal problems that could have been dealt with earlier. Completing the
345 form during the research process has the potential to save researchers' time, by providing a framework
346 for structuring thought and decision-making.

347 Much of the risk-of-bias literature in other disciplines has focused on the effects of interventions (see
348 supplementary material 5). In this type of research the questions asked are causal, because the desired
349 inference concerns whether some action results in some outcome. This has also been the standard focus
350 of evidence-based conservation (e.g. Lortie et al., 2015). ROBITT, on the other hand, is primarily focused
351 on descriptive inference of the type that is often used for ecological indicators (e.g. Gregory et al., 2005)
352 or the EBV literature (e.g. Jetz et al., 2019). However, this distinction is not absolute, and there are many
353 examples of ecological studies that use aggregated species occurrence data in attempts to reach causal
354 conclusions. For example, Woodcock et al. (2016) divided wild bee data for Britain into two subsets
355 based on insecticide use, assessing trends in occupancy for taxa in each subset. Whilst this type of
356 assessment is correlative, there is often a causal motivation (e.g. the title of Woodcock et al. 2016

357 implies causality). Whilst the ROBITT tool has not been explicitly designed to deal with these situations,
358 we suggest that it will still be useful when attempting to make causal inferences from observational
359 data. In the example of Woodcock et al. (2016), the domain representativeness of the data in the two
360 subsets could have been assessed separately to investigate the potential for confounding; additionally,
361 the full dataset could have been assessed for its external validity.

362 One key issue with risk-of-bias assessments is that, whilst it might be easy to define a target population,
363 in some cases it will not be straightforward to determine whether any given sample is representative of
364 that population. For example, a researcher might define their population as wild bees in Chile in the
365 2010s. Mapping the data might reveal that available data are not randomly distributed across the
366 country, but does this reflect the true distribution of wild bees in Chile, or does it reflect non-random
367 sampling? The user might also want to establish whether they have data for all known species of wild
368 bee in Chile: how do they know whether this is the case? The answers to these questions will vary.

369 Whilst it will not always be easy to establish whether a sample is representative of a population, we
370 propose some simple criteria. First, subject-matter experts should be consulted; experts may be able to
371 separate sampling biases from biological phenomena. For example, an expert might know, or suspect,
372 that a species or taxon group occupies areas where it has not been recorded; this is likely to be a strong
373 indication of sampling bias. Second, it might be possible to supplement expert advice with published
374 information. Regional or national Floras etc. may list (undigitised) specimens, or provide information on
375 regional occurrences at some coarse spatio-temporal level. Third, when using presence-only data for a
376 reasonably large number of species in the same group (e.g., bees, birds), it may be acceptable to assume
377 that the combined distribution of records for all species approximates the sampling distribution (Dudík
378 et al., 2005; Phillips et al., 2009). In this case, the combined data would ideally be randomly distributed
379 across the geographical domain. Fourth, presence/absence and abundance data may be a direct
380 reflection of the distribution of sampling (i.e. a species might not be detected but a record is still made
381 of the event), therefore such data may provide reliable information on the distribution of sampling in
382 space and time. If the basis of sampling is known (e.g. random, systematic-random etc.), then data may
383 be representative, at least within the bounds of the original survey. However, even here, such a sample
384 may still be unrepresentative of an analyst's target population if that population pertains to a different
385 spatio-temporal-taxonomic domain to the survey. We can see very few scenarios where it will not be
386 possible to at least approximate the degree to which a dataset is representative of a given population
387 using all the knowledge that could be brought to bear. Indeed, this is the rationale behind qualitative
388 risk-of-bias tools based on expert assessments (supplementary material 5).

389 If analysts cannot reach an informed conclusion with regards to the likely representativeness of a
390 sample, then broader inference is not likely to be meaningful; simple descriptive statistics could be used
391 instead, and this limitation acknowledged, with paper titles, abstracts etc. all reflecting this. This may
392 seem a negative conclusion for an analyst to reach, but we argue that this is likely to be the most
393 honest, and scientific, endpoint for a dataset whose representativeness cannot be clearly assessed.

