Computationally reproducing results from meta-analyses in Ecology and Evolutionary Biology using shared code and data

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ABSTRACT

The rates at which journal articles in ecology and evolutionary biology make data and code available have been studied previously. This study examines how often this data and code, when available, can be used to computationally reproduce results published in articles. This study surveys the data and code sharing practices of 177 meta-analyses published in ecology and evolutionary biology journals published over 2015-17. 26 articles (15%) were found to have obtainable data and code files. Results from these articles were targeted for computational reproduction using the data and code files obtained. Overall, from the sample of 177 articles, 4-13% of articles could be successfully reproduced, depending on the stringency of the criteria applied for a successful reproduction. The low overall success rate was primarily driven by the low rate of code sharing.

CONTENTS

1 INTRODUCTION

Concerns about the replicability and reproducibility of research, perhaps most prominently discussed in psychology (Collaboration, 2015), are also being raised and addressed in the fields of ecology and evolutionary biology. The role of replication in ecology has been discussed and debated in the literature (Ihle et al., 2017; Nakagawa and Parker, 2015; Schnitzer and Carson, 2016; Shavit and Ellison, 2017), and there has been interest and activity in conducting meta-research/meta-science studies in ecology and evolutionary biology (Fidler et al., 2017). For example, Fraser et al. (2018) surveyed ecologists to estimate the prevalence of questionable research practices in ecology and evolutionary biology. Fraser et al. (2020) surveyed ecologists about their opinions about replication studies. Open Science initiatives in the field include the Tools for Transparency in Ecology and Evolution, TTEE (Parker et al., 2016), which was followed by the formation of the Society for Open, Reliable, and Transparent Ecology and Evolutionary biology (SORTEE) for ecologists and biologists with an interest in transparency and open science (O'Dea et al., 2021b).

Closely related to this is the archiving and public availability of data. This is a well-established topic in ecology and evolutionary biology, with numerous efforts to facilitate and improve data sharing, coming from both individual researchers and institutions such as journals. Journals have recognised and stressed the importance of data archiving (Moore et al., 2010; Simmons, 2016; Whitlock et al., 2010). Researchers have created guides and compiled advice for how to best approach data archiving and sharing (Culina et al., 2018; Ihle et al., 2017; Whitlock, 2011). There have also been efforts to review the effectiveness of data archiving policies and assess how the field is doing (Caetano and Aisenberg, 2014; Miller et al., 2021; Roche et al., 2015).

In addition to data availability, the issue of code availability has also been raised. Here, "code" specifically refers to computer code or syntax which is written to perform the data analyses, simulations, and other calculations that are presented as results in articles. Mislan et al. (2016) surveyed 96 ecology journals in 2015, and found that only a small minority (14%) required code to be made available alongside published articles (in contrast to 38% of journals requiring data be made available alongside published articles). Culina et al. (2020) repeated this survey in 2020 and found that of the same 96 journals, 75% mandated or encouraged making code available. However, despite this now common journal policy, Culina et al. (2020) also found that only 27% of a sample of 346 ecology articles published 2015–19 actually shared code.

Computational reproducibility is defined as "obtaining consistent results using the same input data; computational steps, methods, and code; and conditions of analysis" (National Academies of Sciences, Engineering, and Medicine, 2019, p.46). Thus, availability of the data and code underpinning an article is a necessary prerequisite for computational reproducibility. Given available data and code, in theory we should be able to use both to recalculate results that match the published results. Directly evaluating the computational reproducibility of the published literature has been attempted in other fields, especially psychology (Hardwicke et al., 2018, 2021; Minocher et al., 2021; Obels et al., 2020; Stodden et al., 2018), but less often in ecology and evolutionary biology. In their assessment of code availability in ecology articles, Culina et al. (2020) did not attempt to run the code to reproduce results. Archmiller et al. (2020) did attempt to computationally reproduce a sample of 80 studies published in the *The Journal of Wildlife Management* and *Wildlife Society Bulletin*. They were able to obtain data and code for 19 studies, and mostly or fully reproduce the results for 13 of them.

Aims and scope

This exploratory study aims to assess computational reproducibility when using shared data and code by directly attempting the recalculation of specific results from meta-analyses published in ecology and evolution journals (the focus on meta-analyses in particular is explained in section S1 of the Supplementary Information). The primary outcome of this aim is the calculation of an overall computational reproducibility "success rate", similar to Stodden et al. (2018) and Hardwicke et al. (2021).

For this study, we only counted data/code that was reported as already available, rather than data/code that was (potentially) available upon request, as having been "shared" (see Figure 2). It is entirely possible that some authors of the meta-analyses included in this study may have in fact privately shared their data and code in response to requests from other researchers, and so technically have "shared" their data/code. Investigating whether such sharing might have taken place is not part of this study.

That the data and code are publicly available, and not merely available upon request, is important. A request for data requires an interaction between the requesting party and the article authors, and there is a possibility that the request will not be successful, for a variety of reasons (e.g., the authors are no longer contactable via the contact details provided in the article, the authors do not respond in a timely manner, the authors respond but refuse for some reason, the authors respond but can no longer find the data and code). We decided not to request data from article authors in this study: requesting data would introduce a element of the study that may not be reproducible by others: that is, the success or failure of any requests, which rely on a number of factors such as timing, existing connections (of lack thereof) with authors, and the purpose behind the request (i.e., the particulars of this study).

2 METHODS

The structure of the study falls into four distinct domains of activity that we undertook: obtain a sample of meta-analyses from ecology and evolution; assess each meta-analysis for data- and code-sharing; select results to be reproduced using shared data and code; embark on attempts to reproduce the selected results.

We curated a set of meta-analyses to survey by conducting a Scopus abstract and citation database search (see details in Supplementary Information S2). The search query, conducted on 20th December 2017, searched article titles, abstracts, and keywords for the string "meta-anal*", subject to two constraints. The first constraint restricted results to articles published between 2015 and 2017, inclusive. The second constraint restricted results to articles published in one of 21 ecology and evolution journal titles (identified by ISSN), which are the same journal titles as used for the survey of meta-analyses conducted in Nakagawa and Santos (2012).

The search yielded 229 results. One irrelevant result (an article from a non-ecology journal that had not been included in the search) was found to have been included in the results due to a Scopus database error and was immediately excluded, leaving 228 results.

The search results were coded to retain only those articles which were actual meta-analysis studies, details of the coding scheme used are in the Supplementary Information (S2). The final set of ecology and evolutionary biology meta-analyses, to be the basis of the rest of this study, is the set of 177 articles coded as containing claims to be meta-analyses. Figure 1 shows a PRISMA-style flow diagram for this study.

Recording code and data sharing in each article

With the meta-analyses identified, the next task was to ascertain whether data and/or code had been shared alongside each article. These terms are defined in the context of this study in Figure 2.

The availability of data and code for individual articles needs to be evaluated in the context of the publishing journals' policies about making data and code available at the time of publication, especially given that for this study, authors were not contacted regarding code and data availability. A review of the surveyed journals' code and data sharing policies are in the Supplementary Information (S3).

Each meta-analysis article in the set of 177 was assessed for data and code sharing using the coding scheme detailed in the Supplementary Information (S4). We also reviewed the methods section of each article for any and all references to the use of software. If an article did not report any details of software used, we reviewed supplementary documentation, if supplied. The review process is detailed in the Supplementary Information (S5).

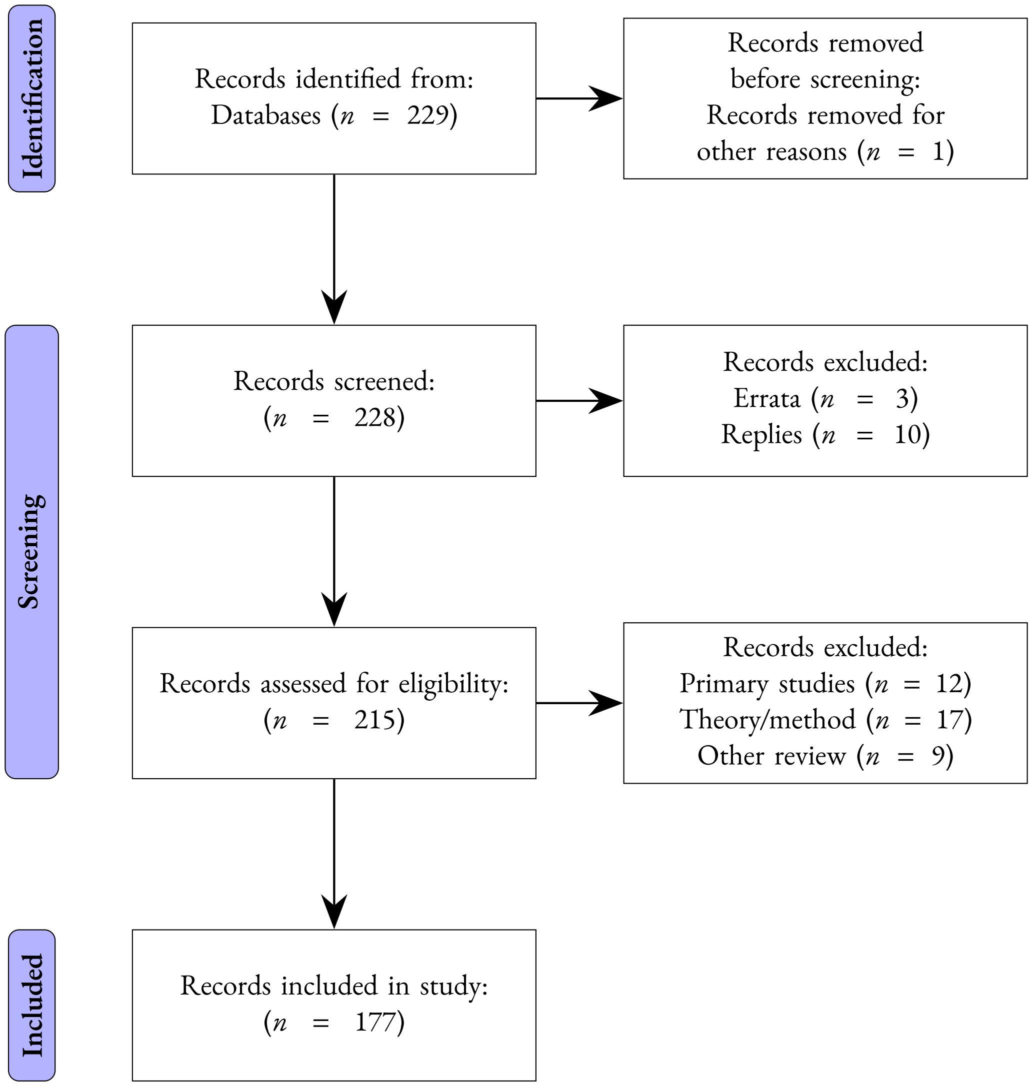

Figure 1: PRISMA-style diagram showing how the final set of meta-analyses was arrived at.

Definitions of data, code, and sharing

Data
"Data" in this context refers to curated, formatted information (both numeric and text-based) that can be considered the "raw material" for calculations and analyses that get presented as results in meta-analysis articles. It's expected that data would be presented in one or more formatted computer files (e.g., in comma separated values format), and perhaps accompanied by additional computer documents containing metadata or some other explanation of the data files' contents. There's a general expectation that the data would be relevant to (at least some of) the results presented in the article it appears alongside.

Code
Following Mislan et al. (2016) and Culina et al. (2020), "code" refers to computer code, specifically analysis code. Analysis code is designed to do tasks such as importing and manipulating data, performing statistical calculations based on data (e.g., calculating summary statistics or fitting models), or conducting simulations. Analysis code may be written in a programming language (e.g., R or Python) or it may be syntax to be run by a dedicated statistical analysis software package such as SPSS, SAS, or STATA. In the context of this study, the code is assumed to be relevant to the calculation of (at least some of) the results reported in the article it appears alongside. It's expected that code would be made available in plain text computer file(s) with the file extensions indicating the language/application, but this may not necessarily be the case.

Sharing
"Sharing" in this context means that the authors of the article have made data and code files available somehow alongside the publication of the article. The use of the term "available" is used here in a specific sense: publishers' websites for journals include provision for supplementary material associated with each published article. For journals which are not Open Access, data and code files provided as supplementary materials on publishers' websites are typically hidden behind subscriber paywalls (much like the articles themselves) and are not available to everyone. We made the decision that data and code provided in this way ought to count as having been shared for the purposes of this study. It is for this reason that we have chosen to refer to "shared" data and code rather than "open" data and code, since "open" carries with it connotations about availability and accessibility that may not apply to data and code files provided as supplementary material behind a publisher's paywall.
Additionally, for this study, we only counted data/code that was reported as already available, rather than data/code that was (potentially) available upon request, as having been "shared". It is entirely possible that some authors of the meta-analyses included in this study may have in fact privately shared their data and code in response to requests from other researchers, and so technically have "shared" their data/code. Investigating whether such sharing might have taken place is not part of this study.

Figure 2: The operational definitions of "data", "code", and "sharing" used for this study.

Selecting target results for computational reproduction

For each article in the subset of meta-analysis articles with both shared data and code, we identified a numeric "target" result that would be the basis of the computational reproduction attempt. Selecting a single result from an article involves subjective judgment, and can potentially be manipulated to increase or decrease the chance of success of reproducing each result. To mitigate this risk, we used the following process to identify a target result: our target result would be the first meta-analytic summary effect (consisting of the point estimate, the sample size, and the measure of uncertainty such as a confidence interval) reported in the results section of each article. The reasoning for this strategy is as follows: (i) in general, summary effects are very commonly reported in meta-analyses, and so this would identify like[1] results across articles; and (ii) identifying the first reported result is a consistent method of selection across articles that minimises (but does not eliminate entirely) the need for interpretation and therefore reduces the risk of bias. A procedure which allowed for results to be deliberately chosen for computational reproduction could potentially be selected on the basis of perceived ease of reproduction (even if only unconsciously). Even though first-reported summary effects might have something in common across articles (e.g., they may tend to be overall mean effects), it seems unlikely that such similarities would be directly correlated with ease of reproduction.

In practice, identifying and extracting the first reported meta-analysis summary effect was complicated by two factors. First, articles presented results in different ways: some articles reported results in the body of the text while others referred to a table or figure. We were able to extract the numerical values directly from in-text results and from results presented in tables. For results presented graphically in figures[2], we extracted numerical results using the software package WebPlotDigitizer version 4.4 for the Windows platform. We rounded all values extracted from figures to two decimal places. Frequently, a result was reported in-text and also expressed in a figure/table; we prioritised extracting in-text results over results reported in figures/tables. The second factor was that not all meta-analysis articles actually reported a summary effect result. In these cases, we extracted numerical values for the first-reported result of any kind associated with the meta-analysis.

Reproducing results and results comparison

For each article, we assessed the shared data and code for its relevance to the identified target result using the following general strategy: (i) Consult documentation accompanying data and code files (if it exists); (ii) Examine comments made within the code syntax files (if such comments exist); (iii) Examine the metadata of

[1] Here, "like" means that results have similar goals (to summarise multiple effect sizes from the literature) and are the result of approximately similar methods (from a family of linear models used in meta-analysis).

[2] Figures required additional interpretation, as they typically plotted multiple summary effects. In these cases, we prioritised extracting the "overall" summary effect if it existed, and otherwise selected the "first" plotted result, according to the layout of the figure (e.g., either the leftmost or topmost result).

data files (if it exists); (iv) Examine the contents of data files directly, looking for clues in variable names and data formats; (v) Examine the syntax of code files directly, looking for clues in the names of functions called and the kinds of calculations made. This approach was sufficient to discern with confidence whether the data and code files were applicable to the re-calculation of the target result. We went ahead with attempting to reproduce the target result for each article where both the shared data and code were found to be relevant.

In cases where we found that the code and/or data were not relevant to the identified target result, our attempt to reproduce those particular target results ended at this point. Rather than do nothing further with these cases, we decided to return to the article and identify an alternative target result that was relevant to the shared data and code, and report the results of these reproduction attempts separately.

Each reproduction attempt was packaged as a reproducible document written in RMarkdown contained with in a controlled computational environment using Docker (details are in the Supplementary Information Section S9). Where code could be successfully run, reproduced target results were compared with the originally published values with the difference expressed as the percent error from the original. For each target result (which consisted of a set of numbers, e.g., summary effect estimate, confidence interval bounds, and sample size), we followed the method used in Hardwicke et al. (2021) and quantified the difference between the original published value and reproduced value by calculating the relative error, expressed as a percentage: $\partial = 100 \times |x_R - x_O|/|x_O|$, where x_O is the original reported result value and x_R is the reproduced result value. Note that the relative error is undefined when the original value is zero. Again following Hardwicke et al. (2021), we distinguished between three magnitudes of error: exact matches ($\partial = 0$), minor numerical discrepancies ($0 < \partial < 10$) and major numerical discrepancies ($\partial \geq 10$).

3 RESULTS

The 177 meta-analyses were located among the 21 journals as shown in Table 1. The table also shows the total number of articles from each journal returned by the literature search. Note that neither *Evolutionary Ecology* or *The Quarterly Review of Biology* were found to have published any articles which claimed to be meta-analyses over 2015–17 (the literature search did not return any results at all from the journal *Evolutionary Ecology*). The journal which was found to have the most meta-analyses during 2015–17 was *Biological Reviews*, followed by *Oikos*. The meta-analyses in the sample were fairly evenly spread across the three years searched, as shown in Table 2. Note that six articles have a publication year of 2018; these articles had all been published online during 2017 (and so were picked up in the literature search), but at the time of the literature search had not yet been assigned to a specific journal issue. These six were subsequently published in journal issues dated in 2018. We decided to keep these six journal articles and regard them as articles published in 2017.

Journal Title	Meta-analysis N	Meta-analysis %	Other N	Other %	Total N	Total %
Biological Reviews	24	13.6	5	9.8	29	12.7
Oikos	22	12.4	2	3.9	24	10.5
Ecology Letters	19	10.7	1	2.0	20	8.8
New Phytologist	18	10.2	5	9.8	23	10.1
Ecology	13	7.3	9	17.6	22	9.6
Journal of Applied Ecology	10	5.6	2	3.9	12	5.3
Molecular Ecology	10	5.6	5	9.8	15	6.6
Oecologia	10	5.6	1	2.0	11	4.8
Functional Ecology	9	5.1	1	2.0	10	4.4
Journal of Ecology	7	4.0	0	0.0	7	3.1
Journal of Animal Ecology	6	3.4	3	5.9	9	3.9
Ecological Monographs	5	2.8	0	0.0	5	2.2
Behavioral Ecology	4	2.3	3	5.9	7	3.1
Evolution	4	2.3	0	0.0	4	1.8
Journal of Evolutionary Biology	4	2.3	10	19.6	14	6.1
Animal Behaviour	3	1.7	2	3.9	5	2.2
Behavioral Ecology and Sociobiology	3	1.7	0	0.0	3	1.3
Ecological Applications	3	1.7	0	0.0	3	1.3
The American Naturalist	3	1.7	1	2.0	4	1.8
The Quarterly Review of Biology	0	0.0	1	2.0	1	0.4
Evolutionary Ecology	0	0.0	0	0.0	0	0.0
Total	*177*	*100.0*	*51*	*100.0*	*228*	*100.0*

Table 1: Breakdown of the 177 identified meta-analysis articles by journal title.

Publication Year	N	%
2015	56	31.6
2016	61	34.5
2017	54	30.5
2018	6	3.4
Total	*177*	*100.0*

Table 2: Breakdown of the 177 identified meta-analysis articles by publication year. Articles with publication year 2018 were all first published online in 2017 before being assigned to a journal issue dated in 2018.

Rates of data and code sharing

The practice of including some kind of supplemental information alongside a published article was very common in this sample. The vast majority (168/177, or 95%) of meta-analysis articles included some kind of supplementary or supporting document (regardless of whether or not they also shared data or code).

When articles were reviewed for data sharing (as per the coding scheme summarised in Table S5), a clear majority of 78% or 138 meta-analyses indicated that data had been shared in some manner. Despite the positive indication, in five cases data files could not actually be obtained. This meant that the effective data sharing rate among this sample of meta-analysis articles was 75% (133 out of 177).

The rates of code sharing were much lower in comparison to data sharing: we were able to obtain shared code files for 16% of meta-analysis articles (28 out of 177). This was one less than the number of articles which had indicated code was available. Of the 28 articles with code, 26 had shared data too, meaning that 15% of articles (26 of 177) in this sample shared both data and code. Section S6 of the Supplementary Information breaks down data and code sharing rates by journal.

Characteristics of shared data and code

Figure 3 shows the online locations where the data files shared by the 133 articles. The majority of data-sharing articles shared some or all of the data files on the journal publisher's website (58%, $n = 77$): in these cases, the data file(s) had been uploaded as supplementary material to the article. The Dryad Digital Repository (Dryad, 2021) was the next most common location to share data (35% or 46 articles), followed by the Figshare (8%, $n = 11$) and Zenodo (1.5%, $n = 2$) repositories. One article was judged to have shared the data for its meta-analyses in tables presented within the published article itself: the article mentioned that the effect sizes and other details for all the individual studies included in the meta-analysis calculations were provided across two tables.

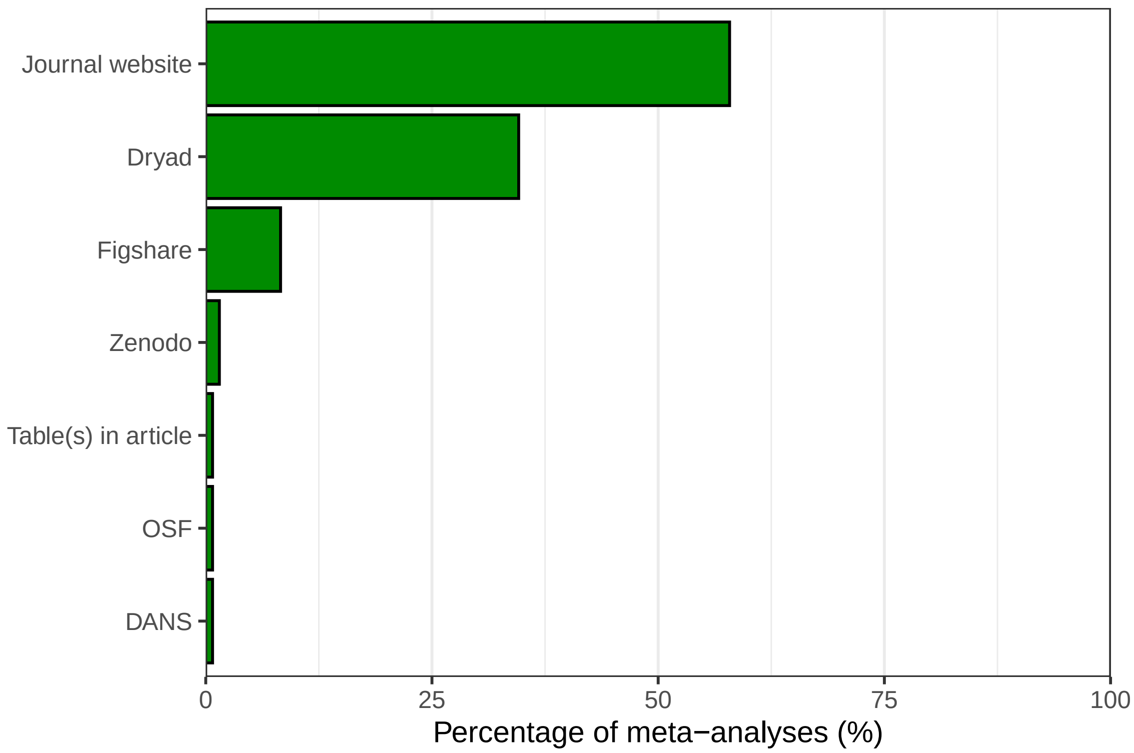

Figure 3: Breakdown of the locations where articles shared data online. Note that some articles shared data files in more than one location; both locations were counted, so the percentages indicated add up to more than 100%.

Figure 4 shows the types (formats) of data files shared by the 133 articles. The most common format for data files was the Microsoft Excel spreadsheet (44%, $n = 59$); this included both the binary XLS format and the Open XML XLSX format. The next most common format was the comma separated values (CSV) format (25%, $n = 33$). Data in a variety of plain text formats was shared by 15% of articles ($n = 20$): this included files containing phylogenetic data in NEXUS or Newick tree format. A substantial minority of articles shared tabular data in document formats like Microsoft Word Document formats DOC and DOCX (17%, $n = 22$), Portable Document Format PDF (14%, $n = 19$), Hypertext Markup Language HTML (2%, $n = 3$), and one article shared data in Rich Text Format RTF (1%). Two articles shared data files with a binary format: one article shared a data file in RData format, a binary file used by the R language, and one article shared multiple data files in a proprietary binary format associated with data logging equipment.

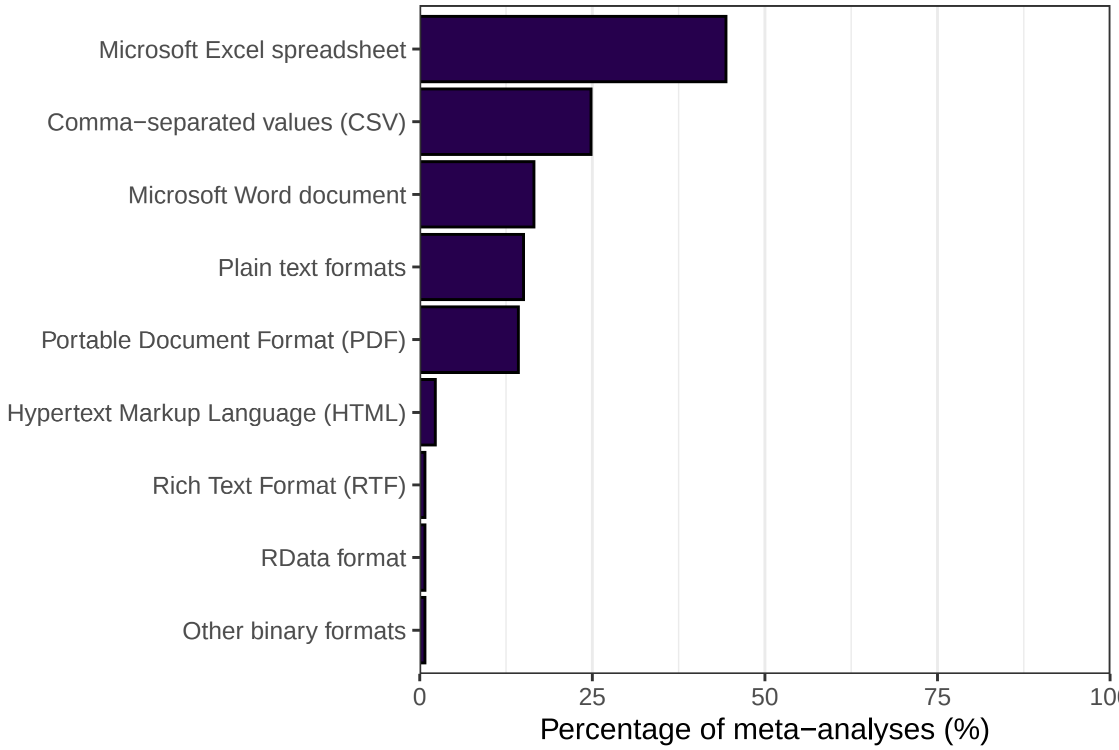

Figure 4: Breakdown of the types of file format shared by each article. Some articles shared data files of more than one type, and both types of file were counted (multiple files of the same file format only counted as one). This means that the percentages will add up to more than 100%.

Table 3 breaks down the type (i.e., language or compatible software environment) of code shared by the 28 meta-analysis articles which shared code. The overwhelming majority of articles shared R code (26 out of 28, 93%): 25 shared only R code, and one article shared R code and C++ code, which were designed to work together. The other two articles shared FORTRAN code and Python code.

Type of code shared	N	%
FORTRAN	1	3.6
Python	1	3.6
R	25	89.3
R and C++	1	3.6
Total	28	100.0

Table 3: The 28 code-sharing meta-analysis articles broken down by the type of code shared.

Software mentioned in articles

Overall, 171 meta-analysis articles (97%) mentioned at least one specific software package that was used during the study, whether mentioned in the article text or in supplementary material. The R software environment was by far the most commonly mentioned software package with nearly 80% of articles mentioning R. The next most commonly mentioned piece of software was MetaWin; 11% of articles mentioned using it. The specialised meta-analysis software package CMA was mentioned by two articles, or 1% of the sample. The full list of all software packages mentioned is in the Supplementary Information (S7). Due to the popularity of R in this sample, and the specifics of its package system, R and R packages are summarised separately from the non-R software packages.

There were 144 mentions of software packages that weren't the R software environment or an R package. The majority of these mentions were accompanied by some kind of reference: 83 (58%) included a complete citation that appeared in the article's reference section, and 39 (27%) included a short in-text reference[3]. Only 15% of these software package mentions had no citation of any kind. A majority of these software package mentions (95, or 66%) also specified which version of the software package was used.

As mentioned above, 141 meta-analysis articles (nearly 80%) mentioned using the R software environment. The majority of these mentions of R included a citation: 86 (61%) included the citation in the reference section and 21 (15%) included a short in-text reference. The version of R used was mentioned in 88 (62%) articles (see Table S9 in the Supplementary Information). In total, there were 257 mentions of specific R packages: 220 (86%) included a full citation and 3 (1%) a short in-text reference. The most common R package mentioned was the *metafor* package (Viechtbauer, 2010), mentioned by 75 articles (53% of the articles which mentioned R). Package versions were mentioned in 58 (23%) cases. A table listing all R packages mentioned in articles is provided in the Supplementary Information (Table S8).

Reproducing target results

The subset of 26 articles with both shared data and shared code was the focus of the reproduction attempts. For each article we selected a target result; in 22 cases, we were able to identify what we termed a "summary effect" result: a mean, correlation, or model parameter such as slope derived from the data collected for the meta-analysis. These target results are detailed in Table 4. In the other 4 cases, the articles did not report such a result, but instead a variety of different results from an eclectic set of analyses. These other results are specified individually for each article in the Supplementary Information (Tables S10-S15).

[3]These short in-text references included simple mentions of the software publisher or author, and/or a URL to the software's website.

ID	Study	Result source	Effect size type	N	Estimate	Uncertainty
MA016	Xu et al. (2017)	in text (p.1100)	Pearson's *r*	49	-0.83	< 0.001 (*p*-value)
MA060	Winternitz et al. (2017)	in text (p.674)	Fisher *z*-transformation	37	0.044	(-0.174, 0.289) (95% HPDI)
MA062	Grueber et al. (2018)	in text (p.1115)	Hedges' *d*	37	-0.205	(-0.444, 0.035) (95% CI)
MA065	Noble et al. (2018)	in text (p.80)	Hedges' *g*	703	-8.42	(-10.73, -6.63) (95% CI)
MA067	Risely et al. (2017)	in text (p.306)	Hedges' *g*	52	-0.21	0.07 (SE), -2.7 (*z*-score), 0.006 (*p*-value)
MA068	Ronget et al. (2017)	in text (p.14)	odds ratio	75	1.82	(1.37, 2.41) (95% HPDI)
MA071	Sievers et al. (2017)	Figure 3A (p.538)	response ratio	50	-0.26	(-1.02, 0.51) (95% CI)
MA074	Harts et al. (2016)	in text (pp.2795-2796)	Pearson's *r*	43	0.183	(0.089, 0.274) (95% CI)
MA081	Jaffé et al. (2016)	in text (p.5351)	slope parameter	1296	1.30	(0.95, 1.66) (95% CI)
MA091	Lemoine et al. (2016)	in text (p.2556)	Cohen's *d*	65	0.56	(0.42, 0.69) (95% CI)
MA095	Gibert et al. (2016)	Figure 3A (pp.1495-1496)	Fisher *z*-transformation	25	0.76	(0.61, 0.91) (95% CI)
MA126	Anderson (2016)	in text (p.83)	log odds ratio	n.s.	-1.11	0.49 (SE), -2.28 (*z*-score), 0.023 (*p*-value), (-2.06, -0.15) (95% CI)
MA145	Moore et al. (2016a)	in text (p.366)	Fisher *z*-transformation	118	-0.08	(-0.22, 0.03) (95% HPDI), 38 ($N_{studies}$), 25 ($N_{species}$)
MA147	Holman (2016)	in text (p.66-69)	percentage	49	0.13	0.030 (SE), (0.074, 0.19) (95% CI)
MA155	Strader et al. (2016)	in text (p.565)	Pearson's *r*	n.s.	0.51	0.01 (*p*-value)
MA188	Senior et al. (2015)	in text (p.653)	log response ratio	818	-0.363	(-0.408, -0.318) (95% CI)
MA191	Voje (2015)	in text (p.92)	slope parameter	553	0.86	(0.77, 0.94) (95% CI)
MA198	Paz-Vinas et al. (2015)	in text (p.4595)	Fisher *z*-transformation	79	-0.41	(-0.55, -0.27) (95% CI)
MA202	Mehrabi and Tuck (2015)	in text (pp.1072-1073)	Hedges' *d*	329	-0.330	(-0.503, -0.156) (95% CI)
MA211	Yuan and Chen (2015)	Figure 2 (p.374)	log response ratio	3298	0.24	(0.23, 0.25) (95% CI)
MA213	Colautti and Lau (2015)	in text (p.2004)	difference in means	654	-0.07	0.362 (*p*-value)
MA229	Gamfeldt et al. (2015)	Figure 3 (p.256)	log response ratio	57	0.40	(0.24, 0.53) (95% CI)

Table 4: Details of the 22 summary effect target results selected for reproduction attempts. In the table, the following abbreviations are used: CI – confidence interval; HPDI – highest posterior density interval; SE – standard error; n.s. – not stated

Across the 26 articles with data and code, there was a total of 173 separate target result values. This includes all summary effect estimate values, sample size values, measures of uncertainty such as lower and upper bounds of confidence intervals described in Table 4 and other values described in Tables S10-S15.

Table 5 summarises our reviews of the articles' shared code for relevance to the target results: Of the 22 articles with summary effect target results, 19 had relevant code, and one had partially relevant code. Of the 4 articles with other target results, one had relevant code, and two had partially relevant code. The remaining cases had code which was not relevant. "Not relevant" means that the shared code performed calculations or analyses that were unrelated to the calculation of the meta-analysis results writ large, let alone the specific meta-analysis target result selected for reproduction. (Such code might instead conduct simulations or analyse experimental data.) Shared code deemed "partially relevant" was code that performed calculations or analyses that related to a subset of the elements that make up the meta-analysis results in total, but not the entirety (and in particular, not the meta-analysis target result selected for reproduction). In the "not relevant" and "partially relevant" cases, the code could not be used to reproduce the target result for each article.

Overall, we judged 20 out of 26 articles with shared data and code (77%) to have code fully relevant to the target result, and therefore we could straightforwardly attempt to reproduce these 20 results.

We attempted to reproduce the 108 target results associated with the 20 articles with relevant code. The reproduction attempt for each article was fully documented in a report, refer to the Supplementary Information (S9) for details. We will regard the 65 target results associated with the six articles with irrelevant/partially relevant code as having failed to be reproduced by default. (We will return to these articles in the next section.) Table 6 summarises the results of the reproduction attempts of the target results.

Table 6 shows that 57% of target results could be reproduced either exactly (to the precision reported in the original article) or within 10% of the original value. Only four reproduced values differed from the original value by 10% or more, and there were six target results from three articles that could not be reproduced at all; the circumstances of these six failures are described in Table 7.

The summary of the reproduction attempts in Table 6 counts every target result value separately, whether an effect size point estimate, a lower or upper bound of a confidence interval, or a sample size. Calculating a reproducibility success rate over the total number of values in this way does not consider that the sets of values from each article are inter-dependent, and so the success or failure in reproducing one value from an article may not be considered to be independent of the success or failure in reproducing another value from the same article. The possibility of dependency of reproduction success between the different target values

ID	Study	Result type	Code relevance
MA016	Xu et al. (2017)	summary effect	not relevant
MA060	Winternitz et al. (2017)	summary effect	relevant
MA062	Grueber et al. (2018)	summary effect	relevant
MA065	Noble et al. (2018)	summary effect	relevant
MA067	Risely et al. (2017)	summary effect	relevant
MA068	Ronget et al. (2017)	summary effect	partially relevant
MA071	Sievers et al. (2017)	summary effect	relevant
MA074	Harts et al. (2016)	summary effect	relevant
MA081	Jaffé et al. (2016)	summary effect	relevant
MA091	Lemoine et al. (2016)	summary effect	relevant
MA092	Xu et al. (2016)	other result	not relevant
MA094	Turney and Buddle (2016)	other result	partially relevant
MA095	Gibert et al. (2016)	summary effect	relevant
MA126	Anderson (2016)	summary effect	relevant
MA129	Crouzeilles and Curran (2016)	other result	relevant
MA145	Moore et al. (2016a)	summary effect	relevant
MA147	Holman (2016)	summary effect	relevant
MA155	Strader et al. (2016)	summary effect	not relevant
MA188	Senior et al. (2015)	summary effect	relevant
MA191	Voje (2015)	summary effect	relevant
MA198	Paz-Vinas et al. (2015)	summary effect	relevant
MA202	Mehrabi and Tuck (2015)	summary effect	relevant
MA211	Yuan and Chen (2015)	summary effect	relevant
MA212	Valls et al. (2015)	other result	partially relevant
MA213	Colautti and Lau (2015)	summary effect	relevant
MA229	Gamfeldt et al. (2015)	summary effect	relevant

Table 5: Summary of the shared code review of articles to gauge the relevance of code to the target result.

Outcome of target result reproduction attempt	N	%
Original and reproduced values match exactly	75	43.4
Original and reproduced values differ by less than 10%	23	13.3
Original and reproduced values differ by 10% or more	4	2.3
Failed, could not calculate any value for target result	6	3.5
Failed, code not relevant to target result	65	37.6
Total	173	100.0

Table 6: Breakdown of target result reproduction attempts.

within an article is examined in the Supplementary Information (S9).

ID	Study	Target result(s)	Description
MA081	Jaffé et al. (2016)	2 values (upper and lower confidence interval limits)	The code uses bootstrapping to calculate the reported confidence interval, but we encountered an error: the bootstrapping procedure as coded creates random data from which the bootstrapped value can't be calculated, making it impossible to complete the bootstrap calculation.
MA211	Yuan and Chen (2015)	4 values (summary effect estimate, upper and lower confidence interval limits, sample size)	There is a mismatch between the supplied data and code: the code that would clearly calculate the target results attempts to subset the supplied data using a variable that does not appear anywhere in any shared data files.

Table 7: Descriptions of the failures to reproduce target results.

The original and reproduced values for the summary effect size target results are compared in Table 8. Overall, apart from one failure to reproduce a summary effect size (MA211), the reproduced values were very close to the originally reported values. Note that for this set of results, all reproduced summary effect sizes are in the same direction as the original. There were nine exact matches between original and reproduced values. Of those that were not exact matches, six (MA060, MA062, MA071, MA191, MA198, MA229) were off by ±0.001 (where reported to 3 decimals places) or ±0.01 (where reported to 2 decimal places); rounding could potentially explain these discrepancies. Also, five cases with discrepancies (MA060, MA062, MA065, MA198, MA202) used methods which relied on random number generation (Markov chain Monte Carlo and multiple imputation). The code for these articles did not include information about setting a random seed, and so it was not practically possible to recover the precise target result value as originally calculated by the code.

ID	Study	Effect size type	Original	Reproduced	Percent error (%)
MA060	Winternitz et al. (2017)	Fisher z-transformation	0.044	0.043	2.27
MA062	Grueber et al. (2018)	Hedges' d	-0.205	-0.204	0.49
MA065	Noble et al. (2018)	Hedges' g	-8.42	-8.87	5.34
MA067	Risely et al. (2017)	Hedges' g	-0.21	-0.21	0.00
MA071	Sievers et al. (2017)	response ratio	-0.26	-0.27	3.85
MA074	Harts et al. (2016)	Pearson's r	0.183	0.185	1.09
MA081	Jaffé et al. (2016)	slope parameter	1.30	1.30	0.00
MA091	Lemoine et al. (2016)	Cohen's d	0.56	0.56	0.00
MA095	Gibert et al. (2016)	Fisher z-transformation	0.76	0.76	0.00
MA126	Anderson (2016)	log odds ratio	-1.11	-1.11	0.00
MA145	Moore et al. (2016a)	Fisher z-transformation	-0.08	-0.08	0.00
MA147	Holman (2016)	percentage	0.13	0.13	0.00
MA188	Senior et al. (2015)	Log response ratio	-0.363	-0.363	0.00
MA191	Voje (2015)	allometric slope parameter	0.86	0.85	1.16
MA198	Paz-Vinas et al. (2015)	Fisher z-transformation	-0.41	-0.42	2.44
MA202	Mehrabi and Tuck (2015)	Hedges' d	-0.330	-0.340	3.03
MA211	Yuan and Chen (2015)	log response ratio	0.24		
MA213	Colautti and Lau (2015)	difference in means	-0.07	-0.07	0.00
MA229	Gamfeldt et al. (2015)	log response ratio	0.40	0.39	2.50

Table 8: The original and reproduced values of the target summary effect sizes, for articles with relevant code.

A full table showing comparisons of original and reproduced values for all target results is provided in the Supplementary Information (Table S16).

Reproducing target results when code not relevant

The previous section identified six cases where the code shared with an article was only partially relevant or not relevant to the article's meta-analysis results. There were three cases with shared code judged partially relevant, and three cases with shared code judged not relevant (these cases are described in detail in the Supplementary Information, Section S10).

As described earlier, the target results for these articles were deemed to have failed their reproduction attempts. However, we reviewed the code and data for these articles again, with the following in mind: (i) where the shared code was at least partially relevant to the meta-analysis in the article, could the code that *had* been shared be used to reproduce an alternative meta-analysis target result, and (ii) where the shared code was clearly not relevant to the meta-analysis, was the shared data and meta-analysis methods description in the article enough to allow us to write code to successfully reproduce the selected target result. The results of assessing two articles fitting scenario (i) are described in the Supplementary Information (Section S10); one article's code despite being partially relevant was judged unworkable and so was treated as part of scenario (ii) along with the three articles with code not relevant.

Table 9 breaks down the outcome of the reproduction attempts when writing new R code: we were able to calculate a value to compare to the original for all target results from the four articles considered. There were 44 exact matches between original and reproduced values (75%), and of the non-exact matches, eleven (19%) reproduced values were within 10% of the original values, and three (5%) reproduced values were more than 10% from the original values. The was also one case of a non-numeric text string not matching the original text string.

Outcome of target result reproduction attempt	N	%
Original and reproduced values match exactly	44	74.6
Original and reproduced values differ by less than 10%	11	18.6
Original and reproduced values differ by 10% or more	3	5.1
Original and reproduced values differ (non-numeric target result)	1	1.7
Total	59	100.0

Table 9: Breakdown of the target result value reproduction attempts for the four articles with irrelevant code (MA016, MA092, MA155, and MA212). The reproduction attempts required the writing of entirely new code.

As these results show, the reproduction attempts using newly-written R code were largely accurate, even though they do not constitute a computational reproducibility attempt evaluating both the shared data and code of the articles, as was the case for the results in the previous section.

Computational reproduction success rates

The overall computational reproducibility success rate for this study depends on how it is defined[4]. Different definitions lead to different values for the numerator and denominator in the calculation. We will consider the success rate in terms of the number of meta-analysis articles with successful reproductions of the target results. Since multiple target result values were identified in each of the 26 articles with shared data and code, the reproduction success on each individual target result value needs to be collapsed into a single result at the article level. There are different approaches to this, with varying levels of strictness.

Table 10 reports the overall computational reproducibility success rates for different collapsing approaches across two scenarios: (i) when all six code-irrelevant cases are considered failures by default (and thus only the 20 articles with target result-relevant code can be potential successes), and (ii) when the reproduction attempts from both the 20 articles with target result-relevant code *and* the four articles where we wrote new R code are included in the success calculations (the two articles where alternative target results were selected in order to evaluate the shared code are still considered failures by default here). In addition, for each scenario, two success rates are calculated: one which expresses the number of successful article reproduction attempts as a percentage of all 177 meta-analysis articles in the sample, and the other which expresses the number of successful article reproduction attempts as a percentage of the subset of 26 meta-analysis articles which shared code and data.

Depending on the level of stringency applied to count as a success, the success rate for the code-relevant cases only is in the range of 4.0–10.7% of all articles in the sample (or 26.9–73.1% of articles with code and data). Including the cases where new code was written for the code-irrelevant cases raises the success rate slightly, with a range of 5.1–13.0% of all articles in the sample (or 34.6–88.5% of articles with code and data).

4 DISCUSSION

In this study, we found that 14.7% of articles in the sample (26/177) shared both code and data, and so slightly less than 15% of articles had the *potential* to have results computationally reproduced. This finding is less than the estimate from Culina et al. (2020) that 21% of the published ecology literature has the potential to be computationally reproducible. The success rates actually achieved in this study as a percentage of the entire sample (4.0–10.7% depending on what is counted as a success, or 5.1–13.0% when including cases requiring new code to be written) are lower compared to the success rate observed in Archmiller et al. (2020): in that study, 13 out of 80 articles surveyed were found to be fully or at least somewhat computationally

[4]Section S11 of the Supplemental Information provides a thorough breakdown of the definition of "computational reproducibility" in the light of the results of this study.

Result for article	All code-irrelevant cases considered failures			Including attempts where new code was written for code-irrelevant cases		
	N	Success rate (%), all	Success rate (%), subset	*N*	Success rate (%), all	Success rate (%), subset
All target result values match original exactly	7	4.0	26.9	9	5.1	34.6
At least 50% of target result values match original exactly	13	7.3	50.0	16	9.0	61.5
All target result values within 10% of original	14	7.9	53.8	16	9.0	61.5
At least 50% of target result values within 10% of original	19	10.7	73.1	23	13.0	88.5

Table 10: Reproducibility success rates at the article level, for different collapsing criteria. In this table, *N* is the number of articles meeting each collapsing criterion, "success rate (%), all" expresses *N* as a percentage of all 177 meta-analysis articles in the sample, and "success rate (%), subset" expresses *N* as a percentage of the subset of 26 articles with shared data and code. In the first three columns of this table, the articles with data and code judged irrelevant to the target results are considered failures by default. In the last three columns, reproduction attempts where we wrote new code to reproduce the target results are included in success calculations.

reproducible, for a success rate of 16%. (In that study, authors of the original articles were contacted to request data and code, which might contribute towards the higher success rate observed.)

The results in Table 10 show that the success rate across all articles changes depending on the definitions for what counts as a success. As indicated earlier, the success rate for this study is effectively capped at a maximum of 14.7% (26/177) since reproduction attempts were never made for articles without both shared data and code. (If we had selected target results in all 177 articles and written code, etc. as necessary to attempt to reproduce all target results, the success rate could potentially have been higher.) Since this study is focused specifically on reusing shared code and data, it is worth recasting the success rate question as "*when both code and data are shared*, what is the computational reproduction success rate?" This changes the denominator in the success rate calculation to 26 for this study, and the resulting success rates become much higher as shown in Table 10.

Although it is obvious that reducing the denominator will inflate the success rate, the success rate range of 27-89% among articles with both shared data and code (again, depending on definitions of success) is still illuminating: these results show that even with data and code, expectations that we might reproduce published results down to the last decimal place are rarely met in practice. However, depending on how stringent our requirements for reproduced results, we can achieve high levels of computational reproduction success. The level of stringency we place on the accuracy of reproduced results will depend on our specific purposes; there may be applications where reproducing most results to within 10% of the original values is acceptable, which this study suggests may be achievable, at least for meta-analyses in ecology and evolution.

The widespread use of R in ecology and evolution for meta-analysis

A noteworthy observation from this study is the popularity of R among ecologists to perform meta-analyses, and in particular, the popularity of the *metafor* and *MCMCglmm* packages. R was the software of choice for a large majority of meta-analyses in the sample. For comparison, Nakagawa and Santos (2012) reported that 42% of meta-analyses included in their survey used the MetaWin software package (Rosenberg et al., 1997), and a total of 19 different meta-analysis software packages across the 100 articles surveyed (18 articles did not report which software package(s) were used for their study). The articles in this sample were published a few years on from the articles surveyed in Nakagawa and Santos (2012), but from articles published over 2015-17, the use of MetaWin had dropped to 11% of articles.

The observed popularity of R agrees with what we already knew about the use of R in ecology: in 2017, around 58% of articles (not just meta-analyses) published across a large sample of ecology journals were reporting that they used R (Lai et al., 2019).

This result bodes well for reproducibility: first, it means that in principle, article authors very likely have R script(s) that could have been shared. Second, R is open source and freely available, making it more accessible for studies like this.