394 Four of the questions in ROBITT provide researchers with an opportunity to consider whether and how
395 they can mitigate biases revealed elsewhere in the tool. It is not possible to review here all possible
396 measures that could be taken by researchers; a full treatment of adjustments and models for dealing
397 with bias would have to cover many topics within statistics and ecological data. However, we note three

398 general approaches. The first is to modify the data in some way (e.g. thinning; Inman et al. 2021). The
 399 second is to model the biases; typically, this will involve incorporation of variables thought to capture
 400 the biasing mechanism in some form of regression analysis (e.g. van Strien et al., 2019), although other
 401 approaches are possible (Ahmad Suhaimi et al., 2021). Third, we suspect that in many cases ROBITT will
 402 reveal the need to restrict the extent of researchers' inferences. This might include redefining the spatial
 403 extent of an analysis to reflect the fact that data are scarcely available in some portion of geographic
 404 space, or coarsening the temporal resolution to "smooth over" temporal biases in geographic or
 405 taxonomic coverage (Pescott et al., 2019). Any modifications to the extents of the statistical population
 406 should be reflected in paper titles, abstracts, etc. We note that it will often be prudent for researchers to
 407 assess the sensitivity of their conclusions to the choice of bias mitigation strategy: some statistical
 408 "fixes" can make aspects of inference worse (Gelman, 2007; Lele, 2010). Nevertheless, we suspect that
 409 by using these general bias mitigation strategies, researchers will usually be able to proceed with their
 410 analyses, even if those analyses relate to more limited statistical populations than initially envisioned.
 411 The problem of inference from biased samples is difficult, and quick fixes do not exist. ROBITT
 412 represents a first attempt to encourage more thoughtful assessment of the potential for bias to
 413 undermine the robust estimation of temporal trends in ecology. We intend to update the tool over time
 414 and welcome feedback from users.

415 References

- 416 Ahmad Suhaimi, S.S., Blair, G.S., Jarvis, S.G., 2021. Integrated species distribution models: A comparison
 417 of approaches under different data quality scenarios. *Divers. Distrib.* 1–10.
 418 <https://doi.org/10.1111/ddi.13255>
- 419 Anon., 2020. PubPeer comments on Soroye et al. 2019. [WWW Document]. URL
 420 <https://pubpeer.com/publications/B2A01E04EBC41DAD2C767B2111972C#1> (accessed 10.8.21).
- 421 Ball-Damerow, J.E., Brenskelle, L., Barve, N., Soltis, P.S., Sierwald, P., Bieler, R., LaFrance, R., Ariño, A.H.,
 422 Guralnick, R., 2019. Research applications of primary biodiversity databases in the digital age. *PLoS*
 423 *One* 1–26. <https://doi.org/10.1101/605071>
- 424 Barnett, V., 1982. *Comparative Statistical Inference.*, 2nd ed. Wiley, Chichester.
- 425 Bero, L., Chartres, N., Diong, J., Fabbri, A., Ghersi, D., Lam, J., Lau, A., McDonald, S., Mintzes, B., Sutton,
 426 P., Turton, J.L., Woodruff, T.J., 2018. The risk of bias in observational studies of exposures (ROBINS-
 427 E) tool: Concerns arising from application to observational studies of exposures. *Syst. Rev.* 7, 1–11.
 428 <https://doi.org/10.1186/s13643-018-0915-2>
- 429 Boyd, R.J., Powney, G., Carvell, C., Pescott, O.L., 2021. occAssess: An R package for assessing potential
 430 biases in species occurrence data. *Ecol. Evol.* <https://doi.org/10.1002/ece3.8299>
- 431 Buckland, S.T., Johnston, A., 2017. Monitoring the biodiversity of regions: Key principles and possible
 432 pitfalls. *Biol. Conserv.* 214, 23–34. <https://doi.org/10.1016/j.biocon.2017.07.034>
- 433 Cardinale, B.J., Gonzalez, A., Allington, G.R.H., Loreau, M., 2018. Is local biodiversity declining or not? A
 434 summary of the debate over analysis of species richness time trends. *Biol. Conserv.* 219, 175–183.