Limitations

A limitation of this study is that the observed rate(s) of computational reproducibility are possibly underestimated. By design, this study did not attempt to contact article authors seeking access to data and code. Although other similar studies (Archmiller et al., 2020; Stodden et al., 2018) report mixed success with receiving data and code from authors, it is still the case that assistance from original authors could have lifted the rate of obtained data and code for articles, and in turn potentially the overall reproducibility rate(s).

Other studies similar to this one have measured the time spent on each reproduction attempt; we did not record this, despite some attempts taking much longer than others. Given that discussions of computational reproducibility have been taking place in contexts where researcher time, effort, and opportunity cost are important considerations, this is perhaps a lost chance to have provided additional information about the activity of reproduction.

Another limitation is the strategy of selecting only a single target result to reproduce per paper. Although this makes it feasible to attempt to reproduce results from more articles, it does not provide a full picture of the reproducibility of the entire articles, and so on the basis of these investigations, we can't claim that any of these articles are in toto "reproducible". However, despite this limitation this strategy needs to be considered in the context of a "triage" approach: articles identified as failing on this relatively simple task raise issues with the data, code, or reliability of published results that must be addressed before further time/work is expended, or before any results are taken to be accurate for particular purposes.

5 CONCLUSION

This study has found that while data sharing is relatively common for meta-analyses in ecology and evolution, with 75% of articles surveyed sharing data, code sharing is much less common (16% of articles). The low rate of code sharing is in broad agreement with other investigations of the levels of code sharing in the discipline (Culina et al., 2020; Mislan et al., 2016).

Assessing the computational reproducibility of the articles with code and data revealed the complexities described. Depending on the strictness of the definition of success and whether cases where new code needed to be written were included, between 4% and 13% of articles in the sample had results that could be successfully reproduced. The low success rate is largely due to the nonavailability of code preventing any attempt from happening in the first place. However, when considering the success rate in terms of the attempts made using data and code, the success rate is much higher, although subject to wide variation depending on the strictness of the criteria for success (27-89%). However, this second interpretation of the success rate is cause for optimism: when code and data are shared, it is possible to use them to reproduce many results accurately. This means that by simply sharing code, the reproducibility of meta-analyses can be expected to be high. The observed widespread adoption of R by researchers in ecology and evolution for meta-analysis suggests that the technical barriers to sharing code that can be used in a reproducible way are relatively low across the discipline.

DATA AVAILABILITY STATEMENT

The data and code files to reproduce all results reported in this article are available on Zenodo at `https://doi.org/10.5281/zenodo.8114702`.

The reproducibility reports created made use of data and code files shared alongside the published meta-analysis articles surveyed in this study; these data/code files are not included in the above Zenodo repository.

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AUTHOR CONTRIBUTIONS

SK: Conceptualization (lead); Methodology (lead); Investigation (lead); Formal Analysis (lead); Writing - Original Draft (lead); Writing - Review & Editing (equal).

DW: Supervision (supporting); Writing - Review & Editing (equal).

ETS: Supervision (supporting); Writing - Review & Editing (equal).

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AUTHOR COMPETING INTERESTS

The authors disclose that they have no competing interests.

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S1 META-ANALYSIS IN ECOLOGY AND EVOLUTIONARY BIOLOGY

Any study reporting numerical results (i.e., not just meta-analyses) can potentially be the subject of an attempt to computationally reproduce results, so why focusing on meta-analyses? First, there is a practical imperative here: narrowing the scope of this study makes it tractable. The ecology and evolution literature is vast and varied, and although the literature at large could be sampled to arrive at a manageable subset of articles to assess, the screening process to identify suitable candidate articles and exclude irrelevant ones would be arduous without some sort of guiding principle. In that sense, "meta-analysis" is just one of many potential ways to winnow down the literature, in that it is a quantitative method that produces numerical results that can (in principle) be subject to a computational reproducibility attempt. But still, why narrow the scope to meta-analyses in particular? To contextualise our answer to this, we start with a brief review of meta-analysis in ecology and evolutionary biology.

Meta-analysis in ecology and evolutionary biology

Meta-analysis, a set of statistical methods for combining the results of multiple studies, is a widely-used tool for research synthesis in medicine, the social sciences, and natural sciences (Lau et al., 2013). Meta-analysis has been used for decades in disciplines such as psychology, education, and especially medicine, where it has become a core tool for assessing the evidence of treatments, in particular via Cochrane systematic reviews (Borenstein et al., 2009; Green et al., 2008). In addition to an enormous literature on methods of meta-analysis, guidelines such as the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) have been developed to standardise how meta-analyses are performed and reported (Moher et al., 2009; Page et al., 2021). PRISMA has been extended to be relevant to meta-analyses in ecology and evolutionary biology specifically (O'Dea et al., 2021a).

Compared to some other disciplines, meta-analysis was adopted by ecology and evolutionary biology relatively recently, but has grown substantially, from a handful of meta-analyses published in the early 1990s to over 500 meta-analyses published in 2010 (Lau et al., 2013). In addition to meta-analyses themselves, there have been numerous methodological papers and handbooks covering how meta-analytical methods can be applied in circumstances specific to ecology/evolutionary biology (e.g., Arnqvist and Wooster, 1995; Gurevitch and Hedges, 1999, 2001; Koricheva et al., 2013). Most relevantly for this paper, there have also been reviews of how meta-analyses have been conducted within the fields of ecology and evolutionary biology.

An early review of methods in meta-analysis (Gates, 2002) reviewed 29 meta-analyses published between 1991 and 1998, and is a useful baseline to track how methodology has progressed since the early years of meta-analysis in ecology. Overall, it was observed that techniques used in the medical meta-analysis literature had not been adopted in ecology, in particular methods of assessing publication bias (only 34% of meta-analyses accounted for publication bias, and all calculated a Rosenthal fail-safe number; none used superior alternatives such as funnel plots, regression or the "trim and fill" method—refer to Nakagawa and Santos (2012) for summaries of these methods). 76% of meta-analyses used the Q statistic to explore heterogeneity in effect sizes, and 17% included a sensitivity analysis of some kind. 28% of meta-analysis provided no information on how the primary studies were located. In terms of the effect sizes used by the meta-analyses, 55% used standardised mean differences, 31% used the Pearson correlation coefficient, and 7% used response ratios.

Nakagawa and Santos (2012) conducted a survey of 100 "biological" meta-analyses (i.e., meta-analyses in ecology and evolutionary biology) published over 2009–2011. They found that only 17% controlled for phylogenetic relatedness between species, and 49% used methods to identify and/or assess the impact of publication bias (specifically, to identify publication bias, about 40% of these meta-analyses used funnel plots, about 10% used a correlation-based method, less than 10% used a quantile plot-based method, and about 5% used a regression-based method. For assessing the impact of publication bias, about 30% calculated Rosenthal fail-safe numbers and less than 10% used the "trim and fill" method). In terms of the effect sizes used by meta-analyses, about 60% used standardised mean differences, about 20% used correlation coefficients and the remainder used other measures.

Vetter et al. (2013) specifically addressed the point about a need for the term "meta-analysis" to be well-defined in the ecology and conservation biology literature. They examined 133 nominal meta-analyses, and applied a two-stage rating system based on the technical requirements for a meta-analysis according to the medical meta-analysis literature. They found that only 45% of the meta-analyses satisfied all requirements in the first stage of rating, ans 25% of the meta-analyses satisfied none. In the second stage of rating which involved only 83 of the meta-analyses which had scored sufficiently highly in the first stage, only a single meta-analysis satisfied all second stage requirements, and 22% of the second stage meta-analyses satisfied none. The authors recommended that going forward, "meta-analyses" in ecology journals ought to include the seven technical requirements outlined in their review.

Koricheva and Gurevitch (2014) performed a similar review to both Nakagawa and Santos (2012) and Vetter et al. (2013), but focused on meta-analyses in plant ecology. They developed a 16-item rubric to assess the quality of meta-analytic methods, based on previous reviews of meta-analytic methods with some additions and refinements. Each item in the rubric listed meta-analyses that were exemplars of relevant method(s).

They used a 14 of these items to assess the methods used in a sample of 322 meta-analyses in plant ecology. The results were mixed: although meta-analyses in plant ecology were highly likely to list all primary studies included in the analysis (87% of meta-analyses in the sample) or explore caused of heterogeneity in results (89%), only 32% reported the full details of their literature searches, only 31% considered publication bias, and only 25% conducted a sensitivity analysis. 5% of meta-analyses considered changes in study effect sizes over time, and 11% took phylogenetic relatedness into account.

ArchMiller et al. (2015) used a 17-item rubric very similar to Koricheva and Gurevitch (2014) to evaluate the methods used by 18 meta-analyses published in the journal *Molecular Ecology*. The goal of this paper was to formalise the definition of meta-analysis for editors, authors, reviewers, and readers of the journal. They found that only 22% of studies met the standard expected for an effective meta-analysis, which required satisfying at least 15 of the 17 items, and 56% of meta-analyses satisfied 9 or fewer of the 17 items. The adherence to the different methods was mixed: While 100% of the meta-analyses provided a list of the primary studies included and documented the meta-data extracted from each, and 94% mentioned the inclusion/exclusion criteria used for selected studies, 50% included details of the literature search terms used and only 22% provided details of both the databases searched and dates the searches were conducted. Only 33% of meta-analyses took publication bias into account, 22% quantified the heterogeneity between effect sizes, and only 33% explicitly reported whether they were using a fixed effect or random effects model.

The common theme of heterogeneity in the methods labelled as "meta-analysis" in the ecology literature has led to the emergence of what might be called the "formal" (Koricheva and Gurevitch, 2014; Vetter et al., 2013) or "narrow" (Nakagawa et al., 2017) definition of meta-analysis: Koricheva and Gurevitch (2014) define meta-analysis "a set of statistical methods for combining outcomes (effect sizes) across different data sets addressing the same research question to examine patterns of response across these data sets and sources of heterogeneity in outcomes", although they do also note that there is no single agreed-upon checklist for assessing whether a given meta-analysis is using the correct methods for this purpose. What does seem clear is that the methods and procedures of the formal/narrow meta-analysis are those mentioned in the checklists/rubrics/rating systems of Vetter et al. (2013), Koricheva and Gurevitch (2014), and ArchMiller et al. (2015).

Focusing on meta-analysis in this study

The first and primary reason for choosing to focus on meta-analysis is this: despite the findings outlined in the previous section, meta-analyses are (relatively) uniform in their statistical methods and data, and so restricting the study to meta-analyses allows for the assessment of "like" studies. This has a few different dimensions that speak to the tractability of the study:

- The great variety in quantitative and statistical methods employed across the entire ecology and evolution literature (with the accompanying variety in computational resource requirements) means that failure to computationally reproduce one study but not another could be a result of radically different scales of computational requirements, which is a confounding factor we'd like to avoid as much as possible, due to limited resources. Potential ways of dealing with this (e.g., screening articles to preclude studies with "too high" computational resource requirements) seem too subjective and difficult to operationalise. Choosing a single type of study, meta-analysis, acts to reduce the likely variation in computational resource requirements.

- In general, meta-analytic models are fitted using relatively small data sets (in the order of tens or hundreds, perhaps thousands, of data points as opposed to "big data" with millions of data points) and require modest computational resources (i.e., can be easily run on a desktop or laptop computer with no high performance computing resources required).

- Meta-analyses in particular benefit from the existence of standards for reporting, e.g., PRISMA. Relevantly for this study, this includes standards around the reporting/sharing of data. While a given meta-analysis may not be obliged to strictly adhere to all PRIMSA reporting guidelines, the existence of such guidelines makes it more likely that different studies can be assessed on a like basis than if no such guidelines or standards existed.

The second reason is, as mentioned earlier, meta-analysis has become an important part of the fields of ecology and evolution. To the extent that meta-analyses become regarded (for better or worse) as a higher standard of evidence, it commensurately raises the stakes of meta-analytic results. In that context, being able to assure the results of meta-analyses through computational reproduction has some value.

S2 LITERATURE SEARCH

We set about curating a set of meta-analyses to survey by conducting a Scopus abstract and citation database search (we accessed the Scopus database via the University of Melbourne library's subscription). The search query, conducted on 20th December 2017, searched article titles, abstracts, and keywords for the string "meta-anal*", subject to two constraints. The first constraint restricted results to articles published between 2015 and 2017, inclusive. The second constraint restricted results to articles published in one of 21 ecology and evolution journal titles (identified by ISSN). The journal titles included are as follows: *The Amer-*

ican Naturalist, *Animal Behaviour*, *Behavioral Ecology*, *Behavioral Ecology and Sociobiology*, *Biological Reviews*, *Ecological Applications*, *Ecological Monographs*, *Ecology*, *Ecology Letters*, *Evolution*, *Evolutionary Ecology*, *Functional Ecology*, *Journal of Animal Ecology*, *Journal of Applied Ecology*, *Journal of Ecology*, *Journal of Evolutionary Biology*, *Molecular Ecology*, *New Phytologist*, *Oecologia*, *Oikos*, *Quarterly Review of Biology*.

The Scopus search string used was as follows:

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TITLE-ABS-KEY ( meta-anal* ) AND ( PUBYEAR = 2015
OR PUBYEAR = 2016 OR PUBYEAR = 2017 )
AND ISSN ( 0003-0147 OR 0003-3472 OR 1045-2249 OR 0340-5443
OR 1464-7931 OR 1051-0761 OR 0012-9615 OR 0012-9658
OR 1461-023x OR 0014-3820 OR 0269-7653 OR 0269-8463
OR 0021-8790 OR 0021-8901 OR 0022-0477 OR 1010-061x
OR 0962-1083 OR 0028-646x OR 0029-8549 OR 0030-1299
OR 0033-5770 )
```

This list of ecology and evolution journal titles is the same as used for the survey of meta-analyses conducted in Nakagawa and Santos (2012). This choice was made to (i) be assured of searching journals that actively published meta-analyses, and (ii) keep the study tractable: Nakagawa and Santos (2012) yielded 390 studies from their three-year (2009–11) search of these journal titles and kept the 100 most recent meta-analyses, so that gave an indication of the approximate number of meta-analysis studies we would need to review. It is unclear if this set of journal titles can be considered a "representative" sample of all ecology and evolutionary biology journals; one obvious factor is that not all journals would necessarily consider meta-analyses to be within their scope. However, it seems clear that the list of journals used for this study is not particularly aberrant, at least: for example, Mislan et al. (2016) reviewed the data and code release policies of 96 "ecology" journals indexed by Web of Science, and the list of 96 journals reviewed includes 17 of the 21 titles surveyed by Nakagawa and Santos (2012).

Identifying meta-analyses

The search results returned articles which contained the string "meta-anal*" somewhere in the article's title, abstract, or list of keywords. However, not all such articles will necessarily be meta-analyses. The next step was to screen the articles to obtain a sample of "meta-analyses". As the review of the ecological meta-analysis methodology literature foreshadowed, this was not straightforward.

The articles were screened using a two-step process: first, some types of articles were checked for and when found, put aside. These article types were (i) errata or corrigenda notices, and (ii) letters or comments in reply to a previously published article. Since errata and comments rely heavily on the context provided by the article they are in reference to (which may or may not be a meta-analysis, and which may or may not be in scope of the literature search), they were considered not suitable to include as "meta-analyses". We considered these article types to be straightforward to identify (due to clear cues in their title, and other contextual clues such as being included in a comments/letters section of a journal issue), and so removed them from consideration without a formal review of their contents.

The second step involved evaluating the remaining articles in the following way: rather than checking they meet a particular set of methodological requirements, meta-analyses were identified by confirming that an article merely includes a *claim* that it is a meta-analysis (or that a meta-analysis was conducted, or words to that effect) or not. This approach to identifying meta-analyses was intended to be as generous as possible and methodologically agnostic.

Identifying a claim that an article is/conducts a meta-analysis still requires judgment and interpretation, and is subjective. To make the claim identification process transparent, we constructed and employed a simple coding scheme with eight items to summarise the "evidence" in support of each article claiming to be a meta-analysis. The coding scheme is outlined in Table S1. This scheme records the use of the term "meta-analysis" in crucial places in the article (title, abstract, keywords if the article includes them), as well as the quoted text of any actual claim found within the body of the article text.

For items 1–4 and 7, the value "Y" indicates an unambiguous "yes" to the question/contention posed in the column "Description" of Table S1, and the value "N" indicates an unambiguous "no". For items 1–4, the value "U" was available to indicate situations where the mention of "meta-analysis" was somehow unclear. For item 3 only, the value "N/A" was used to indicate that an article did not include any keywords.

Items 5 and 6 record the most substantive piece of evidence: text, directly quoted from the article, which contains the claim to be a meta-analysis (if the claim can be found). Item 7 contains the final judgment of whether the article can be considered to include a claim or not (either yes "Y" or no "N"), and item 8 records any additional notes about the judgment.

All articles remaining after the first step were coded using this scheme. In practice, this meant searching the text of each article for the string "meta" (this word fragment was chosen to avoid issues with the matching of the hyphen in "meta-analysis"), and reviewing all matches in order to answer the coding scheme items.

Articles were considered as claiming to be a meta-analysis if the value of item 7 (Claim in article) in the coding scheme was "Y" . Articles found not to include such a claim (a value of "N" for item 7) were put aside.

Index	Field	Values	Description
1	Claim in title	Y, N, U	Does the article include the term “meta-analysis” in its title?
2	Claim in abstract	Y, N, U	Does the article include the term “meta-analysis” in its abstract?
3	Claim in keywords	Y, N, U, N/A	If applicable, is “meta-analysis” one of the article’s keywords?
4	Claim in body text	Y, N, U	Does the article body text contain a claim to be a meta-analysis?
5	Quote of claim	open text	The actual text of the claim as it appears in the article.
6	Quote page number	open text	Page number(s) the quote appears on.
7	Claim in article	Y, N	An overall judgment of whether or not the article claims to be a meta-analysis.
8	Notes	open text	Any additional notes about the article’s meta-analysis claim status.

Table S1: The eight item coding scheme used for determining whether an article claims to be a meta-analysis. In the Values column, “Y” indicates “yes”, “N” indicates “no”, “U” indicates “unclear”, and “N/A” indicates “not applicable”.

The final set of ecology and evolutionary biology meta-analyses, to be the basis of the rest of this study, is simply the set of 177 articles coded as containing claims to be meta-analyses. The bibliographic details of all 177 meta-analysis articles are listed in Table S2.

Table S2: References for all 177 meta-analysis articles in the data set used in this study.

ID	Study
MA001	T. M. Bowles, L. E. Jackson, M. Loeher, and T. R. Cavagnaro. Ecological intensification and arbuscular mycorrhizas: a meta-analysis of tillage and cover crop effects. *Journal of Applied Ecology*, 54(6):1785–1793, dec 2017. doi: 10.1111/1365-2664.12815
MA003	A. S. Mori, S. Tatsumi, and L. Gustafsson. Landscape properties affect biodiversity response to retention approaches in forestry. *Journal of Applied Ecology*, 54(6):1627–1637, dec 2017. doi: 10.1111/1365-2664.12888
MA005	J. A. Charlebois and R. D. Sargent. No consistent pollinator-mediated impacts of alien plants on natives. *Ecology Letters*, 20(11):1479–1490, nov 2017. doi: 10.1111/ele.12831
MA006	N. Martin-StPaul, S. Delzon, and H. Cochard. Plant resistance to drought depends on timely stomatal closure. *Ecology Letters*, 20(11):1437–1447, nov 2017. doi: 10.1111/ele.12851
MA009	A. Romano, N. Saino, and A. P. Møller. Viability and expression of sexual ornaments in the barn swallow hirundo rustica: a meta-analysis. *Journal of Evolutionary Biology*, 30(10):1929–1935, oct 2017b. doi: 10.1111/jeb.13151
MA010	K. E. Davidson, M. S. Fowler, M. W. Skov, S. H. Doerr, N. Beaumont, and J. N. Griffin. Livestock grazing alters multiple ecosystem properties and services in salt marshes: a meta-analysis. *Journal of Applied Ecology*, 54(5):1395–1405, oct 2017. doi: 10.1111/1365-2664.12892

ID	Study
MA011	J. W. A. Grant, L. K. Weir, and S. Ó. Steingrímsson. Territory size decreases minimally with increasing food abundance in stream salmonids: Implications for population regulation. *Journal of Animal Ecology*, 86(6): 1308–1316, nov 2017. doi: 10.1111/1365-2656.12737
MA013	C. Horswill, S. H. O'Brien, and R. A. Robinson. Density dependence and marine bird populations: are wind farm assessments precautionary? *Journal of Applied Ecology*, 54(5):1406–1414, oct 2017. doi: 10.1111/1365-2664.12841
MA014	S. K. Auer, S. S. Killen, and E. L. Rezende. Resting vs. active: a meta-analysis of the intra- and inter-specific associations between minimum, sustained, and maximum metabolic rates in vertebrates. *Functional Ecology*, 31(9):1728–1738, sep 2017. doi: 10.1111/1365-2435.12879
MA015	A. L. Buchanan, S. L. Hermann, M. Lund, and Z. Szendrei. A meta-analysis of non-consumptive predator effects in arthropods: the influence of organismal and environmental characteristics. *Oikos*, 126(9):1233–1240, sep 2017. doi: 10.1111/oik.04384
MA016	X. Xu, D. Medvigy, S. Joseph Wright, K. Kitajima, J. Wu, L. P. Albert, G. A. Martins, S. R. Saleska, and S. W. Pacala. Variations of leaf longevity in tropical moist forests predicted by a trait-driven carbon optimality model. *Ecology Letters*, 20(9):1097–1106, sep 2017. doi: 10.1111/ele.12804
MA017	M. Soria, C. Leigh, T. Datry, L. M. Bini, and N. Bonada. Biodiversity in perennial and intermittent rivers: a meta-analysis. *Oikos*, 126(8):1078–1089, jul 2017. doi: 10.1111/oik.04118
MA018	C. S. Delavaux, L. M. Smith-Ramesh, and S. E. Kuebbing. Beyond nutrients: a meta-analysis of the diverse effects of arbuscular mycorrhizal fungi on plants and soils. *Ecology*, 98(8):2111–2119, aug 2017. doi: 10.1002/ecy.1892
MA019	J. A. LaManna and T. E. Martin. Logging impacts on avian species richness and composition differ across latitudes and foraging and breeding habitat preferences. *Biological Reviews*, 92(3):1657–1674, aug 2017. doi: 10.1111/brv.12300
MA020	L. C. Leal and P. E. C. Peixoto. Decreasing water availability across the globe improves the effectiveness of protective ant–plant mutualisms: a meta-analysis. *Biological Reviews*, 92(3):1785–1794, aug 2017. doi: 10.1111/brv.12307
MA021	A. Romano, A. Costanzo, D. Rubolini, N. Saino, and A. P. Møller. Geographical and seasonal variation in the intensity of sexual selection in the barn swallow hirundo rustica: a meta-analysis. *Biological Reviews*, 92(3): 1582–1600, aug 2017a. doi: 10.1111/brv.12297
MA022	F. Anthelme, R. I. Meneses, N. N. H. Valero, P. Pozo, and O. Dangles. Fine nurse variations explain discrepancies in the stress-interaction relationship in alpine regions. *Oikos*, 126(8):1173–1183, jul 2017. doi: 10.1111/oik.04248

ID	Study
MA023	M. Hindrikson, J. Remm, M. Pilot, R. Godinho, A. V. Stronen, L. Baltrūnaité, S. D. Czarnomska, J. A. Leonard, E. Randi, C. Nowak, M. Åkesson, J. V. López-Bao, F. Álvares, L. Llaneza, J. Echegaray, C. Vilà, J. Ozolins, D. Rungis, J. Aspi, L. Paule, T. Skrbinšek, and U. Saarma. Wolf population genetics in europe: a systematic review, meta-analysis and suggestions for conservation and management. *Biological Reviews*, 92 (3):1601–1629, aug 2017. doi: 10.1111/brv.12298
MA024	J. L. Knapp, L. J. Bartlett, and J. L. Osborne. Re-evaluating strategies for pollinator-dependent crops: How useful is parthenocarpy? *Journal of Applied Ecology*, 54(4):1171–1179, aug 2017. doi: 10.1111/1365-2664.12813
MA025	A. Gázquez and G. T. S. Beemster. What determines organ size differences between species? a meta-analysis of the cellular basis. *New Phytologist*, 215(1):299–308, jul 2017. doi: 10.1111/nph.14573
MA026	J. N. Hendershot, Q. D. Read, J. A. Henning, N. J. Sanders, and A. T. Classen. Consistently inconsistent drivers of microbial diversity and abundance at macroecological scales. *Ecology*, 98(7):1757–1763, jul 2017. doi: 10.1002/ecy.1829
MA027	A. G. Farji-Brener and V. Werenkraut. The effects of ant nests on soil fertility and plant performance: a meta-analysis. *Journal of Animal Ecology*, 86(4):866–877, jul 2017. doi: 10.1111/1365-2656.12672
MA028	D. J. Hitchcock, Ø. Varpe, T. Andersen, and K. Borgå. Effects of reproductive strategies on pollutant concentrations in pinnipeds: a meta-analysis. *Oikos*, 126(6):772–781, jun 2017. doi: 10.1111/oik.03955
MA029	S. E. Miller, M. Barrueto, and D. Schluter. A comparative analysis of experimental selection on the stickleback pelvis. *Journal of Evolutionary Biology*, 30(6):1165–1176, jun 2017. doi: 10.1111/jeb.13085
MA031	P. K. Rowiński and B. Rogell. Environmental stress correlates with increases in both genetic and residual variances: A meta-analysis of animal studies. *Evolution*, 71(5):1339–1351, may 2017. doi: 10.1111/evo.13201
MA033	K. Yue, D. A. Fornara, W. Yang, Y. Peng, C. Peng, Z. Liu, and F. Wu. Influence of multiple global change drivers on terrestrial carbon storage: additive effects are common. *Ecology Letters*, 20(5):663–672, may 2017. doi: 10.1111/ele.12767
MA035	K. A. Wood, J. Ponting, N. D'Costa, J. L. Newth, P. E. Rose, P. Glazov, and E. C. Rees. Understanding intrinsic and extrinsic drivers of aggressive behaviour in waterbird assemblages: a meta-analysis. *Animal Behaviour*, 126: 209–216, apr 2017b. doi: 10.1016/j.anbehav.2017.02.008
MA036	S. Greenwood, P. Ruiz-Benito, J. Martínez-Vilalta, F. Lloret, T. Kitzberger, C. D. Allen, R. Fensham, D. C. Laughlin, J. Kattge, G. Bönisch, N. J. B. Kraft, and A. S. Jump. Tree mortality across biomes is promoted by drought intensity, lower wood density and higher specific leaf area. *Ecology Letters*, 20(4):539–553, apr 2017. doi: 10.1111/ele.12748
MA037	P. A. Martin, A. C. Newton, and J. M. Bullock. Impacts of invasive plants on carbon pools depend on both species' traits and local climate. *Ecology*, 98(4):1026–1035, apr 2017. doi: 10.1002/ecy.1711
MA038	B. Holtmann, M. Lagisz, and S. Nakagawa. Metabolic rates, and not hormone levels, are a likely mediator of between-individual differences in behaviour: a meta-analysis. *Functional Ecology*, 31(3):685–696, mar 2017. doi: 10.1111/1365-2435.12779

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MA040	R. Poulin and G. Pérez-Ponce de León. Global analysis reveals that cryptic diversity is linked with habitat but not mode of life. *Journal of Evolutionary Biology*, 30(3):641–649, mar 2017. doi: 10.1111/jeb.13034
MA041	T. Usui, S. H. M. Butchart, and A. B. Phillimore. Temporal shifts and temperature sensitivity of avian spring migratory phenology: a phylogenetic meta-analysis. *Journal of Animal Ecology*, 86(2):250–261, mar 2017. doi: 10.1111/1365-2656.12612
MA042	A. R. Hrycik, L. Z. Almeida, and T. O. Höök. Sub-lethal effects on fish provide insight into a biologically-relevant threshold of hypoxia. *Oikos*, 126(3):307–317, mar 2017. doi: 10.1111/oik.03678
MA044	M. R. Rossetti, T. Tscharntke, R. Aguilar, and P. Batáry. Responses of insect herbivores and herbivory to habitat fragmentation: a hierarchical meta-analysis. *Ecology Letters*, 20(2):264–272, feb 2017. doi: 10.1111/ele.12723
MA045	G. H. Sorenson, C. J. Dey, C. L. Madliger, and O. P. Love. Effectiveness of baseline corticosterone as a monitoring tool for fitness: a meta-analysis in seabirds. *Oecologia*, 183(2):353–365, feb 2017. doi: 10.1007/s00442-016-3774-3
MA046	Y. Z. Foo, S. Nakagawa, G. Rhodes, and L. W. Simmons. The effects of sex hormones on immune function: a meta-analysis. *Biological Reviews*, 92(1):551–571, feb 2017. doi: 10.1111/brv.12243
MA048	T. Hossie, K. Landolt, and D. L. Murray. Determinants and co-expression of anti-predator responses in amphibian tadpoles: a meta-analysis. *Oikos*, 126(2):n/a–n/a, feb 2017. doi: 10.1111/oik.03305
MA049	I. Booksmythe, B. Mautz, J. Davis, S. Nakagawa, and M. D. Jennions. Facultative adjustment of the offspring sex ratio and male attractiveness: a systematic review and meta-analysis. *Biological Reviews*, 92(1):108–134, feb 2017. doi: 10.1111/brv.12220
MA052	M. Ameye, S. Allmann, J. Verwaeren, G. Smagghe, G. Haesaert, R. C. Schuurink, and K. Audenaert. Green leaf volatile production by plants: a meta-analysis. *New Phytologist*, pages n/a–n/a, 2017. doi: 10.1111/nph.14671
MA053	M. C. Vidal and S. M. Murphy. Bottom-up vs. top-down effects on terrestrial insect herbivores: a meta-analysis. *Ecology Letters*, 21(1):138–150, jan 2018. doi: 10.1111/ele.12874
MA054	Q. Deng, D. E. McMahon, Y. Xiang, C.-L. Yu, R. B. Jackson, and D. Hui. A global meta-analysis of soil phosphorus dynamics after afforestation. *New Phytologist*, 213(1):181–192, jan 2017. doi: 10.1111/nph.14119
MA055	M. R. Lee, E. S. Bernhardt, P. M. van Bodegom, J. H. C. Cornelissen, J. Kattge, D. C. Laughlin, Ü. Niinemets, J. Peñuelas, P. B. Reich, B. Yguel, and J. P. Wright. Invasive species' leaf traits and dissimilarity from natives shape their impact on nitrogen cycling: a meta-analysis. *New Phytologist*, 213(1):128–139, jan 2017. doi: 10.1111/nph.14115

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MA057	Z. Xiao, X. Wang, J. Koricheva, A. Kergunteuil, R.-C. Le Bayon, M. Liu, F. Hu, and S. Rasmann. Earthworms affect plant growth and resistance against herbivores: A meta-analysis. *Functional Ecology*, 32(1):150–160, jan 2018. doi: 10.1111/1365-2435.12969
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MA059	H. Yang, Q. Zhang, R. T. Koide, J. D. Hoeksema, J. Tang, X. Bian, S. Hu, and X. Chen. Taxonomic resolution is a determinant of biodiversity effects in arbuscular mycorrhizal fungal communities. *Journal of Ecology*, 105 (1):219–228, jan 2017. doi: 10.1111/1365-2745.12655
MA060	J. Winternitz, J. L. Abbate, E. Huchard, J. Havlíček, and L. Z. Garamszegi. Patterns of mhc-dependent mate selection in humans and nonhuman primates: a meta-analysis. *Molecular Ecology*, 26(2):668–688, jan 2017. doi: 10.1111/mec.13920
MA061	J. L. Molnar, R. Diogo, J. R. Hutchinson, and S. E. Pierce. Reconstructing pectoral appendicular muscle anatomy in fossil fish and tetrapods over the fins-to-limbs transition. *Biological Reviews*, pages n/a–n/a, nov 2017. doi: 10.1111/brv.12386
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MA063	D. S. Gruner, M. E. S. Bracken, S. A. Berger, B. K. Eriksson, L. Gamfeldt, B. Matthiessen, S. Moorthi, U. Sommer, and H. Hillebrand. Effects of experimental warming on biodiversity depend on ecosystem type and local species composition. *Oikos*, 126(1):8–17, sep 2016. doi: 10.1111/oik.03688
MA064	K. A. Dynarski and B. Z. Houlton. Nutrient limitation of terrestrial free-living nitrogen fixation. *New Phytologist*, 217(3):1050–1061, jan 2018. doi: 10.1111/nph.14905
MA065	D. W. A. Noble, V. Stenhouse, and L. E. Schwanz. Developmental temperatures and phenotypic plasticity in reptiles: a systematic review and meta-analysis. *Biological Reviews*, 93(1):72–97, jan 2018. doi: 10.1111/brv.12333
MA066	R. R. Junker, J. Kuppler, L. Amo, J. D. Blande, R. M. Borges, N. M. van Dam, M. Dicke, S. Dötterl, B. K. Ehlers, F. Etl, J. Gershenzon, R. Glinwood, R. Gols, A. T. Groot, M. Heil, M. Hoffmeister, J. K. Holopainen, S. Jarau, L. John, A. Kessler, J. T. Knudsen, C. Kost, A.-A. C. Larue-Kontic, S. D. Leonhardt, D. Lucas-Barbosa, C. J. Majetic, F. Menzel, A. L. Parachnowitsch, R. S. Pasquet, E. H. Poelman, R. A. Raguso, J. Ruther, F. P. Schiestl, T. Schmitt, D. Tholl, S. B. Unsicker, N. Verhulst, M. E. Visser, B. T. Weldegergis, and T. G. Köllner. Covariation and phenotypic integration in chemical communication displays: biosynthetic constraints and eco-evolutionary implications. *New Phytologist*, pages n/a–n/a, mar 2017. doi: 10.1111/nph.14505

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MA068	V. Ronget, J. Gaillard, T. Coulson, M. Garratt, F. Gueyffier, J. Lega, and J. Lemaître. Causes and consequences of variation in offspring body mass: meta-analyses in birds and mammals. *Biological Reviews*, 93(1):1–27, apr 2017. doi: 10.1111/brv.12329
MA069	P. T. Rohner, T. Teder, T. Esperk, S. Lüpold, and W. U. Blanckenhorn. The evolution of male-biased sexual size dimorphism is associated with increased body size plasticity in males. *Functional Ecology*, In press:n/a–n/a, 2017. doi: 10.1111/1365-2435.13004
MA070	K. Goodell and I. M. Parker. Invasion of a dominant floral resource: effects on the floral community and pollination of native plants. *Ecology*, 98(1):57–69, jan 2017. doi: 10.1002/ecy.1639
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MA081	R. Jaffé, N. Pope, A. L. Acosta, D. A. Alves, M. C. Arias, P. De la Rúa, F. O. Francisco, T. C. Giannini, A. González-Chaves, V. L. Imperatriz-Fonseca, M. G. Tavares, S. Jha, and L. G. Carvalheiro. Beekeeping practices and geographic distance, not land use, drive gene flow across tropical bees. *Molecular Ecology*, 25(21): 5345–5358, sep 2016. doi: 10.1111/mec.13852

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MA090	G. Derroire, P. Balvanera, C. Castellanos-Castro, G. Decocq, D. K. Kennard, E. Lebrija-Trejos, J. A. Leiva, P.-C. Odén, J. S. Powers, V. Rico-Gray, M. Tigabu, and J. R. Healey. Resilience of tropical dry forests – a meta-analysis of changes in species diversity and composition during secondary succession. *Oikos*, 125(10): 1386–1397, oct 2016. doi: 10.1111/oik.03229
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MA097	D. S. W. Katz. The effects of invertebrate herbivores on plant population growth: a meta-regression analysis. *Oecologia*, 182(1):43–53, sep 2016. doi: 10.1007/s00442-016-3602-9
MA098	L. F. Fuzessy, T. G. Cornelissen, C. Janson, and F. A. O. Silveira. How do primates affect seed germination? a meta-analysis of gut passage effects on neotropical plants. *Oikos*, 125(8):1069–1080, aug 2016. doi: 10.1111/oik.02986
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MA103	Q. He and B. R. Silliman. Consumer control as a common driver of coastal vegetation worldwide. *Ecological Monographs*, 86(3):278–294, aug 2016. doi: 10.1002/ecm.1221
MA106	M. Delgado-Baquerizo, F. T. Maestre, P. B. Reich, P. Trivedi, Y. Osanai, Y.-R. Liu, K. Hamonts, T. C. Jeffries, and B. K. Singh. Carbon content and climate variability drive global soil bacterial diversity patterns. *Ecological Monographs*, 86(3):373–390, aug 2016. doi: 10.1002/ecm.1216
MA107	D. Thom and R. Seidl. Natural disturbance impacts on ecosystem services and biodiversity in temperate and boreal forests. *Biological Reviews*, 91(3):760–781, aug 2016. doi: 10.1111/brv.12193