 435 <https://doi.org/10.1016/j.biocon.2017.12.021>
- 436 Clark, P., Evans, F., 1954. Distance to Nearest Neighbour as a Measure of Spatial Relationships in

- 437 Populations. *Ecology* 35, 445–453. <https://doi.org/10.1007/BF02315373>
- 438 Collen, B., Pettorelli, N., Baillie, J., Durant, S., 2013. *Biodiversity Monitoring and Conservation: Bridging*
439 *the Gap Between Global Commitment and Local Action - Conservation Science and Practice Series.*
440 Wiley.
- 441 Crossley, M.S., Meier, A.R., Baldwin, E.M., Berry, L.L., Crenshaw, L.C., Hartman, G.L., Lagos-Kutz, D.,
442 Nichols, D.H., Patel, K., Varriano, S., Snyder, W.E., Moran, M.D., 2020. No net insect abundance and
443 diversity declines across US Long Term Ecological Research sites. *Nat. Ecol. Evol.* 4, 1368–1376.
444 <https://doi.org/10.1038/s41559-020-1269-4>
- 445 Dengler, J., Jansen, F., Glöckler, F., Peet, R.K., de Cáceres, M., Chytrý, M., Ewald, J., Oldeland, J., Lopez-
446 Gonzalez, G., Finckh, M., Mucina, L., Rodwell, J.S., Schaminée, J.H.J., Spencer, N., 2011. The Global
447 Index of Vegetation-Plot Databases (GIVD): A new resource for vegetation science. *J. Veg. Sci.* 22,
448 582–597. <https://doi.org/10.1111/j.1654-1103.2011.01265.x>
- 449 Dennis, E.B., Brereton, T.M., Morgan, B.J.T., Fox, R., Shortall, C.R., Prescott, T., Foster, S., 2019. Trends
450 and indicators for quantifying moth abundance and occupancy in Scotland. *J. Insect Conserv.* 23,
451 369–380. <https://doi.org/10.1007/s10841-019-00135-z>
- 452 Desquilbet, M., Cornillon, P.A., Gaume, L., Bonmatin, J.M., 2021. Adequate statistical modelling and data
453 selection are essential when analysing abundance and diversity trends. *Nat. Ecol. Evol.* 5, 592–594.
454 <https://doi.org/10.1038/s41559-021-01427-x>
- 455 Desquilbet, M., Gaume, L., Grippa, M., Céréghino, R., Jean-François, H., Bonmatin, J.-M., Cornillon, P.-A.,
456 Maes, D., Van Dyck, H., Goulson, D., 2020. Comment on “Meta-analysis reveals declines in
457 terrestrial but increases in freshwater insect abundances.” *Science* (80-).
458 <https://doi.org/10.1126/science.abd8947>
- 459 Dornelas, M., Antão, L.H., Moyes, F., Bates, A.E., Magurran, A.E., Adam, D., Akhmetzhanova, A.A.,
460 Appeltans, W., Arcos, J.M., Arnold, H., Ayyappan, N., Badihi, G., Baird, A.H., Barbosa, M., Barreto,
461 T.E., Bässler, C., Bellgrove, A., Belmaker, J., Benedetti-Cecchi, L., Bett, et al. BioTIME: A database of
462 biodiversity time series for the Anthropocene. *Glob. Ecol. Biogeogr.* 27, 760–786.
463 <https://doi.org/10.1111/geb.12729>
- 464 Dornelas, M., Gotelli, N.J., McGill, B., Shimadzu, H., Moyes, F., Sievers, C., Magurran, A.E., 2014.