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MA110	G. Arceo-Gómez and T.-L. Ashman. Invasion status and phylogenetic relatedness predict cost of heterospecific pollen receipt: implications for native biodiversity decline. *Journal of Ecology*, 104(4):1003–1008, jul 2016. doi: 10.1111/1365-2745.12586
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MA118	A. M. Smilanich, R. M. Fincher, and L. A. Dyer. Does plant apparency matter? thirty years of data provide limited support but reveal clear patterns of the effects of plant chemistry on herbivores. *New Phytologist*, 210(3):1044–1057, may 2016. doi: 10.1111/nph.13875
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MA121	J. S. Wesner. Contrasting effects of fish predation on benthic versus emerging prey: a meta-analysis. *Oecologia*, 180(4):1205–1211, apr 2016. doi: 10.1007/s00442-015-3539-4
MA122	M. P. Moore, R. Riesch, and R. A. Martin. The predictability and magnitude of life-history divergence to ecological agents of selection: a meta-analysis in livebearing fishes. *Ecology Letters*, 19(4):435–442, apr 2016b. doi: 10.1111/ele.12576
MA123	E. Rowen and I. Kaplan. Eco-evolutionary factors drive induced plant volatiles: a meta-analysis. *New Phytologist*, 210(1):284–294, apr 2016. doi: 10.1111/nph.13804
MA124	T. J. Thurman and R. D. H. Barrett. The genetic consequences of selection in natural populations. *Molecular Ecology*, 25(7):1429–1448, apr 2016. doi: 10.1111/mec.13559
MA125	M.-P. Hébert, B. E. Beisner, and R. Maranger. A meta-analysis of zooplankton functional traits influencing ecosystem function. *Ecology*, 97(4):1069–1080, apr 2016. doi: 10.1890/15-1084.1
MA126	J. T. Anderson. Plant fitness in a rapidly changing world. *New Phytologist*, 210(1):81–87, apr 2016. doi: 10.1111/nph.13693
MA127	S. Lorenz, V. Martinez-Fernández, C. Alonso, E. Mosselman, D. García de Jalón, M. González del Tánago, B. Belletti, D. Hendriks, and C. Wolter. Fuzzy cognitive mapping for predicting hydromorphological responses to multiple pressures in rivers. *Journal of Applied Ecology*, 53(2):559–566, apr 2016. doi: 10.1111/1365-2664.12569
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MA138	K. E. Barton. Tougher and thornier: general patterns in the induction of physical defence traits. *Functional Ecology*, 30(2):181–187, feb 2016. doi: 10.1111/1365-2435.12495
MA140	S. E. Street, C. P. Cross, and G. R. Brown. Exaggerated sexual swellings in female nonhuman primates are reliable signals of female fertility and body condition. *Animal Behaviour*, 112(Supplement C):203–212, feb 2016. doi: 10.1016/j.anbehav.2015.11.023
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MA146	I. T. Roca, L. Desrochers, M. Giacomazzo, A. Bertolo, P. Bolduc, R. Deschesnes, C. A. Martin, V. Rainville, G. Rheault, and R. Proulx. Shifting song frequencies in response to anthropogenic noise: a meta-analysis on birds and anurans. *Behavioral Ecology*, 27(5):1269–1274, jan 2016. doi: 10.1093/beheco/arw060
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MA150	R. M. Gunton and J. Pöyry. Scale-specific spatial density dependence in parasitoids: a multi-factor meta-analysis. *Functional Ecology*, 30(9):1501–1510, sep 2016. doi: 10.1111/1365-2435.12627
MA151	R. N. German, C. E. Thompson, and T. G. Benton. Relationships among multiple aspects of agriculture's environmental impact and productivity: a meta-analysis to guide sustainable agriculture. *Biological Reviews*, 92(2):716–738, may 2017. doi: 10.1111/brv.12251
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MA155	M. E. Strader, G. V. Aglyamova, and M. V. Matz. Red fluorescence in coral larvae is associated with a diapause-like state. *Molecular Ecology*, 25(2):559–569, jan 2016. doi: 10.1111/mec.13488
MA157	K. A. Wood, M. T. O'Hare, C. McDonald, K. R. Searle, F. Daunt, and R. A. Stillman. Herbivore regulation of plant abundance in aquatic ecosystems. *Biological Reviews*, 92(2):1128–1141, may 2017a. doi: 10.1111/brv.12272

ID	Study
MA158	Q. Deng, D. Hui, Y. Luo, J. Elser, Y.-P. Wang, I. Loladze, Q. Zhang, and S. Dennis. Down-regulation of tissue n:p ratios in terrestrial plants by elevated co2. *Ecology*, 96(12):3354–3362, dec 2015. doi: 10.1890/15-0217.1
MA159	L. Z. Garamszegi, G. Markó, E. Szász, S. Zsebők, M. Azcárate, G. Herczeg, and J. Török. Among-year variation in the repeatability, within- and between-individual, and phenotypic correlations of behaviors in a natural population. *Behavioral Ecology and Sociobiology*, 69(12):2005–2017, dec 2015. doi: 10.1007/s00265-015-2012-z
MA160	S. Lüpold, L. W. Simmons, J. L. Tomkins, and J. L. Fitzpatrick. No evidence for a trade-off between sperm length and male premating weaponry. *Journal of Evolutionary Biology*, 28(12):2187–2195, dec 2015. doi: 10.1111/jeb.12742
MA162	D. Moreno-Mateos, P. Meli, M. I. Vara-Rodríguez, and J. Aronson. Ecosystem response to interventions: lessons from restored and created wetland ecosystems. *Journal of Applied Ecology*, 52(6):1528–1537, dec 2015. doi: 10.1111/1365-2664.12518
MA163	I. Katano, H. Doi, B. K. Eriksson, and H. Hillebrand. A cross-system meta-analysis reveals coupled predation effects on prey biomass and diversity. *Oikos*, 124(11):1427–1435, nov 2015. doi: 10.1111/oik.02430
MA164	S. Graham, E. Chapuis, S. Meconcelli, N. Bonel, K. Sartori, A. Christophe, P. Alda, P. David, and T. Janicke. Size-assortative mating in simultaneous hermaphrodites: an experimental test and a meta-analysis. *Behavioral Ecology and Sociobiology*, 69(11):1867–1878, nov 2015. doi: 10.1007/s00265-015-1999-5
MA168	J. M. Goessling, H. Kennedy, M. T. Mendonça, and A. E. Wilson. A meta-analysis of plasma corticosterone and heterophil : lymphocyte ratios – is there conservation of physiological stress responses over time? *Functional Ecology*, 29(9):1189–1196, sep 2015. doi: 10.1111/1365-2435.12442
MA169	G. Q. Romero, T. Gonçalves-Souza, C. Vieira, and J. Koricheva. Ecosystem engineering effects on species diversity across ecosystems: a meta-analysis. *Biological Reviews*, 90(3):877–890, aug 2015. doi: 10.1111/brv.12138
MA170	J. M. Nielsen, B. N. Popp, and M. Winder. Meta-analysis of amino acid stable nitrogen isotope ratios for estimating trophic position in marine organisms. *Oecologia*, 178(3):631–642, jul 2015. doi: 10.1007/s00442-015-3305-7
MA171	J. James, F. M. Slater, I. P. Vaughan, K. A. Young, and J. Cable. Comparing the ecological impacts of native and invasive crayfish: could native species' translocation do more harm than good? *Oecologia*, 178(1):309–316, may 2015. doi: 10.1007/s00442-014-3195-0
MA176	R. Esteban, O. Barrutia, U. Artetxe, B. Fernández-Marín, A. Hernández, and J. I. García-Plazaola. Internal and external factors affecting photosynthetic pigment composition in plants: a meta-analytical approach. *New Phytologist*, 206(1):268–280, apr 2015. doi: 10.1111/nph.13186
MA178	D. J. Becker, D. G. Streicker, and S. Altizer. Linking anthropogenic resources to wildlife–pathogen dynamics: a review and meta-analysis. *Ecology Letters*, 18(5):483–495, may 2015. doi: 10.1111/ele.12428
MA179	S. Starko, B. Z. Claman, and P. T. Martone. Biomechanical consequences of branching in flexible wave-swept macroalgae. *New Phytologist*, 206(1):133–140, apr 2015. doi: 10.1111/nph.13182

ID	Study
MA180	Y.-H. Hsu, J. Schroeder, I. Winney, T. Burke, and S. Nakagawa. Are extra-pair males different from cuckolded males? a case study and a meta-analytic examination. *Molecular Ecology*, 24(7):1558–1571, apr 2015. doi: 10.1111/mec.13124
MA181	C. A. Mazza and C. L. Ballaré. Photoreceptors uvr8 and phytochrome b cooperate to optimize plant growth and defense in patchy canopies. *New Phytologist*, 207(1):4–9, jul 2015. doi: 10.1111/nph.13332
MA182	M. C. Jackson. Interactions among multiple invasive animals. *Ecology*, 96(8):2035–2041, aug 2015. doi: 10.1890/15-0171.1
MA183	A. Arct, S. M. Drobniak, and M. Cichoń. Genetic similarity between mates predicts extrapair paternity—a meta-analysis of bird studies. *Behavioral Ecology*, 26(4):959–968, jul 2015. doi: 10.1093/beheco/arv004
MA184	S. A. Boudreau, S. C. Anderson, and B. Worm. Top-down and bottom-up forces interact at thermal range extremes on american lobster. *Journal of Animal Ecology*, 84(3):840–850, may 2015. doi: 10.1111/1365-2656.12322
MA185	L.-Y. Yang, C. A. Machado, X.-D. Dang, Y.-Q. Peng, D.-R. Yang, D.-Y. Zhang, and W.-J. Liao. The incidence and pattern of copollinator diversification in dioecious and monoecious figs. *Evolution*, 69(2):294–304, feb 2015. doi: 10.1111/evo.12584
MA186	A. Siefert, C. Violle, L. Chalmandrier, C. H. Albert, A. Taudiere, A. Fajardo, L. W. Aarssen, C. Baraloto, M. B. Carlucci, M. V. Cianciaruso, V. de L. Dantas, F. de Bello, L. D. S. Duarte, C. R. Fonseca, G. T. Freschet, S. Gaucherand, N. Gross, K. Hikosaka, B. Jackson, V. Jung, C. Kamiyama, M. Katabuchi, S. W. Kembel, E. Kichenin, N. J. B. Kraft, A. Lagerström, Y. L. Bagousse-Pinguet, Y. Li, N. Mason, J. Messier, T. Nakashizuka, J. M. Overton, D. A. Peltzer, I. M. Pérez-Ramos, V. D. Pillar, H. C. Prentice, S. Richardson, T. Sasaki, B. S. Schamp, C. Schöb, B. Shipley, M. Sundqvist, M. T. Sykes, M. Vandewalle, and D. A. Wardle. A global meta-analysis of the relative extent of intraspecific trait variation in plant communities. *Ecology Letters*, 18(12): 1406–1419, dec 2015. doi: 10.1111/ele.12508
MA187	J. Beninde, M. Veith, and A. Hochkirch. Biodiversity in cities needs space: a meta-analysis of factors determining intra-urban biodiversity variation. *Ecology Letters*, 18(6):581–592, jun 2015. doi: 10.1111/ele.12427
MA188	A. M. Senior, S. Nakagawa, M. Lihoreau, S. J. Simpson, and D. Raubenheimer. An overlooked consequence of dietary mixing: A varied diet reduces interindividual variance in fitness. *The American Naturalist*, 186(5): 649–659, nov 2015. doi: 10.1086/683182
MA189	L. K. Albertson and D. C. Allen. Meta-analysis: abundance, behavior, and hydraulic energy shape biotic effects on sediment transport in streams. *Ecology*, 96(5):1329–1339, may 2015. doi: 10.1890/13-2138.1
MA190	R. Frankham. Genetic rescue of small inbred populations: meta-analysis reveals large and consistent benefits of gene flow. *Molecular Ecology*, 24(11):2610–2618, jun 2015. doi: 10.1111/mec.13139
MA191	K. L. Voje. Scaling of morphological characters across trait type, sex, and environment: A meta-analysis of static allometries. *The American Naturalist*, 187(1):89–98, nov 2015. doi: 10.1086/684159
MA192	M. Slot and K. Kitajima. General patterns of acclimation of leaf respiration to elevated temperatures across biomes and plant types. *Oecologia*, 177(3):885–900, mar 2015. doi: 10.1007/s00442-014-3159-4

ID	Study
MA193	M. Jahnke, J. L. Olsen, and G. Procaccini. A meta-analysis reveals a positive correlation between genetic diversity metrics and environmental status in the long-lived seagrass posidonia oceanica. *Molecular Ecology*, 24 (10):2336–2348, may 2015. doi: 10.1111/mec.13174
MA194	J. C. Iacarella, J. T. A. Dick, M. E. Alexander, and A. Ricciardi. Ecological impacts of invasive alien species along temperature gradients: testing the role of environmental matching. *Ecological Applications*, 25(3):706–716, apr 2015. doi: 10.1890/14-0545.1
MA195	P. E. Quesnelle, K. E. Lindsay, and L. Fahrig. Relative effects of landscape-scale wetland amount and landscape matrix quality on wetland vertebrates: a meta-analysis. *Ecological Applications*, 25(3):812–825, apr 2015. doi: 10.1890/14-0362.1
MA197	L. R. Dougherty and D. M. Shuker. The effect of experimental design on the measurement of mate choice: a meta-analysis. *Behavioral Ecology*, 26(2):311–319, mar 2015. doi: 10.1093/beheco/aru125
MA198	I. Paz-Vinas, G. Loot, V. M. Stevens, and S. Blanchet. Evolutionary processes driving spatial patterns of intraspecific genetic diversity in river ecosystems. *Molecular Ecology*, 24(18):4586–4604, sep 2015. doi: 10.1111/mec.13345
MA199	S. A. Sistla, A. P. Appling, A. M. Lewandowska, B. N. Taylor, and A. A. Wolf. Stoichiometric flexibility in response to fertilization along gradients of environmental and organismal nutrient richness. *Oikos*, 124(7): 949–959, jul 2015. doi: 10.1111/oik.02385
MA200	M. Jauni, S. Gripenberg, and S. Ramula. Non-native plant species benefit from disturbance: a meta-analysis. *Oikos*, 124(2):122–129, feb 2015. doi: 10.1111/oik.01416
MA201	R. A. Bunn, P. W. Ramsey, and Y. Lekberg. Do native and invasive plants differ in their interactions with arbuscular mycorrhizal fungi? a meta-analysis. *Journal of Ecology*, 103(6):1547–1556, nov 2015. doi: 10.1111/1365-2745.12456
MA202	Z. Mehrabi and S. L. Tuck. Relatedness is a poor predictor of negative plant–soil feedbacks. *New Phytologist*, 205(3):1071–1075, feb 2015. doi: 10.1111/nph.13238
MA203	X. Wang, D. R. Taub, and L. M. Jablonski. Reproductive allocation in plants as affected by elevated carbon dioxide and other environmental changes: a synthesis using meta-analysis and graphical vector analysis. *Oecologia*, 177(4):1075–1087, apr 2015. doi: 10.1007/s00442-014-3191-4
MA204	A. Albert, A. G. Auffret, E. Cosyns, S. A. O. Cousins, B. D'hondt, C. Eichberg, A. E. Eycott, T. Heinken, M. Hoffmann, B. Jaroszewicz, J. E. Malo, A. Mårell, M. Mouissie, R. J. Pakeman, M. Picard, J. Plue, P. Poschlod, S. Provoost, K. A. Schulze, and C. Baltzinger. Seed dispersal by ungulates as an ecological filter: a trait-based meta-analysis. *Oikos*, 124(9):1109–1120, sep 2015. doi: 10.1111/oik.02512
MA205	J. L. Mijangos, C. Pacioni, P. B. S. Spencer, and M. D. Craig. Contribution of genetics to ecological restoration. *Molecular Ecology*, 24(1):22–37, jan 2015. doi: 10.1111/mec.12995
MA206	L. Tamburello, E. Maggi, L. Benedetti-Cecchi, G. Bellistri, A. J. Rattray, C. Ravaglioli, L. Rindi, J. Roberts, and F. Bulleri. Variation in the impact of non-native seaweeds along gradients of habitat degradation: a meta-analysis and an experimental test. *Oikos*, 124(9):1121–1131, sep 2015. doi: 10.1111/oik.02197

ID	Study
MA207	V. Ferreira, B. Castagneyrol, J. Koricheva, V. Gulis, E. Chauvet, and M. A. S. Graça. A meta-analysis of the effects of nutrient enrichment on litter decomposition in streams. *Biological Reviews*, 90(3):669–688, aug 2015. doi: 10.1111/brv.12125
MA208	A. E. A. Stephens and M. Westoby. Effects of insect attack to stems on plant survival, growth, reproduction and photosynthesis. *Oikos*, 124(3):266–273, mar 2015. doi: 10.1111/oik.01809
MA210	W. R. L. Anderegg. Spatial and temporal variation in plant hydraulic traits and their relevance for climate change impacts on vegetation. *New Phytologist*, 205(3):1008–1014, feb 2015. doi: 10.1111/nph.12907
MA211	Z. Y. Yuan and H. Y. H. Chen. Negative effects of fertilization on plant nutrient resorption. *Ecology*, 96(2): 373–380, feb 2015. doi: 10.1890/14-0140.1
MA212	A. Valls, M. Coll, and V. Christensen. Keystone species: toward an operational concept for marine biodiversity conservation. *Ecological Monographs*, 85(1):29–47, feb 2015. doi: 10.1890/14-0306.1
MA213	R. I. Colautti and J. A. Lau. Contemporary evolution during invasion: evidence for differentiation, natural selection, and local adaptation. *Molecular Ecology*, 24(9):1999–2017, may 2015. doi: 10.1111/mec.13162
MA214	L. A. Fuiman, T. L. Connelly, S. K. Lowerre-Barbieri, and J. W. McClelland. Egg boons: central components of marine fatty acid food webs. *Ecology*, 96(2):362–372, feb 2015. doi: 10.1890/14-0571.1
MA215	L. Baeten, T. J. Davies, K. Verheyen, H. V. Calster, and M. Vellend. Disentangling dispersal from phylogeny in the colonization capacity of forest understorey plants. *Journal of Ecology*, 103(1):175–183, jan 2015. doi: 10.1111/1365-2745.12333
MA217	Z. E. Taranu, I. Gregory-Eaves, P. R. Leavitt, L. Bunting, T. Buchaca, J. Catalan, I. Domaizon, P. Guilizzoni, A. Lami, S. McGowan, H. Moorhouse, G. Morabito, F. R. Pick, M. A. Stevenson, P. L. Thompson, and R. D. Vinebrooke. Acceleration of cyanobacterial dominance in north temperate-subarctic lakes during the anthropocene. *Ecology Letters*, 18(4):375–384, apr 2015. doi: 10.1111/ele.12420
MA218	L. M. Pintor and J. E. Byers. Do native predators benefit from non-native prey? *Ecology Letters*, 18(11): 1174–1180, nov 2015. doi: 10.1111/ele.12496
MA220	K. A. Harper, S. E. Macdonald, M. S. Mayerhofer, S. R. Biswas, P.-A. Esseen, K. Hylander, K. J. Stewart, A. U. Mallik, P. Drapeau, B.-G. Jonsson, D. Lesieur, J. Kouki, and Y. Bergeron. Edge influence on vegetation at natural and anthropogenic edges of boreal forests in canada and fennoscandia. *Journal of Ecology*, 103(3): 550–562, may 2015. doi: 10.1111/1365-2745.12398
MA222	A. Culina, R. Radersma, and B. C. Sheldon. Trading up: the fitness consequences of divorce in monogamous birds. *Biological Reviews*, 90(4):1015–1034, nov 2015. doi: 10.1111/brv.12143
MA223	M. E. S. Bracken, H. Hillebrand, E. T. Borer, E. W. Seabloom, J. Cebrian, E. E. Cleland, J. J. Elser, D. S. Gruner, W. S. Harpole, J. T. Ngai, and J. E. Smith. Signatures of nutrient limitation and co-limitation: responses of autotroph internal nutrient concentrations to nitrogen and phosphorus additions. *Oikos*, 124(2):113–121, feb 2015. doi: 10.1111/oik.01215
MA224	S. Périquet, H. Fritz, and E. Revilla. The lion king and the hyaena queen: large carnivore interactions and coexistence. *Biological Reviews*, 90(4):1197–1214, nov 2015. doi: 10.1111/brv.12152

ID	Study
MA226	K. H. Elliott, J. F. Hare, M. L. Vaillant, A. J. Gaston, Y. Ropert-Coudert, and W. G. Anderson. Ageing gracefully: physiology but not behaviour declines with age in a diving seabird. *Functional Ecology*, 29(2):219–228, feb 2015. doi: 10.1111/1365-2435.12316
MA227	A. Lafuente, P. Pérez-Palacios, B. Doukkali, M. D. Molina-Sánchez, J. I. Jiménez-Zurdo, M. A. Caviedes, I. D. Rodríguez-Llorente, and E. Pajuelo. Unraveling the effect of arsenic on the model medicago–ensifer interaction: a transcriptomic meta-analysis. *New Phytologist*, 205(1):255–272, jan 2015. doi: 10.1111/nph.13009
MA229	L. Gamfeldt, J. S. Lefcheck, J. E. K. Byrnes, B. J. Cardinale, J. E. Duffy, and J. N. Griffin. Marine biodiversity and ecosystem functioning: what's known and what's next? *Oikos*, 124(3):252–265, mar 2015. doi: 10.1111/oik.01549

S3 REVIEW OF JOURNAL POLICIES ON DATA AND CODE SHARING

The availability of data and code for individual articles needs to be evaluated in the context of the publishing journals' policies about making data and code available at the time of publication. Due to the retrospective nature of this study, we could not collect information about the journals' data and code policies contemporaneous with the articles published 2015–17. Despite this, the journals' policies on data and code can be inferred from other sources, including previous studies of journal policies and initiatives such as the Joint Data Archiving Policy (JDAP). We deal with data policies and then code policies in turn.

Data policies

JDAP was adopted by a number of journals in the fields of ecology and evolutionary biology in 2011 (Dryad, 2020). JDAP introduced data archiving as a requirement for publication: the data that underlie the results of the article must be deposited in a public data repository, such as the Dryad Digital Repository (Dryad, 2021). Four of the journals in this study adopted JDAP in 2011: *Evolution* (Rausher et al., 2010), *Journal of Evolutionary Biology* (Moore et al., 2010), *Molecular Ecology* (Rieseberg et al., 2010), and *The American Naturalist* (Whitlock et al., 2010). *Functional Ecology* adopted a slight variation of JDAP in 2014 (Fox et al., 2014), along with other journals published by the British Ecological Society: *Journal of Animal Ecology*, *Journal of Applied Ecology*, and *Journal of Ecology* (Sandhu and Baker, 2014). Therefore, assuming the journals' adoption of JDAP (or slight variation thereof) has persisted, we expect that these eight journals would have mandated data archiving for all studies published through 2015–17.

Mislan et al. (2016) investigated both the data and code policies for 17 of the 21 journal titles in this study. The policies checked were as of 1st June 2015, which is within the 2015–17 time period. Specifically, regarding data, Mislan et al. (2016) recorded whether journals' policies *required* data to be released as a condition of publication—that is, beyond mere encouragement to make data available. We shall regard the findings in Mislan et al. (2016) as representing journals' policies on data and code at the start of 2015 (it is possible that some meta-analyses published in the first five months of 2015 were published under a different journal policy that then changed to the policy found by Mislan et al. (2016), but for simplicity we will discount this possibility).

The four journals that were not reviewed in Mislan et al. (2016) are *Animal Behaviour*, *Biological Reviews*, *New Phytologist*, and *Quarterly Review of Biology*. We examined other sources to get an indication of their data and code policies. The data policy of the journal *Animal Behaviour* was surveyed in January 2014 by Caetano and Aisenberg (2014). This survey found that the journal encouraged authors to make data available, but did not make it mandatory. In the absence of other information (which was searched for in e.g., editorials or news releases, but not found), we assume that this was the data policy of the journal during 2015–17. (When checked again in 2021, the journal was found to have the same policy of encouraging data sharing, so it seems safe to assume the policy has been consistently in place since 2014.) When checked in 2021, the journal *Biological Reviews* "encourages" authors to make data available, but does not require authors to do so, or to include data availability statements (John Wiley & Sons, 2021). In the absence of other information, we assume that this was the data policy of the journal during 2015–17. The data policy of the journal *New Phytologist* was surveyed in August/September 2013 by Magee et al. (2014). This survey classified the policy of *New Phytologist* as *weak*, meaning that data sharing was encouraged but not required. In the absence of other information, we assume that this was the data policy of the journal during 2015–17. When checked in 2021, the instructions to authors webpage for the journal *Quarterly Review of Biology*[5] makes no mention of data sharing, archiving, or availability. Similarly, an archived snapshot of the instructions to authors webpage as it was on 28th May 2016[6] made no mention of any data policy. In the absence of other information, we assume that not requiring data sharing was the effective data policy of the journal during 2015–17. A summary of the data-sharing policies of the journals in this study is given in Table S3.