465 Assemblage time series reveal biodiversity change but not systematic loss. *Science* (80-). 344,
466 296–299. <https://doi.org/10.1126/science.1248484>
- 467 Dudík, M., Schapire, R.E., Phillips, S.J., 2005. Correcting sample selection bias in maximum entropy
468 density estimation. *Adv. Neural Inf. Process. Syst.* 323–330.
- 469 Gelman, A., 2007. Struggles with survey weighting and regression modeling. *Stat. Sci.* 22, 153–164.
470 <https://doi.org/10.1214/088342306000000691>
- 471 Gelman, A., 2006. Multilevel (hierarchical) modeling: What It can and cannot do. *Technometrics* 48,
472 432–435. <https://doi.org/10.1198/004017005000000661>
- 473 GEO BON Secretariat, 2015. *Global Biodiversity Change Indicators Version 1.2* 1–20.
- 474 Gonzalez, A., Cardinale, B.J., Allington, G.R.H., Byrnes, J., Endsley, K.A., Brown, D.G., Hooper, D.U., Isbell,
475 F., O’Connor, M.I., Loreau, M., 2016. Estimating local biodiversity change: A critique of papers

- 476 claiming no net loss of local diversity. *Ecology* 97, 1949–1960. <https://doi.org/10.1890/15-1759.1>
- 477 Gregory, R.D., Van Strien, A., Vorisek, P., Meyling, A.W.G., Noble, D.G., Foppen, R.P.B., Gibbons, D.W.,
478 2005. Developing indicators for European birds. *Philos. Trans. R. Soc. B Biol. Sci.* 360, 269–288.
479 <https://doi.org/10.1098/rstb.2004.1602>
- 480 Grimm, V., Berger, U., Bastiansen, F., Eliassen, S., Ginot, V., Giske, J., Goss-Custard, J., Grand, T., Heinz,
481 S.K., Huse, G., Huth, A., Jepsen, J.U., Jørgensen, C., Mooij, W.M., Müller, B., Pe'er, G., Piou, C.,
482 Railsback, S.F., Robbins, A.M., Robbins, et al., 2006. A standard protocol for describing individual-
483 based and agent-based models. *Ecol. Modell.* 198, 115–126.
484 <https://doi.org/10.1016/j.ecolmodel.2006.04.023>
- 485 Grimm, V., Berger, U., DeAngelis, D.L., Polhill, J.G., Giske, J., Railsback, S.F., 2010. The ODD protocol: A
486 review and first update. *Ecol. Modell.* 221, 2760–2768.
487 <https://doi.org/10.1016/j.ecolmodel.2010.08.019>
- 488 Guzman, L.M., Johnson, S.A., Mooers, A.O., Gonigle, L.K.M., 2021. Using historical data to estimate
489 bumble bee occurrence : Variable trends across species provide little support for community-level
490 declines. *Biol. Conserv.* 257, 109141. <https://doi.org/10.1016/j.biocon.2021.109141>
- 491 Higgins, J.P.T., Altman, D.G., Gøtzsche, P.C., Jüni, P., Moher, D., Oxman, A.D., Savović, J., Schulz, K.F.,
492 Weeks, L., Sterne, J.A.C., 2011. The Cochrane Collaboration's tool for assessing risk of bias in
493 randomised trials. *BMJ* 343, 1–9. <https://doi.org/10.1136/bmj.d5928>
- 494 Hudson, L.N., Newbold, T., Contu, S., Hill, S.L.L., Lysenko, I., De Palma, A., Phillips, H.R.P., Alhusseini, T.I.,
495 Bedford, F.E., Bennett, D.J., Booth, H., Burton, V.J., Chng, C.W.T., Choimes, A., Correia, D.L.P., Day,
496 J., Echeverría-Londoño, S., Emerson, S.R., Gao, D., Garon, M., et al., 2017. The database of the
497 PREDICTS (Projecting Responses of Ecological Diversity In Changing Terrestrial Systems) project.
498 *Ecol. Evol.* 7, 145–188. <https://doi.org/10.1002/ece3.2579>
- 499 Hughes, A., Orr, M., Ma, K., Costello, M., Waller, J., Provoost, P., Zhu, C., Qiao, H., 2020. Sampling biases
500 shape our view of the natural world. *Ecography (Cop.)*. 1–11. <https://doi.org/10.1111/ecog.05926>
- 501 Inman, R., Franklin, J., Esque, T., Nussear, K., 2021. Comparing sample bias correction methods for
502 species distribution modeling using virtual species. *Ecosphere* 12.
503 <https://doi.org/10.1002/ecs2.3422>
- 504 Jähnig, S.C., Baranov, V., Altermatt, F., Cranston, P., Friedrichs-Manthey, M., Geist, J., He, F., Heino, J.,
505 Hering, D., Hölker, F., Jourdan, J., Kalinkat, G., Kiesel, J., Leese, F., Maasri, A., Monaghan, M.T.,
506 Schäfer, R.B., Tockner, K., Tonkin, J.D., Domisch, S., 2021. Revisiting global trends in freshwater
507 insect biodiversity. *Wiley Interdiscip. Rev. Water* 8, 1–5. <https://doi.org/10.1002/wat2.1506>
- 508 Jetz, W., McGeoch, M.A., Guralnick, R., Ferrier, S., Beck, J., Costello, M.J., Fernandez, M., Geller, G.N.,
509 Keil, P., Merow, C., Meyer, C., Muller-Karger, F.E., Pereira, H.M., Regan, E.C., Schmeller, D.S., Turak,
510 E., 2019. Essential biodiversity variables for mapping and monitoring species populations. *Nat.*
511 *Ecol. Evol.* 3, 539–551. <https://doi.org/10.1038/s41559-019-0826-1>
- 512 Kéry, M., Royle, J.A., 2016. *Applied hierarchical modelling in ecology: analysis of species distribution,*
513 *abundance and species richness in R and BUGS.* Academic press, London.
- 514 Kim, S.Y., Park, J.E., Lee, Y.J., Seo, H.J., Sheen, S.S., Hahn, S., Jang, B.H., Son, H.J., 2013. Testing a tool for
515 assessing the risk of bias for nonrandomized studies showed moderate reliability and promising

- 516 validity. *J. Clin. Epidemiol.* 66, 408–414. <https://doi.org/10.1016/j.jclinepi.2012.09.016>
- 517 Kissling, W.D., Ahumada, J.A., Bowser, A., Fernandez, M., Fernández, N., García, E.A., Guralnick, R.P.,
518 Isaac, N.J.B., Kelling, S., Los, W., McRae, L., Mihoub, J.B., Obst, M., Santamaria, M., Skidmore, A.K.,
519 Williams, K.J., Agosti, D., Amariles, D., Arvanitidis, C., Bastin, L., De Leo, F., et al., 2018. Building
520 essential biodiversity variables (EBVs) of species distribution and abundance at a global scale. *Biol.*
521 *Rev.* 93, 600–625. <https://doi.org/10.1111/brv.12359>
- 522 Lehmann, E., 1959. *Testing Statistical Hypotheses*. John Wiley & Sons Inc., New York.
- 523 Lele, S.R., 2010. Model complexity and information in the data: Could it be a house built on sand?
524 *Ecology* 91, 3493–3496. <https://doi.org/10.1890/10-0099.1>
- 525 Lister, B.C., Garcia, A., 2018. Climate-driven declines in arthropod abundance restructure a rainforest
526 food web. *Proc. Natl. Acad. Sci. U. S. A.* 115, E10397–E10406.
527 <https://doi.org/10.1073/pnas.1722477115>
- 528 Lortie, C. J., Stewart, G., Rothstein, H., & Lau, J. (2015). How to critically read ecological meta-analyses.
529 *Research Synthesis Methods*, 6(2), 124–133. <https://doi.org/10.1002/jrsm.1109>
- 530 Meng, X.L., 2018. Statistical paradises and paradoxes in big data (I): Law of large populations, big data
531 paradox, and the 2016 us presidential election. *Ann. Appl. Stat.* 12, 685–726.