Code policies

The principal source for information about journals' code policies comes from the survey conducted in Mislan et al. (2016). This survey was followed up and repeated in Culina et al. (2020), which updated the status of journals' code policies in 2020. Both surveys have recorded information about the code policies of 17 of the journals included in this present study. Mislan et al. (2016) recorded whether journals required

[5] https://www.journals.uchicago.edu/journals/qrb/instruct
[6] https://web.archive.org/web/20160528051141/http://www.journals.uchicago.edu/journals/qrb/instruct

Journal	JDAP member	Data sharing required?	Source
Animal Behaviour	N	N	Caetano and Aisenberg (2014)
Behavioral Ecology	N	N	Mislan et al. (2016)
Behavioral Ecology and Sociobiology	N	N	Mislan et al. (2016)
Biological Reviews	N	N	Journal website
Ecological Applications	N	Y	Mislan et al. (2016)
Ecological Monographs	N	Y	Mislan et al. (2016)
Ecology	N	Y	Mislan et al. (2016)
Ecology Letters	N	Y	Mislan et al. (2016)
Evolution	Y	Y	Mislan et al. (2016)
Evolutionary Ecology	N	N	Mislan et al. (2016)
Functional Ecology	Y	Y	Mislan et al. (2016)
Journal of Animal Ecology	Y	Y	Mislan et al. (2016)
Journal of Applied Ecology	Y	Y	Mislan et al. (2016)
Journal of Ecology	Y	Y	Mislan et al. (2016)
Journal of Evolutionary Biology	Y	Y	Mislan et al. (2016)
Molecular Ecology	Y	Y	Mislan et al. (2016)
New Phytologist	N	N	Magee et al. (2014)
Oecologia	N	N	Mislan et al. (2016)
Oikos	N	Y	Mislan et al. (2016)
The American Naturalist	Y	Y	Mislan et al. (2016)
The Quarterly Review of Biology	N	N	Journal website

Table S3: Summary of whether data sharing was found to be required for each journal surveyed in this study, along with JDAP member status and source of the information. In the columns "JDAP member" and "Data sharing required?", "Y" indicates "yes" and "N" indicates "no".

the release of code as a requirement for publication as a binary yes/no variable (the same way as how journals' data policies were recorded). The updated survey in Culina et al. (2020) distinguished between policies where code sharing was "encouraged" and policies where code sharing was "mandatory" (the authors note that some journal policies were ambiguously worded such that it could not be determined whether code sharing was merely encouraged or a mandatory requirement; they designated such policies "encouraged/mandatory"). For the four journals not covered in the Mislan et al. (2016) survey, we could not find contemporary assessments of their code policies over the period 2015–17. The best we could do was to inspect the current (as of 2021) journal policy information for these four journals. We found that *Animal Behaviour* had a policy of encouraging code sharing, but we could not find mention of polic(ies) about code in the online information for *Biological Reviews*, *New Phytologist*, and *The Quarterly Review of Biology*. For the purposes of this study, we shall regard these four journals as not having had a policy requiring code sharing during 2015–17. A summary of the code policies of the journals in this study is given in Table S4.

Journal	2015 survey	2020 survey	2021 check
Animal Behaviour	-	-	E
Behavioral Ecology	N	N	-
Behavioral Ecology and Sociobiology	N	N	-
Biological Reviews	-	-	N.F.
Ecological Applications	Y	M	-
Ecological Monographs	Y	M	-
Ecology	Y	M	-
Ecology Letters	N	E/M	-
Evolution	N	M	-
Evolutionary Ecology	N	E	-
Functional Ecology	Y	E/M	-
Journal of Animal Ecology	Y	E/M	-
Journal of Applied Ecology	Y	E/M	-
Journal of Ecology	Y	E/M	-
Journal of Evolutionary Biology	N	M	-
Molecular Ecology	Y	E	-
New Phytologist	-	-	N.F.
Oecologia	N	N	-
Oikos	N	N	-
The American Naturalist	Y	E	-
The Quarterly Review of Biology	-	-	N.F.

Table S4: Summary of the code sharing policies found for each journal. The column "2015 survey" refers to Mislan et al. (2016), the column "2020 survey" refers to Culina et al. (2020), and the column "2021 check" refers to our own checks made in 2021. Within the table columns, "Y" indicates "yes", "N" indicates "no", "E" indicates "encouraged", "M" indicates "mandatory", and "N.F." indicates "not found".

S4 CODING SCHEME FOR CODE AND DATA SHARING

The assessment process for each article for shared data and code was as follows: first, we inspected the end sections of each article for any mention of supplemental material, and for the existence of a data/code availability statement of any kind. In cases without an explicit data availability statement, or where data/code were not listed as supplements, we reviewed the methods and results sections for any possible in-text mention of data/code availability, first by performing a keyword search for “data”. Regardless of what was mentioned in the article, we also inspected the journal webpage for each article (accessed via The University of Melbourne library) for indications and details of supplemental materials, shared data and shared code. We attempted to download and briefly inspect all files at the journal webpage that we found. Where supplemental material, data and/or code were reported as existing at other web links (e.g., an online data archive), we followed the web links and attempted to download and inspect all files we found. The coding scheme in Table S5 captures the results of this process.

This coding scheme assumes that if data and/or code were shared, there would be some positive indication of this fact somewhere in the article itself, or on the journal publisher’s web page for the article (either as supplemental material, or as a link to an independent resource). An absence of any such indication was taken to mean that data/code was not shared. This approach does not account for the possibility that authors may have in fact shared the data and code associated with their article (say, by publishing it in a data repository such as Dryad) but not included any indication either in the article itself, or on the journal web page for the article. (One possible reason this might occur is when authors decide to share the data/code after the article had been published.) We decided not to attempt to check for such possibilities when assessment of an article and its journal web page found no indications of shared data or code.

In this coding scheme, items 1–4 concern supplemental material in general, items 5–12 concern shared data in particular, and items 13–20 concern shared code in particular (item 21 was used to record any additional notes). The items recording the existence (or not) of shared supplemental materials, data, and code are items 1, 5–6, and 13–14. For the data and code sharing, we separated out the nominal sharing of these from the actual sharing of these (in retrospect, we should have done the same for supplemental materials too). In this context, data and code were recorded as having been actually shared only if we were personally able to successfully download (via The University of Melbourne library) and inspect the relevant file(s).

The numbers of files shared (items 2, 7, and 15) were recorded to help keep track of downloaded files. These values were recorded only if the respective preceding items indicated that such files existed. This did lead to some anomalies: the number of files was recorded as 0 in cases where the article stated that all relevant data was made available within tables of the article itself (and not as a separate data file).

S5 RECORDING MENTIONS OF SOFTWARE USED

The review process for mentions of software in an article consisted of checking the text of each article/supplementary document for the following keywords (using a case-insensitive search):

- "CMA", referring to the software package *Comprehensive Meta-Analysis* (Borenstein et al., 2013);
- "MetaWin", referring to the software package *Meta Win* (Rosenberg et al., 1997);
- "metafor", referring to the R package *metafor* (Viechtbauer, 2010);
- "mcmcglmm", referring to the R package *mcmcglmm* (Hadfield, 2010).

In the absence of these keywords being found, the methods section/supplementary document was manually scanned for statements along the lines of "analyses were performed using [software package]".

For each mention of software used (allowing for multiple mentions per article), the details were recorded using a ten-item coding scheme outlined in Table S6. The coding scheme was designed around an expectation of the frequent mention of R and R packages.

Items 1 and 2 record the name of the software package/platform as reported in the article and the page number of the mention respectively.

Items 3 and 4 record whether a specific version of the software was reported. Items 5, 6, and 7 are specific to the R software environment.

Item 5 is a flag indicating whether the mentioned software package was an R package or not. This required judgment beyond what was reported in the article: For most software mentioned, we were able to code this item based on our own knowledge of R and its packages; where we were not already familiar with the software package, we used contextual clues in the article (e.g., mentions of the function of the software or details from the citation if provided) and online searches of the software name to determine whether or not it was an R package.

Item 6 was only applicable to software identified as an R package: this recorded the location where the R package was hosted. We anticipated that there would be few discrete categories here: "base" referring to packages which are part of the base R installation; "Bioconductor" referring to R packages released as

Index	Field	Values	Description
1	Supplements included	Y, N	Does the article include supplementary information?
2	No. supplement files	0-99	Number of discrete files or documents included as supplementary information
3	Supplements mentioned	Y, N	Does the article *mention* the existence of the supplementary information?
4	Supplements detailed	Y, N	Does the article provide details of the contents of supplementary information?
5	Datasets nominally included	Y, N	Does the article *indicate* that data has been shared, included?
6	Datasets included	Y, N	Was the data actually included (shared) and obtainable?
7	No. data files	0-99	Number of discrete data files included
8	Dataset sources	open text	Location of the datasets (e.g., repository name)
9	Dataset URL	open text	Link to data as applicable
10	Dataset info in article	Y, N	Is the availability of data referred to in the article?
11	Dataset info on website	Y, N	Is the availability of data referred to on the journal web page for the article?
12	Data format	open text	File format(s) of data files
13	Code nominally included	Y, N	Does the article *indicate* that code has been shared, included?
14	Code included	Y, N	Was the code actually included (shared) and obtainable?
15	No. code files	0-99	Number of discrete code files included
16	Code sources	open text	Location of the code (e.g., repository name)
17	Code URL	open text	Link to code as applicable
18	Code info in article	Y, N	Is the availability of code referred to in the article?
19	Code info on website	Y, N	Is the availability of code referred to on the journal web page for the article?
20	Code type	open text	Language or software package the code is associated with
21	Notes	open text	Any additional notes about the article's data and code sharing.

Table S5: The twenty-one item coding scheme used for recording data and code sharing in meta-analysis articles. In the Values column, "Y" indicates "yes" and "N" indicates "no".

components of the Bioconductor project; "CRAN" referring to the Comprehensive R Archive Network, a repository for R packages; and "other" for all remaining cases.

Item 7 is applicable only to mentions of the R software environment at large: this records whether in addition to the mention of R, specific R packages mentioned as well.

Items 8 and 9 record whether and how the article cited/provided a reference for the software mentioned. Item 8 was initially "Y"/"N" (yes/no), during the coding process we decided to introduce an addition code "T" which was for instances of an "in text" reference for the software (e.g., the website for the software package in parentheses immediately following the software name) but with no corresponding details in the "References" section of the article. As a result, a value of "Y" indicates that the article includes a full reference to the software in the References section. The full reference (or in-text only citation) as reported in the article is recorded in Item 9.

Finally, Item 10 was used to record additional notes/context about the mention of the software as applicable.

Index	Field	Values	Description
1	Software details	open text	The name of the software as reported in the article.
2	Page reference	open text	Specify the page number of the mention.
3	Version specified	Y, N	Does the article specify the version of the software?
4	Version details	open text	The version details as reported in the article.
5	Is R package	Y, N	Is the software mentioned an R package?
6	R package location	base, Bioconductor, CRAN, other, N/A	If the software mentioned is an R package, where is the package located/hosted?
7	R packages mentioned	Y, N, N/A	If the software mentioned is R, are packages mentioned elsewhere in the article?
8	Software cited	Y, N, T	Does the article include a citation for the software package?
9	Citation details	open text	The full reference to the software as reported in the article.
10	Notes	open text	Any additional notes about this mention of software.

Table S6: The ten item coding scheme used for recording software mentions. In the Values column, "Y" indicates "yes", "N" indicates "no", "T" indicates "in-text only", and "N/A" indicates "not applicable".

S6 DATA AND CODE SHARING

For the 133 articles with data, we had found some kind of indication about data availability somewhere in the article itself or in the supplementary documentation for all but one article (in this one case, the information indicating that data was available was on the journal's web page for the article instead). This took the form of either an explicit data availability statement in the article, or a mention in the body of the article, as part of an in-article statement about the content of supplemental/supporting information, or in the supplemental/supporting information itself. For example, *Evolution* articles included a data availability statement in a dedicated section titled "Data Archiving" located at the end of the article, just before the references section.

Failures to obtain data and code

We failed to obtain data for five articles for three reasons: for the first three cases, a supplemental document indicated that data files were included as part of the supplemental material. However, the files referred to could not be found as part of the online supplement; it is possible that while the documentation for the data was uploaded, the actual files themselves were not. In the fourth case, the data availability statement said that data would be uploaded to Dryad upon acceptance of the article, however no link or details of how to find the data were provided (failing to update the data availability statement may have been an oversight when the article was being finalised for publication). In the final case, the article stated that data had been deposited in a research institute's database, but failed to provide any details apart from a link to the institute's main web page. The institute maintains a number of databases, and there was no clear way to identify which data in which database was relevant to the meta-analysis.

The one case where we could not obtain code is the one of the articles discussed above in reference to data availability, where files listed as being part of the supplement could not be found.

Data and Code Sharing by Journal

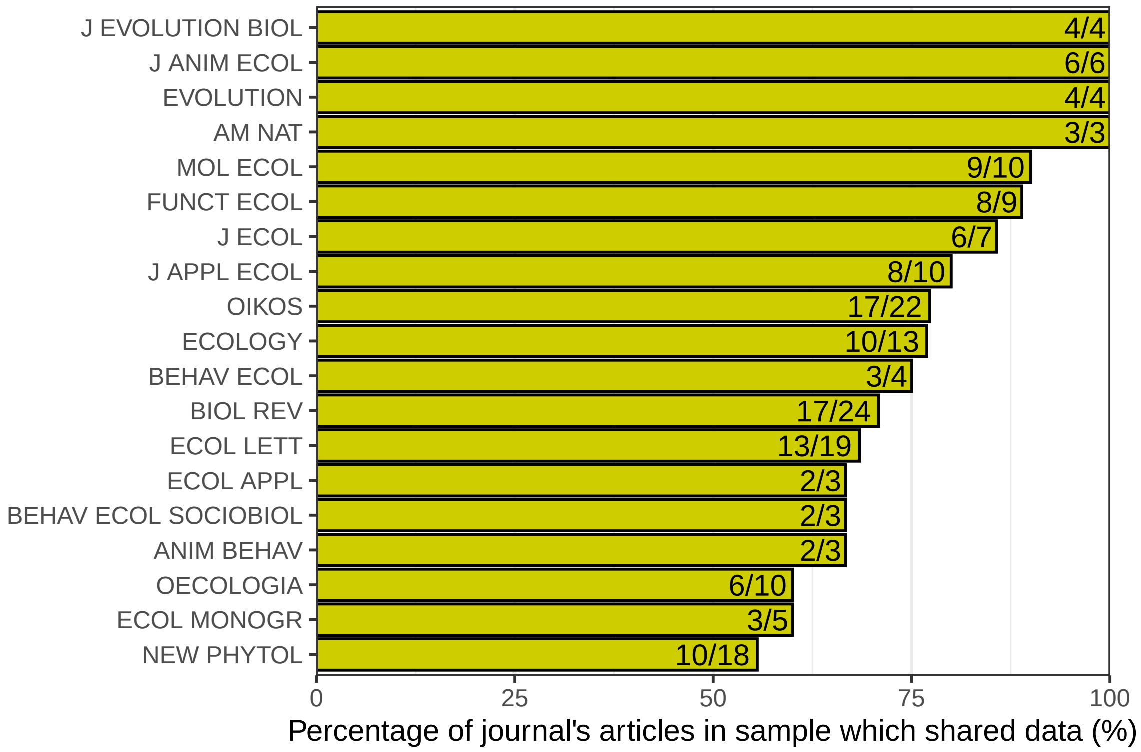

Figure S1: Comparison of data sharing rates in articles by journal.

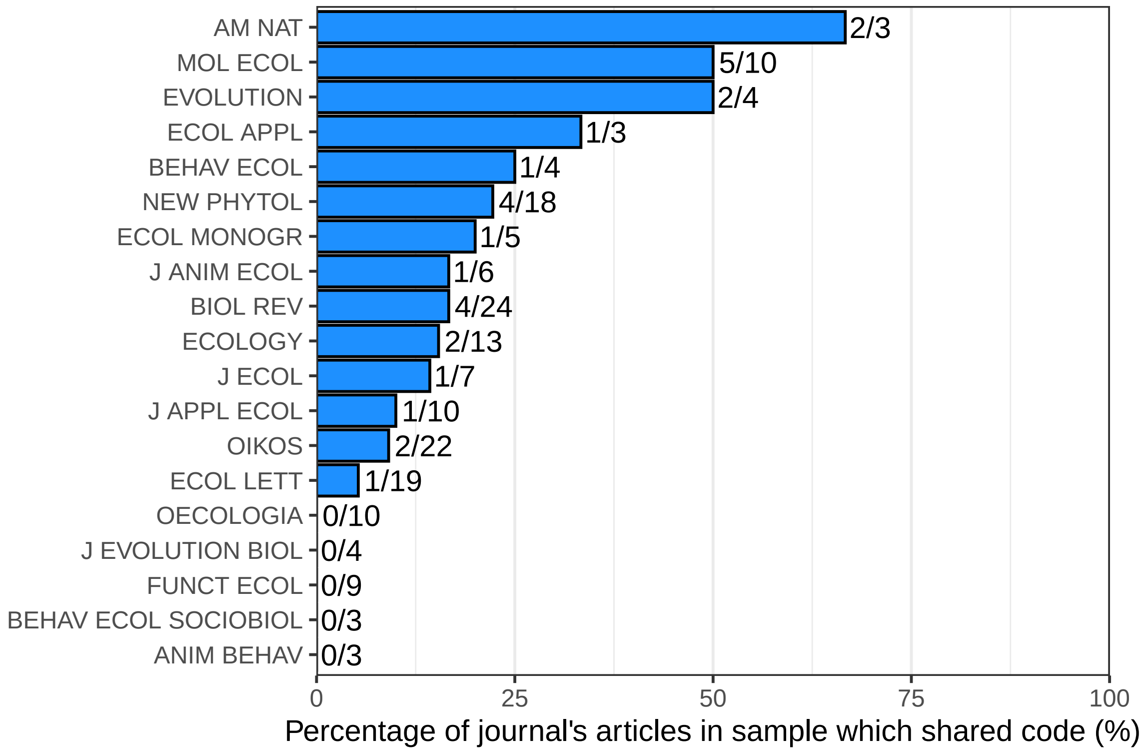

Figure S2: Comparison of code sharing rates in articles by journal.

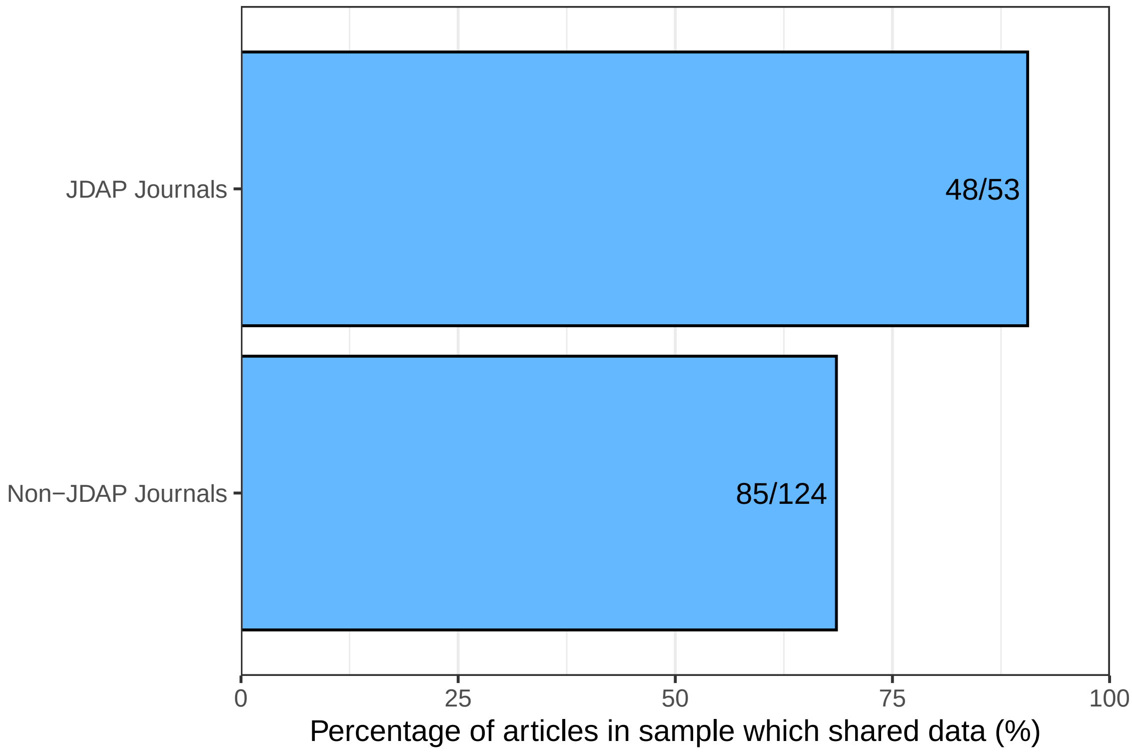

Figure S3: Comparison of data sharing rates in articles by journal JDAP membership status.

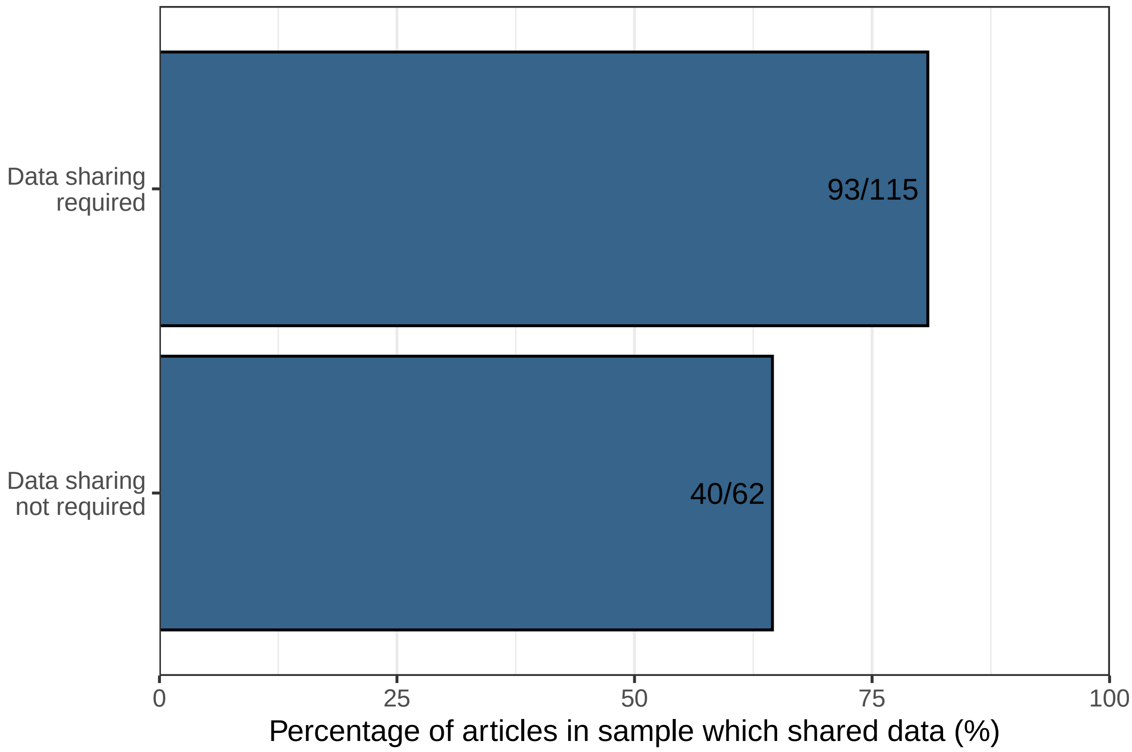

Figure S4: Comparison of data sharing rates in articles by journal data policy 2015–17.

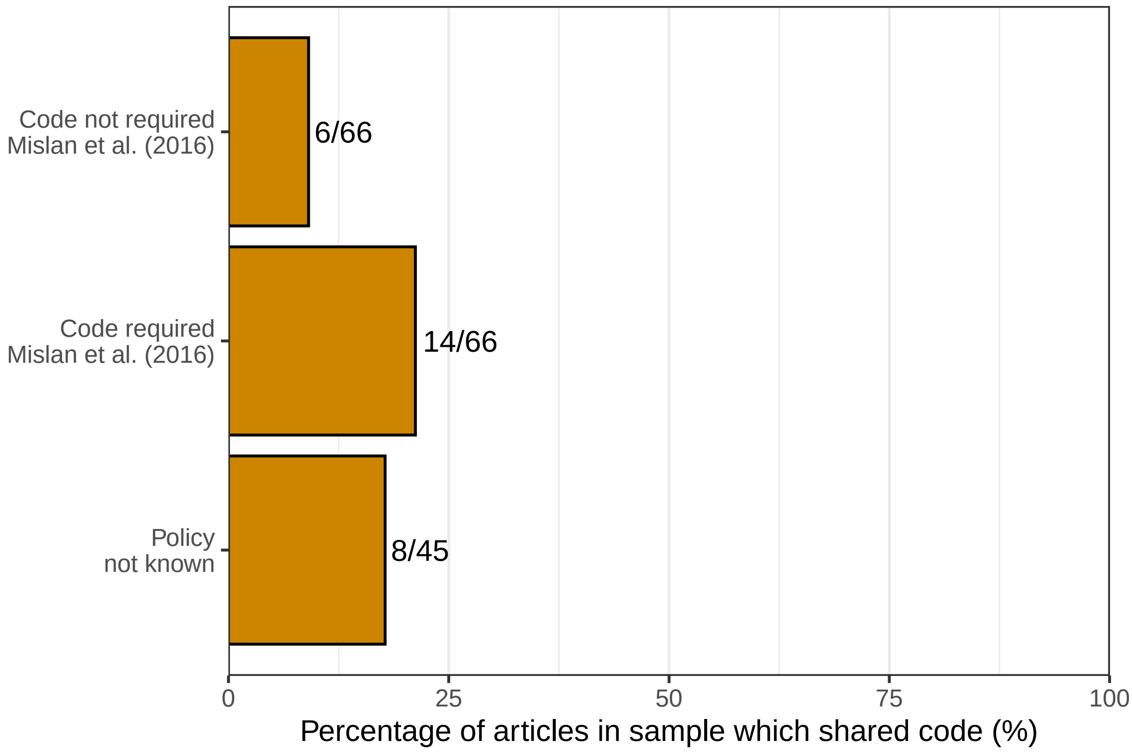

Figure S5: Comparison of code sharing rates in articles by journal code policy according to Mislan et al. (2016).

S7 SOFTWARE MENTIONED IN ARTICLES

Figure S6 shows the distribution of the number of different software packages mentioned in each article (or in its supplementary material). Here, R packages have been treated as special cases: articles mentioning multiple R packages have been treated as just mentioning the R software environment. For example, an article which mentioned the R software environment and four R packages was regarded as mentioning one software package (the R software environment) rather than five software packages.

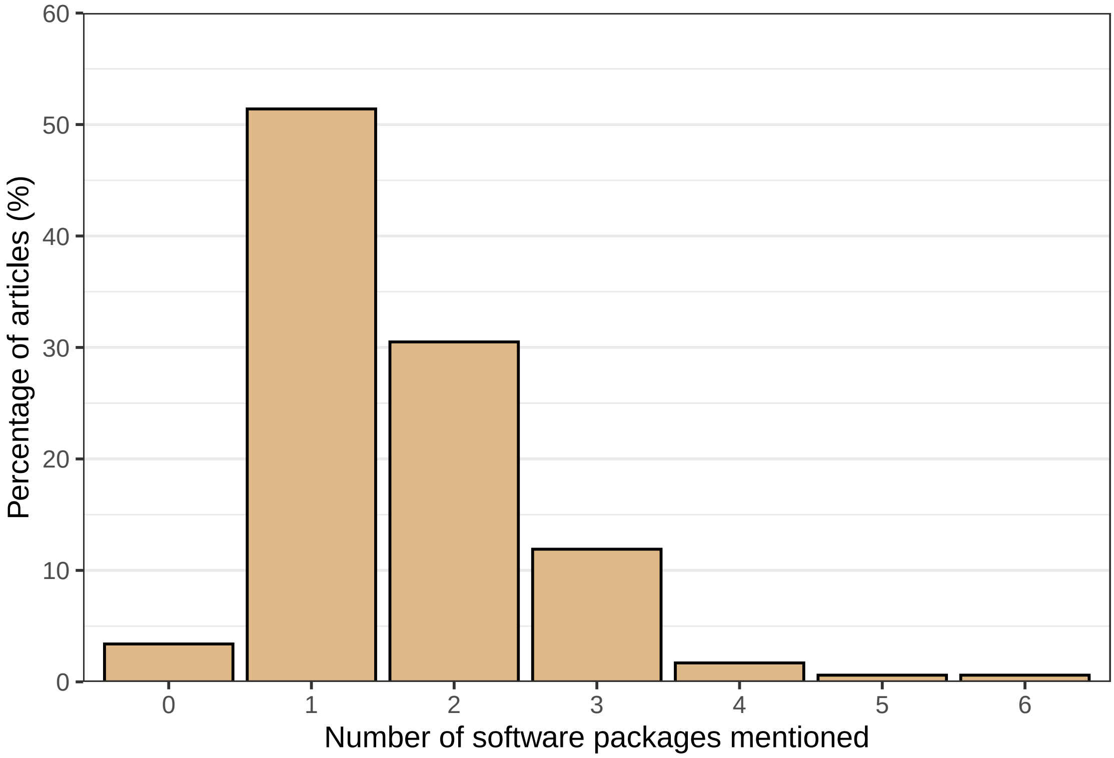

Figure S6: Distribution of the number of different software packages mentioned in each article (or its supplementary material).

Figure S7 is a version of Figure S6 which shows the distribution of the number of different software packages mentioned in each article (or in its supplementary material), *including* mentions of R packages. For example, an article which mentioned the R software environment and four R packages was regarded as mentioning five software packages rather than one software package (i.e., the R software in general).

Table S7 lists all software packages mentioned in the 177 meta-analysis articles. This table includes all mentions of the R software environment, but specifically excludes mentions of R packages, which are listed in the following table.

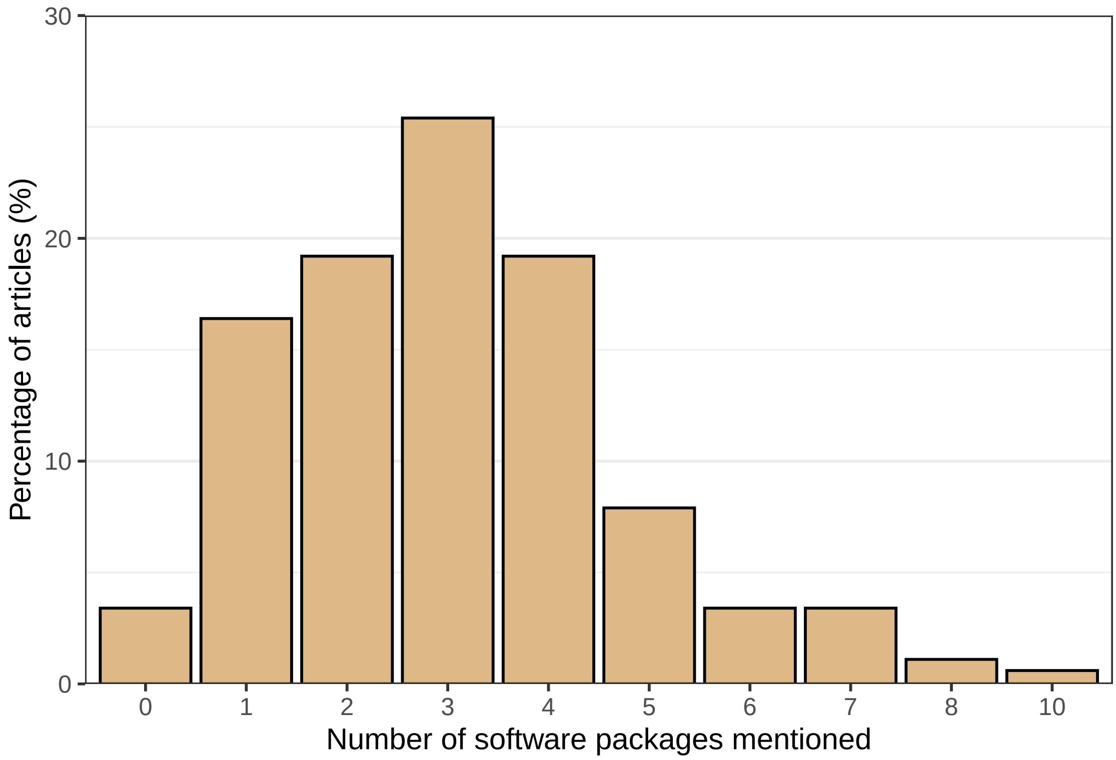

Figure S7: Distribution of the number of different software packages mentioned in each article (or its supplementary material), including mentions of R packages.

Table S7: All software packages mentioned in the 177 meta-analysis articles. Note that this table does not list individual R packages.

Name of software package	N	%
R	141	79.7
MetaWin	20	11.3
WebPlotDigitizer	10	5.6
DataThief III	9	5.1
SAS	9	5.1
ImageJ	7	4.0
GraphClick	6	3.4
PlotDigitizer	5	2.8
GetData Graph Digitizer	4	2.3
JMP	4	2.3
RStudio	4	2.3
SPSS/PASW	4	2.3
Minitab	3	1.7

Name of software package	N	%
Phylocom	3	1.7
Phylomatic	3	1.7
RAxML	3	1.7
ArcGIS	2	1.1
ArcMap	2	1.1
CMA	2	1.1
Engauge Digitizer	2	1.1
GENALEX	2	1.1
MAFFT	2	1.1
Python	2	1.1
Stan	2	1.1
AbstrackR	1	0.6
ADZE	1	0.6
AMOS	1	0.6
ARLSUMSTAT	1	0.6
ASReml-R	1	0.6
Bowtie2	1	0.6
Cervus	1	0.6
Circuitscape	1	0.6
Cytoscape	1	0.6
Digitize It 2010	1	0.6
Ecopath	1	0.6
ED2 (FORTRAN)	1	0.6
Excel	1	0.6
FigTree	1	0.6
GenClone	1	0.6
GrabIt! XP	1	0.6
GRASS GIS	1	0.6
Image Pro Plus	1	0.6
JAGS	1	0.6

Name of software package	N	%
LocARNA	1	0.6
MEGA 4	1	0.6
Mesquite	1	0.6
Modeltest	1	0.6
MrBayes	1	0.6
OpenBUGS	1	0.6
OriginPro	1	0.6
Perl	1	0.6
Photoshop	1	0.6
phyloMeta	1	0.6
PRIMER	1	0.6
QGIS	1	0.6
SigmaPlot	1	0.6
Techdig	1	0.6
xyscan	1	0.6

In total, there were 398 mentions of R and R packages across the articles: 141 mentions of the R software environment, and 257 mentions of specific R packages. Figure S8 shows the distribution of the number of packages mentioned by each R-using article. As the figure shows, it was most common for R-using articles to mention only one or two packages (68%); only 6% of R-using articles mentioned more than three R packages.

Table S8 lists all R packages mentioned in the 141 meta-analysis articles that mentioned using R. The table includes the location of each R package (whether CRAN, Bioconductor, a base R package, or from another source). Note: At the time of checking (2nd August 2022), four packages (*empiricalFDR.DESeq2*, *foodweb*, *MAc*, and *VIF*) have been removed from CRAN[7]. The vast majority (74, or 92%) of the mentioned R packages were from the Comprehensive R Archive Network (CRAN), with 3 (4%) from the Bioconductor project and 2 from other websites. One article mentioned the package *stats*, which is part of the "base" set of R packages that are an integral part of the R software.

[7] Package *empiricalFDR.DESeq2* was archived 13th June 2022 (`https://cran.r-project.org/package=empiricalFDR.DESeq2`); package *foodweb* was archived 21st June 2022 (`https://cran.r-project.org/package=foodweb`); package *MAc* was archived 4th March 2022 (`https://cran.r-project.org/package=MAc`); package *VIF* was archived 9th May 2022 (`https://cran.r-project.org/package=VIF`).

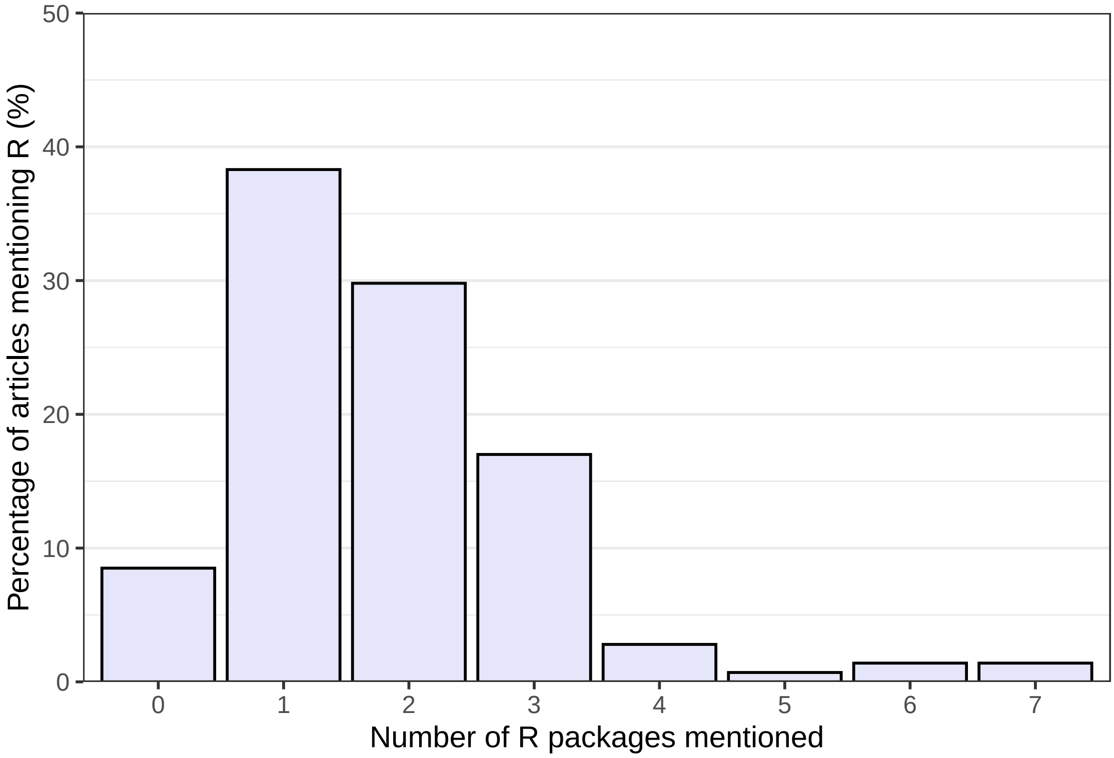

Figure S8: Distribution of the number of different R packages mentioned in each article which mentioned using R.

Table S8: All R packages mentioned in the sample of 141 meta-analysis articles which mentioned using R.

Name of R package	Package source	N	%
metafor	CRAN	75	53.2
MCMCglmm	CRAN	26	18.4
lme4	CRAN	20	14.2
ape	CRAN	13	9.2
MuMIn	CRAN	8	5.7
vegan	CRAN	7	5.0
nlme	CRAN	6	4.3
ggplot2	CRAN	5	3.5
phytools	CRAN	5	3.5
compute.es	CRAN	4	2.8
glmulti	CRAN	4	2.8
multcomp	CRAN	3	2.1
raster	CRAN	3	2.1
ade4	CRAN	2	1.4

Name of R package	Package source	N	%
boot	CRAN	2	1.4
lmerTest	CRAN	2	1.4
meta	CRAN	2	1.4
mgcv	CRAN	2	1.4
mice	CRAN	2	1.4
party	CRAN	2	1.4
picante	CRAN	2	1.4
randomForest	CRAN	2	1.4
rjags	CRAN	2	1.4
rmeta	CRAN	2	1.4
A3	CRAN	1	0.7
abc	CRAN	1	0.7
adegenet	CRAN	1	0.7
AICcmodavg	CRAN	1	0.7
arrayQualityMetrics	BioConductor	1	0.7
betareg	CRAN	1	0.7
caper	CRAN	1	0.7
coda	CRAN	1	0.7
coin	CRAN	1	0.7
DESeq2	BioConductor	1	0.7
dismo	CRAN	1	0.7
ecodist	CRAN	1	0.7
effects	CRAN	1	0.7
empiricalFDR.DESeq2	CRAN	1	0.7
foodweb	CRAN	1	0.7
gbm	CRAN	1	0.7
GENHET	other	1	0.7
Hmisc	CRAN	1	0.7
ICC	CRAN	1	0.7
igraph	CRAN	1	0.7

Name of R package	Package source	N	%
inext	CRAN	1	0.7
Kendall	CRAN	1	0.7
KOGMWU	CRAN	1	0.7
languageR	CRAN	1	0.7
leaps	CRAN	1	0.7
lmodel2	CRAN	1	0.7
lsmeans	CRAN	1	0.7
MAc	CRAN	1	0.7
maps	CRAN	1	0.7
maptools	CRAN	1	0.7
MASS	CRAN	1	0.7
merTools	CRAN	1	0.7