532 <https://doi.org/10.1214/18-AOAS1161SF>
- 533 Navarro, L.M., Fernández, N., Guerra, C., Guralnick, R., Kissling, W.D., Londoño, M.C., Muller-Karger, F.,
534 Turak, E., Balvanera, P., Costello, M.J., Delavaud, A., El Serafy, G.Y., Ferrier, S., Geijzendorffer, I.,
535 Geller, G.N., Jetz, W., Kim, E.S., Kim, H.J., Martin, C.S., McGeoch, et al., 2017. Monitoring
536 biodiversity change through effective global coordination. *Curr. Opin. Environ. Sustain.* 29, 158–
537 169. <https://doi.org/10.1016/j.cosust.2018.02.005>
- 538 Nelson, G., Ellis, S., 2019. The history and impact of digitization and digital data mobilization on
539 biodiversity research. *Philos. Trans. R. Soc. B Biol. Sci.* 374, 2–10.
540 <https://doi.org/10.1098/rstb.2017.0391>
- 541 Outhwaite, C.L., Powney, G.D., August, T.A., Chandler, R.E., Rorke, S., Pescott, O., Harvey, M., Roy, H.E.,
542 Fox, R., Walker, K., Roy, D.B., Alexander, K., Ball, S., Bantock, T., Barber, T., Beckmann, B.C., Cook,
543 T., Flanagan, J., Fowles, A., Hammond, P., et al., 2019. Annual estimates of occupancy for
544 bryophytes, lichens and invertebrates in the UK (1970-2015) 1–12.
545 <https://doi.org/10.5285/0ec7e549-57d4-4e2d-b2d3-2199e1578d84>
- 546 Page, L.M., Macfadden, B.J., Fortes, J.A., Soltis, P.S., Riccardi, G., 2015. Digitization of Biodiversity
547 Collections Reveals Biggest Data on Biodiversity. *Bioscience* 65, 841–842.
548 <https://doi.org/10.1093/biosci/biv104>
- 549 Page, M.J., Moher, D., Bossuyt, P.M., Boutron, I., Hoffmann, T.C., Mulrow, C.D., Shamseer, L., Tetzlaff,
550 J.M., Akl, E.A., Brennan, S.E., Chou, R., Glanville, J., Grimshaw, J.M., Hróbjartsson, A., Lalu, M.M., Li,
551 T., Loder, E.W., Mayo-Wilson, E., Mcdonald, S., McGuinness, L.A., et al., 2021b. PRISMA 2020
552 explanation and elaboration: Updated guidance and exemplars for reporting systematic reviews.
553 *BMJ* 372. <https://doi.org/10.1136/bmj.n160>
- 554 Pereira, H.M., Ferrier, S., Walters, M., Geller, G.N., Jongman, R.H.G., Scholes, R.J., Bruford, M.W.,
555 Brummitt, N., Butchart, S.H.M., Cardoso, A.C., Coops, N.C., Dulloo, E., Faith, D.P., Freyhof, J.,

- 556 Gregory, R.D., Heip, C., Höft, R., Hurtt, G., Jetz, W., Karp, D.S., et al., 2013. Essential biodiversity
557 variables. *Science* (80-). 339, 277–278. <https://doi.org/10.1126/science.1229931>
- 558 Pescott, O.L., Humphrey, T.A., Stroh, P.A., Walker, K.J., 2019. Temporal changes in distributions and the
559 species atlas: How can British and Irish plant data shoulder the inferential burden? *Br. Irish Bot.* 1,
560 250–282. <https://doi.org/10.33928/bib.2019.01.250>
- 561 Peters, R.H., 1991. *A critique for ecology*. Cambridge University Press, Cambridge.