metahdep	BioConductor	1	0.7
MODISTools	CRAN	1	0.7
pez	CRAN	1	0.7
pheatmap	CRAN	1	0.7
plotmcmc	CRAN	1	0.7
plyr	CRAN	1	0.7
PVR	CRAN	1	0.7
R2WinBUGS	CRAN	1	0.7
rfPermute	CRAN	1	0.7
rgdal	CRAN	1	0.7
RInSp	CRAN	1	0.7
rms	CRAN	1	0.7
rotl	CRAN	1	0.7
rstan	CRAN	1	0.7
rvest	CRAN	1	0.7
segmented	CRAN	1	0.7
shape	CRAN	1	0.7
smatr	CRAN	1	0.7

Name of R package	Package source	N	%
STANDARICH	other	1	0.7
stats	base	1	0.7
vif	CRAN	1	0.7
visreg	CRAN	1	0.7
weights	CRAN	1	0.7
zoo	CRAN	1	0.7

Table S9 shows all R versions mentioned in the articles, as they originally appeared in the articles. This includes one article where the authors mention using two different versions of R for their study (v2.14.1 and v3.0.0), a study which included the R version twice, first in the body of the text and second as part of the citation in the references section, but where the versions differed (v3.1.0 and v3.0.1, which might be due to a typing error), and six articles where the version information provided was not complete (v2.12, v2.13, v2.14, v2.15, v3.1, v3.2). In the case of the six incomplete R version statements, it is possible that the authors were intending to refer to the "0" versions, i.e., 2.12.0, 2.13.0, etc.

R version	N	%
2.12	1	0.7
2.13	1	0.7
2.14	1	0.7
2.14.1	4	2.8
2.15	1	0.7
2.15.2	3	2.1
3.0.0/2.14.1	1	0.7
3.0.1	8	5.7
3.0.2	14	9.9
3.0.3	3	2.1
3.1	2	1.4
3.1.0	2	1.4
3.1.0/3.0.1	1	0.7
3.1.1	4	2.8
3.1.2	12	8.5
3.1.3	3	2.1
3.2	1	0.7
3.2.0	1	0.7
3.2.1	6	4.3
3.2.2	6	4.3
3.2.3	6	4.3
3.2.4	1	0.7
3.3.0	2	1.4
3.3.1	1	0.7
3.3.2	1	0.7
3.4.0	1	0.7
3.4.1	1	0.7
(No version mentioned)	53	37.6

Table S9: All R versions as originally mentioned in the sample of 141 meta-analysis articles which mentioned using R.

Variable	Value
ID	MA092
Study	Xu et al. (2016)
Result source	in text and from Table 1 (pp.84-85)
Result type	Regression model results for all data
Regression result	$\text{TLP} = -4.67 + 0.725 \times \log(\text{SLA}) - 0.937 \times \log(\text{WD})$
N	68
R^2_{adj}	0.32 (p-value < 0.001)
RMSE	0.55

Table S10: Details of the target result for article MA092, Xu et al. (2016). For context, TLP – turgor loss point, SLA – specific leaf area, WD – wood density, RMSE – root mean square error.

Variable	Value
ID	MA094
Study	Turney and Buddle (2016)
Result source	in text (p.1227)
Result type	Ordination analysis result
N	n.s.
R^2	0.494 ($p < 0.0001$)

Table S11: Details of the target result for article MA094, Turney and Buddle (2016). n.s. – not stated.

Variable	Value
ID	MA129
Study	Crouzeilles and Curran (2016)
Result source	Table 1 (A) (p.444)
Result type	Comparison of models by AICc
Result values	See Table S13

Table S12: Summary of the target result for article MA129, Crouzeilles and Curran (2016).

Buffer	Δ_i	w_i	R^2
Null	0.00	0.20	
50	0.96	0.12	
25	0.98	0.12	
75	1.17	0.11	
200	1.34	0.10	
150	1.56	0.09	
10	1.56	0.09	
100	1.61	0.09	
5	1.70	0.08	

Table S13: Details of the target result for article MA129, Crouzeilles and Curran (2016). The table headings and values are taken directly from Table 1 (A), p.444. Note that blank/missing values in the R^2 column are as per the original table. Here, Buffer is radius in km, Δ_i is AICc_i − minimum AICc (where AICc is the corrected Akaike information criterion), w_i is Akaike weight, R^2 is coefficient of determination, omitted in this table.

Variable	Value
ID	MA212
Study	Valls et al. (2015)
Result source	Table 2 (p.38)
Result type	Counts of matches
Result values	See Table S15

Table S14: Summary of the target result for article MA212, Valls et al. (2015).

KS index	Match impact	Match biomass	No match	Overall match
KS_1	91	10	0	match impact
KS_2	5	81	15	match biomass
KS_3	50	28	23	
KS_4	25	54	22	match biomass
KS_5	86	12	3	match impact
KS_6	0	94	7	match biomass
KS_7	32	35	34	
KS_8	11	70	20	match biomass
KS_9	91	10	0	match impact
KS_{10}	25	54	22	match biomass
KS_{11}	71	20	10	match impact
KS_{12}	46	39	16	

Table S15: Details of the target result for article MA212, Valls et al. (2015). The table headings and values are taken directly from Table 2, p.38. Note that blank/missing values in rows 3, 7, and 12 of column “Overall match” are as per the original table.

S9 REPRODUCIBILITY REPORTS

Reproducibility report design

We decided to record all the steps of each reproduction attempt in a document integrating the running of analysis code with explanatory prose to contextualise the attempt and its outcome. This an attempt to follow the literate programming approach (Knuth, 1984), which emphasises that computer programs ought to be human-readable and understandable. It's been recognised that this integration of analysis code and word processing facilitates reproducibility (Buckheit and Donoho, 1995; Claerbout and Karrenbach, 1992), especially when the document is packaged with the data files required for the analysis into a compendium (Gentleman and Temple Lang, 2007). As will be described in section 3 of the results, nearly all code that was shared was code for the R language (R Core Team, 2022). We mention this here because this fact determined the specifics of our technical approach to constructing the reproducibility reports.

We wrote a reproducibility report template using RMarkdown, a format for reproducible documents in the R language. An RMarkdown file can be compiled to produce a formatted, human-readable output document (such as an HTML or PDF document), which reports the results of running all included R code. The R source code in the RMarkdown document is re-run each time the document is compiled. We structured the template similarly to the RMarkdown reproducibility reports used in Hardwicke et al. (2021) to reproduce results from articles published in *Psychological Science*. Each report was structured as follows:

- A reference to the article and numerical details of the target result to be reproduced;
- Details of the shared data and code files;
- As assessment of the applicability of the shared data and code files;
- Set up of the R environment as required for the analyses;
- Importing and cleaning of data;
- Running the analysis code to reproduce the target result;
- Comparison of the original and reproduced target result value(s);
- A summary of information about the R computational environment used.

Within the RMarkdown source file, each report section consists of a combination of text marked up for appropriate formatting and "chunks" of R code which, when executed, perform in order the relevant tasks for the analysis (e.g., importing data from a file).

We set up each reproducibility report to run within its own Docker container. A container is a structured package of software designed to run a particular application in a virtual computing environment. The advantage of this approach is that applications can run on different computers without users needing to deal with software or system dependencies or settings. Docker is a tool for creating and running containers (Boettiger, 2015; Nüst et al., 2020). In particular, Docker allows users to build upon existing containers in an easy way. We created a container for each reproducibility report by starting with a pre-built container running R maintained by the Rocker project (Boettiger and Eddelbuettel, 2017). The Rocker container already included all elements required to run an R session in an isolated computational environment. On top of this pre-built "layer" we built containers which installed all additional R packages required for the analyses in the reproducibility reports, including custom functions written by us to facilitate comparison of the original and reproduced values. We controlled the versions of both R and all R packages: the Rocker project maintains multiple containers with different versions of R; we selected version 3.5.0. We installed R packages from a snapshot of the Comprehensive R Archive Network (CRAN) frozen at 2 July 2018, to ensure compatibility with R 3.5.0[8] The final layer of the container for each reproducibility report incorporated the specific data and code files required for data analysis. The result of this work was a small, self-contained application with everything required to compile the reproducibility report for each of the articles with shared data and code. This is a variation on the "research compendium" (Marwick et al., 2018): a research compendium is usually envisioned as being created by the original authors of a research project, to facilitate the reproducibility of their own results, rather than being created by a third party after the fact.

Running code

The core of each reproducibility report was the section which conducted the data analysis and calculated the target result. Because each reproducibility report is fundamentally an assessment of the shared data and code, we envisioned that each report would by default only execute lines of code taken directly from the shared code file(s) except where unavoidable. Importing data files was the principle situation where we anticipated we would need to modify lines of code and/or write new code.[9] In order to differentiate original lines of code from additional lines of code written by us, we wrote a function to specify which particular lines of an external code file to execute. This way, the original shared code could be run by a call to a function, rather than needing to be manually inserted into the source of the RMarkdown report. All additional, custom

[8]The date 2 July 2018 is the last day before the release of the succeeding version of R. We used the Microsoft mirror of CRAN: https://cran.microsoft.com/snapshot/2018-07-02/.

[9]We anticipated that most if not all shared code concerning operations involving external files would require modification. This was due to the fact that at the very least, file paths to data files, etc. would need to be changed to match the file system structure set up within each Docker container.

code would be written directly into the RMarkdown source file. Running individual lines of code from the original files in this way also had the advantage that only the code that was required to calculate the target result could be run, rather than the entire code file. For analyses that involved random number generation, we set an arbitrary random seed so that the specific set of numbers calculated would be reproduced over successive compilations of the report.

Table S16: The original and reproduced values of all target results.

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA016	Xu et al. (2017)	correlation	Pearson's *r*	point est.	N	-0.83	-0.83	0.00	E
MA016	Xu et al. (2017)	correlation	Pearson's *r*	*p*-value	N	< 0.001	< 0.001		E
MA016	Xu et al. (2017)	correlation	Pearson's *r*	*N*	N	49	49	0.00	E
MA060	Winternitz et al. (2017)	mean	Fisher *z*-transformation	point est.	N	0.044	0.043	2.27	< 10%
MA060	Winternitz et al. (2017)	mean	Fisher *z*-transformation	HPDI lower	N	-0.174	-0.194	11.49	10%+
MA060	Winternitz et al. (2017)	mean	Fisher *z*-transformation	HPDI upper	N	0.289	0.268	7.27	< 10%
MA060	Winternitz et al. (2017)	mean	Fisher *z*-transformation	*N*	N	37	37	0.00	E
MA062	Grueber et al. (2018)	mean	Hedges' *d*	point est.	N	-0.205	-0.204	0.49	< 10%
MA062	Grueber et al. (2018)	mean	Hedges' *d*	CI lower	N	-0.444	-0.446	0.45	< 10%
MA062	Grueber et al. (2018)	mean	Hedges' *d*	CI upper	N	0.035	0.039	11.43	10%+
MA062	Grueber et al. (2018)	mean	Hedges' *d*	*N*	N	37	37	0.00	E
MA065	Noble et al. (2018)	mean	Hedges' *g*	point est.	N	-8.42	-8.87	5.34	< 10%
MA065	Noble et al. (2018)	mean	Hedges' *g*	CI lower	N	-10.73	-10.85	1.12	< 10%
MA065	Noble et al. (2018)	mean	Hedges' *g*	CI upper	N	-6.63	-6.68	0.75	< 10%
MA065	Noble et al. (2018)	mean	Hedges' *g*	*N*	N	703	703	0.00	E
MA067	Risely et al. (2017)	mean	Hedges' *g*	point est.	N	-0.21	-0.21	0.00	E

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA067	Risely et al. (2017)	mean	Hedges' *g*	SE	N	0.07	0.07	0.00	E
MA067	Risely et al. (2017)	mean	Hedges' *g*	*z*-score	N	-2.7	-2.8	3.70	< 10%
MA067	Risely et al. (2017)	mean	Hedges' *g*	*p*-value	N	0.006	0.005	16.67	10%+
MA067	Risely et al. (2017)	mean	Hedges' *g*	*N*	N	52	52	0.00	E
MA068	Ronget et al. (2017)	mean	odds ratio	point est.	N	1.82			F
MA068	Ronget et al. (2017)	mean	odds ratio	HPDI lower	N	1.37			F
MA068	Ronget et al. (2017)	mean	odds ratio	HPDI upper	N	2.41			F
MA068	Ronget et al. (2017)	mean	odds ratio	*N*	N	75			F
MA071	Sievers et al. (2017)	mean	response ratio	point est.	N	-0.26	-0.27	3.85	< 10%
MA071	Sievers et al. (2017)	mean	response ratio	CI lower	N	-1.02	-1.03	0.98	< 10%
MA071	Sievers et al. (2017)	mean	response ratio	CI upper	N	0.51	0.49	3.92	< 10%
MA071	Sievers et al. (2017)	mean	response ratio	*N*	N	50	50	0.00	E
MA074	Harts et al. (2016)	correlation	Pearson's *r*	point est.	N	0.183	0.185	1.09	< 10%
MA074	Harts et al. (2016)	correlation	Pearson's *r*	CI lower	N	0.089	0.089	0.00	E
MA074	Harts et al. (2016)	correlation	Pearson's *r*	CI upper	N	0.274	0.281	2.55	< 10%
MA074	Harts et al. (2016)	correlation	Pearson's *r*	*N*	N	43	43	0.00	E
MA081	Jaffé et al. (2016)	mean	slope parameter	point est.	N	1.30	1.30	0.00	E
MA081	Jaffé et al. (2016)	mean	slope parameter	CI lower	N	0.95			F
MA081	Jaffé et al. (2016)	mean	slope parameter	CI upper	N	1.66			F
MA081	Jaffé et al. (2016)	mean	slope parameter	*N*	N	1296	1296	0.00	E
MA091	Lemoine et al. (2016)	mean	Cohen's *d*	point est.	N	0.56	0.56	0.00	E
MA091	Lemoine et al. (2016)	mean	Cohen's *d*	CI lower	N	0.42	0.42	0.00	E

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA091	Lemoine et al. (2016)	mean	Cohen's *d*	CI upper	N	0.69	0.69	0.00	E
MA091	Lemoine et al. (2016)	mean	Cohen's *d*	N	N	65	65	0.00	E
MA092	Xu et al. (2016)	model output	n.a.	R^2_{adj}	N	0.32	0.33	3.13	< 10%
MA092	Xu et al. (2016)	model output	n.a.	RMSE	N	0.55	0.55	0.00	E
MA092	Xu et al. (2016)	model output	n.a.	intercept	N	-4.67	-4.18	10.49	10%+
MA092	Xu et al. (2016)	model output	n.a.	log(SLA) coeff.	N	0.725	0.730	0.69	< 10%
MA092	Xu et al. (2016)	model output	n.a.	log(WD) coeff.	N	-0.937	-0.980	4.59	< 10%
MA092	Xu et al. (2016)	model output	n.a.	N	N	68	68	0.00	E
MA094	Turney and Buddle (2016)	model output	n.a.	R^2	N	0.494			F
MA094	Turney and Buddle (2016)	model output	n.a.	p-value	N	< 0.0001			F
MA095	Gibert et al. (2016)	mean	Fisher z-transformation	point est.	N	0.76	0.76	0.00	E
MA095	Gibert et al. (2016)	mean	Fisher z-transformation	CI lower	N	0.61	0.61	0.00	E
MA095	Gibert et al. (2016)	mean	Fisher z-transformation	CI upper	N	0.91	0.91	0.00	E
MA095	Gibert et al. (2016)	mean	Fisher z-transformation	N	N	25	25	0.00	E
MA126	Anderson (2016)	mean	log odds ratio	point est.	N	-1.11	-1.11	0.00	E
MA126	Anderson (2016)	mean	log odds ratio	SE	N	0.49	0.49	0.00	E

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA126	Anderson (2016)	mean	log odds ratio	CI lower	N	-2.06	-2.06	0.00	E
MA126	Anderson (2016)	mean	log odds ratio	CI upper	N	-0.15	-0.15	0.00	E
MA126	Anderson (2016)	mean	log odds ratio	*z*-score	N	-2.28	-2.28	0.00	E
MA126	Anderson (2016)	mean	log odds ratio	*p*-value	N	0.023	0.023	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank1	n.a.	Δ_i	N	0.00	0.00		E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank1	n.a.	w_i	N	0.20	0.20	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank1	n.a.	buffer (km radius)	C	Null	Null		E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank2	n.a.	Δ_i	N	0.96	0.96	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank2	n.a.	w_i	N	0.12	0.12	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank2	n.a.	buffer (km radius)	C	50	50		E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank3	n.a.	Δ_i	N	0.98	0.98	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank3	n.a.	w_i	N	0.12	0.12	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank3	n.a.	buffer (km radius)	C	25	25		E

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA129	Crouzeilles and Curran (2016)	Table 1A, rank4	n.a.	Δ_i	N	1.17	1.17	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank4	n.a.	w_i	N	0.11	0.11	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank4	n.a.	buffer (km radius)	C	75	75		E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank5	n.a.	Δ_i	N	1.34	1.34	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank5	n.a.	w_i	N	0.10	0.10	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank5	n.a.	buffer (km radius)	C	200	200		E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank6	n.a.	Δ_i	N	1.56	1.56	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank6	n.a.	w_i	N	0.09	0.09	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank6	n.a.	buffer (km radius)	C	150	150		E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank7	n.a.	Δ_i	N	1.56	1.56	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank7	n.a.	w_i	N	0.09	0.09	0.00	E

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA129	Crouzeilles and Curran (2016)	Table 1A, rank7	n.a.	buffer (km radius)	C	10	10		E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank8	n.a.	Δ_i	N	1.61	1.61	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank8	n.a.	w_i	N	0.09	0.09	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank8	n.a.	buffer (km radius)	C	100	100		E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank9	n.a.	Δ_i	N	1.70	1.70	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank9	n.a.	w_i	N	0.08	0.08	0.00	E
MA129	Crouzeilles and Curran (2016)	Table 1A, rank9	n.a.	buffer (km radius)	C	5	5		E
MA145	Moore et al. (2016a)	mean	Fisher z-transformation	point est.	N	-0.08	-0.08	0.00	E
MA145	Moore et al. (2016a)	mean	Fisher z-transformation	HPDI lower	N	-0.22	-0.21	4.55	$< 10\%$
MA145	Moore et al. (2016a)	mean	Fisher z-transformation	HPDI upper	N	0.03	0.05	66.67	10%+
MA145	Moore et al. (2016a)	mean	Fisher z-transformation	N	N	118	118	0.00	E

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA145	Moore et al. (2016a)	mean	Fisher *z*-transformation	$N_{studies}$	N	38	38	0.00	E
MA145	Moore et al. (2016a)	mean	Fisher *z*-transformation	$N_{species}$	N	25	25	0.00	E
MA147	Holman (2016)	mean	percentage	point est.	N	0.13	0.13	0.00	E
MA147	Holman (2016)	mean	percentage	SE	N	0.03	0.03	0.00	E
MA147	Holman (2016)	mean	percentage	CI lower	N	0.074	0.074	0.00	E
MA147	Holman (2016)	mean	percentage	CI upper	N	0.19	0.19	0.00	E
MA147	Holman (2016)	mean	percentage	N	N	49	49	0.00	E
MA155	Strader et al. (2016)	correlation	Pearson's r	point est.	N	0.51	0.51	0.00	E
MA155	Strader et al. (2016)	correlation	Pearson's r	p-value	N	0.01	0.01	0.00	E
MA188	Senior et al. (2015)	mean	Log response ratio	point est.	N	-0.363	-0.363	0.00	E
MA188	Senior et al. (2015)	mean	Log response ratio	CI lower	N	-0.408	-0.408	0.00	E
MA188	Senior et al. (2015)	mean	Log response ratio	CI upper	N	-0.318	-0.318	0.00	E
MA188	Senior et al. (2015)	mean	Log response ratio	N	N	818	818	0.00	E
MA191	Voje (2015)	mean	allometric slope parameter	point est.	N	0.86	0.85	1.16	$< 10\%$
MA191	Voje (2015)	mean	allometric slope parameter	CI lower	N	0.77	0.77	0.00	E
MA191	Voje (2015)	mean	allometric slope parameter	CI upper	N	0.94	0.94	0.00	E

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA191	Voje (2015)	mean	allometric slope parameter	*N*	N	553	553	0.00	E
MA198	Paz-Vinas et al. (2015)	mean	Fisher *z*-transformation	point est.	N	-0.41	-0.42	2.44	< 10%
MA198	Paz-Vinas et al. (2015)	mean	Fisher *z*-transformation	CI lower	N	-0.55	-0.55	0.00	E
MA198	Paz-Vinas et al. (2015)	mean	Fisher *z*-transformation	CI upper	N	-0.27	-0.28	3.70	< 10%
MA198	Paz-Vinas et al. (2015)	mean	Fisher *z*-transformation	*N*	N	79	80	1.27	< 10%
MA202	Mehrabi and Tuck (2015)	mean	Hedges' *d*	point est.	N	-0.330	-0.340	3.03	< 10%
MA202	Mehrabi and Tuck (2015)	mean	Hedges' *d*	CI lower	N	-0.503	-0.521	3.58	< 10%
MA202	Mehrabi and Tuck (2015)	mean	Hedges' *d*	CI upper	N	-0.156	-0.159	1.92	< 10%
MA202	Mehrabi and Tuck (2015)	mean	Hedges' *d*	*N*	N	329	329	0.00	E
MA211	Yuan and Chen (2015)	mean	log response ratio	point est.	N	0.24			F
MA211	Yuan and Chen (2015)	mean	log response ratio	CI lower	N	0.23			F

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA211	Yuan and Chen (2015)	mean	log response ratio	CI upper	N	0.25			F
MA211	Yuan and Chen (2015)	mean	log response ratio	*N*	N	3298			F
MA212	Valls et al. (2015)	Table 2, Match biomass	n.a.	KS1	N	10	10	0.00	E
MA212	Valls et al. (2015)	Table 2, Match biomass	n.a.	KS2	N	81	81	0.00	E
MA212	Valls et al. (2015)	Table 2, Match biomass	n.a.	KS3	N	28	28	0.00	E
MA212	Valls et al. (2015)	Table 2, Match biomass	n.a.	KS4	N	54	54	0.00	E
MA212	Valls et al. (2015)	Table 2, Match biomass	n.a.	KS5	N	12	12	0.00	E
MA212	Valls et al. (2015)	Table 2, Match biomass	n.a.	KS6	N	94	94	0.00	E
MA212	Valls et al. (2015)	Table 2, Match biomass	n.a.	KS7	N	35	35	0.00	E
MA212	Valls et al. (2015)	Table 2, Match biomass	n.a.	KS8	N	70	70	0.00	E
MA212	Valls et al. (2015)	Table 2, Match biomass	n.a.	KS9	N	10	10	0.00	E

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA212	Valls et al. (2015)	Table 2, Match biomass	n.a.	KS10	N	54	54	0.00	E
MA212	Valls et al. (2015)	Table 2, Match biomass	n.a.	KS11	N	20	20	0.00	E
MA212	Valls et al. (2015)	Table 2, Match biomass	n.a.	KS12	N	39	39	0.00	E
MA212	Valls et al. (2015)	Table 2, Match impact	n.a.	KS1	N	91	91	0.00	E
MA212	Valls et al. (2015)	Table 2, Match impact	n.a.	KS2	N	5	5	0.00	E
MA212	Valls et al. (2015)	Table 2, Match impact	n.a.	KS3	N	50	51	2.00	< 10%
MA212	Valls et al. (2015)	Table 2, Match impact	n.a.	KS4	N	25	25	0.00	E
MA212	Valls et al. (2015)	Table 2, Match impact	n.a.	KS5	N	86	87	1.16	< 10%
MA212	Valls et al. (2015)	Table 2, Match impact	n.a.	KS6	N	0	0		E
MA212	Valls et al. (2015)	Table 2, Match impact	n.a.	KS7	N	32	33	3.12	< 10%
MA212	Valls et al. (2015)	Table 2, Match impact	n.a.	KS8	N	11	11	0.00	E

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA212	Valls et al. (2015)	Table 2, Match impact	n.a.	KS9	N	91	91	0.00	E
MA212	Valls et al. (2015)	Table 2, Match impact	n.a.	KS10	N	25	25	0.00	E
MA212	Valls et al. (2015)	Table 2, Match impact	n.a.	KS11	N	71	72	1.41	< 10%
MA212	Valls et al. (2015)	Table 2, Match impact	n.a.	KS12	N	46	47	2.17	< 10%
MA212	Valls et al. (2015)	Table 2, No match	n.a.	KS1	N	0	0		E
MA212	Valls et al. (2015)	Table 2, No match	n.a.	KS2	N	15	15	0.00	E
MA212	Valls et al. (2015)	Table 2, No match	n.a.	KS3	N	23	22	4.35	< 10%
MA212	Valls et al. (2015)	Table 2, No match	n.a.	KS4	N	22	22	0.00	E
MA212	Valls et al. (2015)	Table 2, No match	n.a.	KS5	N	3	2	33.33	10%+
MA212	Valls et al. (2015)	Table 2, No match	n.a.	KS6	N	7	7	0.00	E
MA212	Valls et al. (2015)	Table 2, No match	n.a.	KS7	N	34	33	2.94	< 10%