- 562 Phillips, S.J., Dudík, M., Elith, J., Graham, C.H., Lehmann, A., Leathwick, J., Ferrier, S., 2009. Sample
563 selection bias and presence-only distribution models: Implications for background and pseudo-
564 absence data. *Ecol. Appl.* 19, 181–197. <https://doi.org/10.1890/07-2153.1>
- 565 Powney, G.D., Carvell, C., Edwards, M., Morris, R.K.A., Roy, H.E., Woodcock, B.A., Isaac, N.J.B., 2019.
566 Widespread losses of pollinating insects in Britain. *Nat. Commun.* 1–6.
567 <https://doi.org/10.1038/s41467-019-08974-9>
- 568 Prendergast, J. R., Wood, S. N., Lawton, J. H., Eversham, B. C., 1993. Correcting for Variation in
569 Recording Effort in Analyses of Diversity Hotspots. *Biodivers. Lett.* 1, 39–53.
- 570 Royle, J.A., 2006. Site occupancy models with heterogeneous detection probabilities. *Biometrics* 62, 97–
571 102. <https://doi.org/10.1111/j.1541-0420.2005.00439.x>
- 572 Sánchez-Bayo, F., Wyckhuys, K.A.G., 2019. Worldwide decline of the entomofauna: A review of its
573 drivers. *Biol. Conserv.* 232, 8–27. <https://doi.org/10.1016/j.biocon.2019.01.020>
- 574 Saunders, M.E., Janes, J.K., O’Hanlon, J.C., 2020. Moving on from the Insect Apocalypse Narrative:
575 Engaging with Evidence-Based Insect Conservation. *Bioscience* 70, 80–89.
576 <https://doi.org/10.1093/biosci/biz143>
- 577 Schmolke, A., Thorbek, P., DeAngelis, D.L., Grimm, V., 2010. Ecological models supporting environmental
578 decision making: A strategy for the future. *Trends Ecol. Evol.* 25, 479–486.
579 <https://doi.org/10.1016/j.tree.2010.05.001>
- 580 Schünemann, H., Brožek, J., Guyatt, G., Oxman, A., 2013. *GRADE handbook*.
- 581 Simmons, B.I., Balmford, A., Bladon, A.J., Christie, A.P., De Palma, A., Dicks, L. V., Gallego-Zamorano, J.,
582 Johnston, A., Martin, P.A., Purvis, A., Rocha, R., Wauchope, H.S., Wordley, C.F.R., Worthington,
583 T.A., Finch, T., 2019. Worldwide insect declines: An important message, but interpret with caution.
584 *Ecol. Evol.* 9, 3678–3680. <https://doi.org/10.1002/ece3.5153>
- 585 Simons, D.J., Shoda, Y., Lindsay, D.S., 2017. Constraints on Generality (COG): A Proposed Addition to All
586 Empirical Papers. *Perspect. Psychol. Sci.* 12, 1123–1128.
587 <https://doi.org/10.1177/1745691617708630>
- 588 Soroye, P., Newbold, T., Kerr, J., 2020. Among Bumble Bees Across Continents. *Science* (80-). 367, 685–
589 688.
- 590 Sterne, J.A., Hernán, M.A., Reeves, B.C., Savović, J., Berkman, N.D., Viswanathan, M., Henry, D., Altman,
591 D.G., Ansari, M.T., Boutron, I., Carpenter, J.R., Chan, A.W., Churchill, R., Deeks, J.J., Hróbjartsson,
592 A., Kirkham, J., Jüni, P., Loke, Y.K., Pigott, T.D., Ramsay, C.R., et al., 2016. ROBINS-I: A tool for
593 assessing risk of bias in non-randomised studies of interventions. *BMJ* 355, 4–10.

- 594 <https://doi.org/10.1136/bmj.i4919>
- 595 Sterne, J.A.C., Savović, J., Page, M.J., Elbers, R.G., Blencowe, N.S., Boutron, I., Cates, C.J., Cheng, H.Y.,
596 Corbett, M.S., Eldridge, S.M., Emberson, J.R., Hernán, M.A., Hopewell, S., Hróbjartsson, A.,
597 Junqueira, D.R., Jüni, P., Kirkham, J.J., Lasserson, T., Li, T., McAleenan, A., Reeves, et al., 2019. RoB
598 2: A revised tool for assessing risk of bias in randomised trials. *BMJ* 366, 1–8.
599 <https://doi.org/10.1136/bmj.l4898>
- 600 Sullivan, B.L., Aycrigg, J.L., Barry, J.H., Bonney, R.E., Bruns, N., Cooper, C.B., Damoulas, T., Dhondt, A.A.,
601 Dietterich, T., Farnsworth, A., Fink, D., Fitzpatrick, J.W., Fredericks, T., Gerbracht, J., Gomes, C.,
602 Hochachka, W.M., Iloff, M.J., Lagoze, C., La Sorte, F.A., Merrifield, M., et al., 2014. The eBird
603 enterprise: An integrated approach to development and application of citizen science. *Biol.*
604 *Conserv.* 169, 31–40. <https://doi.org/10.1016/j.biocon.2013.11.003>
- 605 van Klink, R., Bowler, D., Gongalsky, K., Swengel, A., Gentile, A., Chase, J., 2020. Meta-analysis reveals
606 declines in terrestrial but increases in freshwater insect abundances. *Science* (80-.). 368, 417–420.
607 <https://doi.org/10.1126/science.aax9931>
- 608 van Strien, A.J., van Swaay, C.A.M., van Strien-van Liempt, W.T.F.H., Poot, M.J.M., WallisDeVries, M.F.,
609 2019. Over a century of data reveal more than 80% decline in butterflies in the Netherlands. *Biol.*
610 *Conserv.* 234, 116–122. <https://doi.org/10.1016/j.biocon.2019.03.023>
- 611 Vellend, M., Baeten, L., Myers-Smith, I.H., Elmendorf, S.C., Beauséjour, R., Brown, C.D., De Frenne, P.,
612 Verheyen, K., Wipf, S., 2013. Global meta-analysis reveals no net change in local-scale plant
613 biodiversity over time. *Proc. Natl. Acad. Sci. U. S. A.* 110, 19456–19459.
614 <https://doi.org/10.1073/pnas.1312779110>
- 615 Willig, M.R., Woolbright, L., Presley, S.J., Schowalter, T.D., Waide, R.B., Heartsill Scalley, T., Zimmerman,
616 J.K., González, G., Lugo, A.E., 2019. Populations are not declining and food webs are not collapsing
617 at the Luquillo Experimental Forest. *Proc. Natl. Acad. Sci. U. S. A.* 116, 12143–12144.
618 <https://doi.org/10.1073/pnas.1820456116>
- 619 Wolff, R.F., Moons, K.G.M., Riley, R.D., Whiting, P.F., Westwood, M., Collins, G.S., Reitsma, J.B., Kleijnen,
620 J., Mallett, S., 2019. PROBAST: A tool to assess the risk of bias and applicability of prediction model
621 studies. *Ann. Intern. Med.* 170, 51–58. <https://doi.org/10.7326/M18-1376>
- 622 Woodcock, B.A., Isaac, N.J.B., Bullock, J.M., Roy, D.B., Garthwaite, D.G., Crowe, A., Pywell, R.F., 2016.
623 Impacts of neonicotinoid use on long-term population changes in wild bees in England. *Nat.*
624 *Commun.* 7. <https://doi.org/10.1038/ncomms12459>
- 625 Zurell, D., Franklin, J., König, C., Bouchet, P.J., Dormann, C.F., Elith, J., Fandos, G., Feng, X., Guillera-
626 Arroita, G., Guisan, A., Lahoz-Monfort, J.J., Leitão, P.J., Park, D.S., Peterson, A.T., Rapacciuolo, G.,
627 Schmatz, D.R., Schröder, B., Serra-Diaz, J.M., Thuiller, W., Yates, K.L., et al., 2020. A standard
628 protocol for reporting species distribution models. *Ecography* (Cop.). 43, 1261–1277.
629 <https://doi.org/10.1111/ecog.04960>
- 630
- 631