MA212	Valls et al. (2015)	Table 2, No match	n.a.	KS8	N	20	20	0.00	E
MA212	Valls et al. (2015)	Table 2, No match	n.a.	KS9	N	0	0		E
MA212	Valls et al. (2015)	Table 2, No match	n.a.	KS10	N	22	22	0.00	E
MA212	Valls et al. (2015)	Table 2, No match	n.a.	KS11	N	10	9	10.00	10%+
MA212	Valls et al. (2015)	Table 2, No match	n.a.	KS12	N	16	15	6.25	< 10%
MA212	Valls et al. (2015)	Table 2, Overall match	n.a.	KS1	C	match impact	match impact		E

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA212	Valls et al. (2015)	Table 2, Overall match	n.a.	KS2	C	match biomass	match biomass		E
MA212	Valls et al. (2015)	Table 2, Overall match	n.a.	KS3	C	(none)	match impact		NC
MA212	Valls et al. (2015)	Table 2, Overall match	n.a.	KS4	C	match biomass	match biomass		E
MA212	Valls et al. (2015)	Table 2, Overall match	n.a.	KS5	C	match impact	match impact		E
MA212	Valls et al. (2015)	Table 2, Overall match	n.a.	KS6	C	match biomass	match biomass		E
MA212	Valls et al. (2015)	Table 2, Overall match	n.a.	KS7	C	(none)	(none)		E
MA212	Valls et al. (2015)	Table 2, Overall match	n.a.	KS8	C	match biomass	match biomass		E
MA212	Valls et al. (2015)	Table 2, Overall match	n.a.	KS9	C	match impact	match impact		E
MA212	Valls et al. (2015)	Table 2, Overall match	n.a.	KS10	C	match biomass	match biomass		E
MA212	Valls et al. (2015)	Table 2, Overall match	n.a.	KS11	C	match impact	match impact		E
MA212	Valls et al. (2015)	Table 2, Overall match	n.a.	KS12	C	(none)	(none)		E

ID	Study	Result type	Effect size type	Target result	Value type	Original	Reproduced	Percent error (%)	Status
MA213	Colautti and Lau (2015)	mean	difference in means	point est.	N	-0.07	-0.07	0.00	E
MA213	Colautti and Lau (2015)	mean	difference in means	*p*-value	N	0.362	0.362	0.00	E
MA213	Colautti and Lau (2015)	mean	difference in means	*N*	N	654	654	0.00	E
MA229	Gamfeldt et al. (2015)	mean	log response ratio	point est.	N	0.40	0.39	2.50	< 10%
MA229	Gamfeldt et al. (2015)	mean	log response ratio	CI lower	N	0.24	0.26	8.33	< 10%
MA229	Gamfeldt et al. (2015)	mean	log response ratio	CI upper	N	0.53	0.53	0.00	E
MA229	Gamfeldt et al. (2015)	mean	log response ratio	*N*	N	57	57	0.00	E

Examining dependency between reproduced values within articles

Table 5 lists 19 articles where (i) the result type is a summary effect and (ii) the code is relevant. For these 19 articles, the set of target result values are broadly similar in type: there is a point estimate, a sample size, and some kind of measure of uncertainty (e.g., the upper and lower bounds of a confidence interval). To gauge the level of dependency between the reproductions of these different types of values within articles, Table S17 breaks down the results for each article by target value type, specifying how closely the target result value was reproduced (using the same categories reported in Table 6). For this summary, measures of uncertainty other than confidence interval bounds (e.g., standard errors) were ignored.

ID	N	Point est.	CI lower	CI upper
MA091	Exact	Exact	Exact	Exact
MA095	Exact	Exact	Exact	Exact
MA147	Exact	Exact	Exact	Exact
MA188	Exact	Exact	Exact	Exact
MA145	Exact	Exact	Within 10%	At Least 10%
MA081	Exact	Exact	Failure	Failure
MA067	Exact	Exact	n.a.	n.a.
MA213	Exact	Exact	n.a.	n.a.
MA191	Exact	Within 10%	Exact	Exact
MA074	Exact	Within 10%	Exact	Within 10%
MA229	Exact	Within 10%	Within 10%	Exact
MA065	Exact	Within 10%	Within 10%	Within 10%
MA071	Exact	Within 10%	Within 10%	Within 10%
MA202	Exact	Within 10%	Within 10%	Within 10%
MA062	Exact	Within 10%	Within 10%	At Least 10%
MA060	Exact	Within 10%	At Least 10%	Within 10%
MA198	Within 10%	Within 10%	Exact	Within 10%
MA211	Failure	Failure	Failure	Failure
MA126	n.a.	Exact	Exact	Exact

Table S17: A breakdown of how closely target result values were reproduced for each article with relevant code and a summary effect result type. The target result value types are sample size N, point estimate, and confidence interval bounds (CI lower and CI upper). Values of "n.a." indicate that that particular target result value type was not reported for that article.

Table S17 considers how closely the sample size, point estimate, lower confidence interval bound, and upper confidence interval bound could be reproduced for each article. The closeness of the reproduced values were considered progressively, from left to right. The table shows that most values of sample size could be reproduced exactly, but the closeness of the reproduced values dropped off considerably after that for the point estimate, etc. There are two identifiable clusters: a cluster of four articles (MA091, MA095, MA147, MA188) where all target values could be reproduced exactly, and a cluster of three articles (MA065, MA071, MA202) where the sample size was reproduced exactly, and the remaining values were within 10%. This clustering may indicate that there is some dependency between values from the same article regarding how closely they will be reproduced. However, the sample is small and the categories of reproduction closeness are relatively coarse.

S10 REPRODUCING TARGET RESULTS WHEN CODE NOT RELEVANT

Table S18 details the circumstances of the six cases where shared code was judged not relevant to reproducing the target result.

ID	Study	Code language	Description
MA016	Xu et al. (2017)	Python	Not relevant. The code shared is for simulations of leaf longevity, reported separately from the meta-analysis.
MA068	Ronget et al. (2017)	R	Partially relevant. The code shared regards the extraction of effect sizes from primary studies used in the meta-analysis. The code does not conduct the meta-analysis itself.
MA092	Xu et al. (2016)	Fortran	Not relevant. The code shared is the source code for a modified version of the Ecosystem Demography Biosphere Model, ED2 (Medvigy et al., 2009). Simulations using this model were reported separately from the meta-analysis.
MA094	Turney and Buddle (2016)	R	Partially relevant. The code shared is for generating null food web models. Although necessary, the code is not sufficient to reproduce the chosen result. Further, there was a "missing" code file: in the Oikos online appendix, one listed code file was actually missing (`hierarchy_measure.R`), while the other listed code file (`null_models.R`) was duplicated, resulting in two code files in the appendix with the same contents.
MA155	Strader et al. (2016)	R	Not relevant. The code shared is for conducting Gene Ontology analyses, and for producing article Figure 1D. These are separate results from the meta-analysis.
MA212	Valls et al. (2015)	R	Partially relevant. The code shared runs Spearman rank correlation tests, relevant to meta-analysis results presented in Table 3 of article. The code is not relevant to the selected meta-analysis result.

Table S18: The articles with shared code which was either not relevant or only partially relevant to reproducing the chosen meta-analysis results.

In the cases of MA016, MA092, and MA155, the shared code had nothing to do with the reported meta-analysis results. In the case of MA212, the shared code was partially relevant, but was practically unusable for the purposes of reproducing the specific results in the article. (Specifically, the shared code for MA212, written to calculate Spearman's rank correlation coefficient for multiple sets of data and summarise the corresponding p-values, seemed to be an extract from a larger code base; the code assumed a specific data structure that was not defined anywhere in the shared materials, nor did the data structure implied by the code correspond to any of the shared data files. Lacking contextual information on the setup required for the code to work, we decided that the code as provided for MA212 was unusable.) For these four cases we attempted to reproduce the originally selected target results detailed in Tables 4 and S10 by writing entirely new R code.

There were 59 target result values across MA016, MA092, MA155, and MA212. This set of target result values included 12 non-numeric values: these were entries from the table in article MA212, see Table S15. Percent error was not applicable to these non-numeric values, and so the reproduced values were assessed as being either exact text string matches with the original or non-matches. The details of the individual reproduction attempts for all these values are reported in Table S16.

In the cases of MA068 and MA094, the code was relevant to other parts of the meta-analysis described in the articles. We selected alternative target results from these articles that were directly relevant to the shared code. For MA068, the shared code performed simulations of logistic regression slopes and standard errors; these simulations were performed to supplement under-reported results from two primary studies included in the meta-analysis. The target results were the values of the simulations as reported in the article. For MA094, the shared code simulated species richness in food webs using different food web models; the simulation results were compared with the results from a sample of published food webs in a figure. The target results were the widths of bars in that figure, which represented the average proportion of species richness at different trophic levels for the published and simulated food webs. There were 3 target result values for MA068, and 21 target result values for MA094. The details of the alternative target results are reported in Tables S19-S21, and the results of comparing the reproduced values with the original values of these target results are in Table S22.

Variable	Value
ID	MA068
Study	Ronget et al. (2017)
Result source	Table 1 (pp.7-8)
Result type	Simulated slope parameters and standard errors to supplement incompletely reported primary study results
Standard error 1	0.001
Mean slope parameter 2	-0.001
Standard error 2	0.113

Table S19: Detail of the alternative target results selected for article MA068, Ronget et al. (2017). These alternative target results were selected due to being relevant to the shared code. Standard error 1 is simulated to supplement a result from Rödel et al. (2004), mean slope parameter 2 and standard error 2 are simulated to supplement a result from Barber-Meyer et al. (2008).

We used the shared code for these two articles to successfully calculate values for all 24 alternative target values. This perfect success rate is perhaps to be expected, since the alternative target results were specifically selected on the basis of being relevant to the shared code. Seven values out of the 24 (29%) were reproduced exactly (to the same precision as reported), another seven reproduced values (29%) were within 10% of the

Variable	Value
ID	MA094
Study	Turney and Buddle (2016)
Result source	in text (p.1227)
Result type	Descriptive statistics of species richness (i.e., N_{species}) in a sample of published food webs
$N_{\text{food webs}}$	72
Mean	90.21
Standard deviation	31.27
Minimum	50
Maximum	209

Table S20: Detail of the first set of alternative target results selected for article MA094, Turney and Buddle (2016). These alternative target results were selected due to being relevant to the shared code.

original value, and the remaining ten (42%) reproduced values were 10% or more from the original value. All ten reproduced values with substantial percent errors (10% or more) compared to the original were target results from simulations, which use pseudo-random number generation, and neither R script set a random seed which would have facilitated the exact reproduction of the simulations. For one target result in MA068, the mean slope parameter for a logistic regression, the reproduced value was 0.001, compared with an original value of -0.001. This is the only case in this study of a reproduced target result not being in the same direction as the original target result value. However, by using different random seeds, repeated simulations of this target result could yield different results, which might more closely agree with the original value.

Variable	Value
ID	MA094
Study	Turney and Buddle (2016)
Result source	Figure 1 (p.1227)
Result type	Bar widths (in pixels) representing average proportions of species richness at different trophic levels for different food web types
Published food webs, top trophic level	215
Published food webs, intermediate trophic level	475
Published food webs, herbivore trophic level	430
Published food webs, basal trophic level	549
Random food webs, top trophic level	589
Random food webs, intermediate trophic level	521
Random food webs, herbivore trophic level	51
Random food webs, basal trophic level	108
Cascade food webs, top trophic level	79
Cascade food webs, intermediate trophic level	934
Cascade food webs, herbivore trophic level	158
Cascade food webs, basal trophic level	221
Niche food webs, top trophic level	441
Niche food webs, intermediate trophic level	408
Niche food webs, herbivore trophic level	102
Niche food webs, basal trophic level	385

Table S21: Detail of the second set of alternative target results selected for article MA094, Turney and Buddle (2016). These alternative target results were selected due to being relevant to the shared code.

Table S22: The original and reproduced values of all alternative target results for MA068 and MA094. All target result values are numeric.

ID	Study	Result type	Effect size type	Target result	Original	Reproduced	Percent error (%)	Status
MA068	Ronget et al. (2017)	logistic regression model (Rödel)	slope parameter	SE	0.001	0.001	0.00	E
MA068	Ronget et al. (2017)	logistic regression model (Barber-Meyer)	slope parameter	point est.	-0.001	0.001	200.00	10%+
MA068	Ronget et al. (2017)	logistic regression model (Barber-Meyer)	slope parameter	SE	0.113	0.113	0.00	E
MA094	Turney and Buddle (2016)	mean	species richness	point est.	90.21	90.21	0.00	E
MA094	Turney and Buddle (2016)	mean	species richness	SD	31.27	31.27	0.00	E
MA094	Turney and Buddle (2016)	mean	species richness	minimum	50	50	0.00	E
MA094	Turney and Buddle (2016)	mean	species richness	maximum	209	209	0.00	E
MA094	Turney and Buddle (2016)	mean	species richness	N	72	72	0.00	E
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	published food webs, top trophic level	215	212	1.40	$<$ 10%
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	published food webs, intermediate trophic level	475	476	0.21	$<$ 10%

ID	Study	Result type	Effect size type	Target result	Original	Reproduced	Percent error (%)	Status
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	published food webs, herbivore trophic level	430	434	0.93	< 10%
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	published food webs, basal trophic level	549	550	0.18	< 10%
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	random food webs, top trophic level	589	96	83.70	10%+
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	random food webs, intermediate trophic level	521	1078	106.91	10%+
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	random food webs, herbivore trophic level	51	27	47.06	10%+
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	random food webs, basal trophic level	108	64	40.74	10%+
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	cascade food webs, top trophic level	79	252	218.99	10%+
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	cascade food webs, intermediate trophic level	934	759	18.74	10%+
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	cascade food webs, herbivore trophic level	158	160	1.27	< 10%
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	cascade food webs, basal trophic level	221	227	2.71	< 10%
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	niche food webs, top trophic level	441	359	18.59	10%+

ID	Study	Result type	Effect size type	Target result	Original	Reproduced	Percent error (%)	Status
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	niche food webs, intermediate trophic level	408	441	8.09	< 10%
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	niche food webs, herbivore trophic level	102	129	26.47	10%+
MA094	Turney and Buddle (2016)	average proportion of species present	pixel width	niche food webs, basal trophic level	385	439	14.03	10%+

S11 REVISITING THE DEFINITION OF REPRODUCIBILITY

In this section, we return to the definition of reproducibility provided in the introduction, "reproducibility is obtaining consistent results using the same input data; computational steps, methods, and code; and conditions of analysis" (National Academies of Sciences, Engineering, and Medicine, 2019, p.43) and consider each component of this definition in turn, in the context of the results of this study.

Consistent As is noted in the NAS report, there can be different standards for what is considered "consistent". In some scenarios, bitwise consistency may be required. In others, obtaining results in the same direction as the original might be considered good enough. The reproduced results in this study were compared to their original counterparts by looking at the percentage error. Looking at Tables 6 and 9, relaxing standards for consistency from exact matches to matches within 10% of the original boosted the percentage of target results considered consistent substantially, from 43% to 56% in Table 6, and from 75% to 93% in Table 9. In the context of meta-analysis, what might be considered sufficient consistency will likely depend on the purposes that the results are put to use, and the sensitivity of those purposes to variation in the inputs. Meta-analysis in particular is an interesting case because meta-analyses can be updated with additional primary studies, and is complicated by differences of judgment over which primary studies ought to be included and excluded, etc. Given this, there may be an expectation that meta-analytic summary effects are already subject to variation beyond formal statistical error. In this context, there may be a tolerance for a certain amount of inconsistency in any asserted summary effect, such that small discrepancies of up to 10% in value when reproduced are not fatal (albeit perhaps still worthy of rigorous checking).

Results In the context of reproducing a numerical result, "results" are those numbers printed in the published article. Ordinarily, we take them as they are presented. However, in this study, we have the example of a result reported in article MA062 (Grueber et al., 2018) which contains a typo (a missing minus sign). Here, the code and data produce the "correct" result, with a value less than zero. Here, interpretation and judgement is required: a reader can see that there is supposed to be a minus sign in front of the reported effect size, since that would then agree with the stated confidence interval. This example is particularly straightforward and obvious.

This is important to note because a lot of the challenge of evaluating computational reproducibility of results is in getting the data and code to "work"; understandably, that's where a lot of the focus is. But this perhaps takes for granted that the target value in the published article that is being reproduced is valid, and has not been corrupted during rounds of revision, copy editing, type setting, etc. (This is of course the chief motivation behind reproducible reports/documents, where analysis and text are contained within the one document, and so issues such as transcription error, etc. are mitigated.)

Another issue is the coverage/completeness of results. Do all "results" (e.g., all numerical values reported in text, all tables and figures) in an article need to be reproducible? For tractability, this study selected a single target result for reproduction across a number of articles, with the goal of selecting the first mentioned summary effect where possible. Even though this "bare minimum" attempt for each article covered only a tiny proportion of all results reported, the successes and failures were still informative.

Same input data Data sharing policies and advocacy perhaps may take for granted that the data file(s) that get shared are the same as the data file(s) that were actually used for the calculations reported in the article. But, this may not necessarily be the case: (i) Authors may "clean up" their data files in preparation for them to be shared. This may involve recoding of data values, or renaming of variables to make them more explicable to outside readers. This could introduce changes to how the data needs to be pre-processed or recoded for analysis. (ii) Some data files may be updated or edited over time, especially if used in projects which span more than a single article. It may become a non-trivial task to identify a single version of the data file(s) that applies to all results reported in an article.

In one meta-analysis (Yuan and Chen, 2015), the data file shared was not the data file used with the provided code, and according to the content of the article itself, could not have been the data file used to calculate all results reported. This was due to a missing variable in the data set.

There is one meta-analysis where the authors explicitly provide two different versions of their data: the first which is the one actually used in the meta-analysis (and so is the one to be used to "reproduce" the results in the article), and the second which is a corrected version of the first, and which the authors recommend be used for further analysis. This example is particularly striking because of the transparency of the authors and the delineation they provide between "original" results and what might be called "correct" results.

The point of this is to say that when we say "the same data", we might not necessarily mean or intend to refer to "the specific original file(s) used by the authors in the calculation of the results". What we mean is a set of data that has the same substantive content as the original data, regardless of whether that version of the data was used by the authors to calculate the results or not.

Same computational steps, methods, and code This has multiple components: first, the sharing of code files has the same issues as the sharing of data files, as detailed above. Code files may be "cleaned up" for public release, or comments may be added, or code might be passed through a tool to format the code for easier reading. The point of this is to say that when we say "the same code", we may not necessarily mean the "specific original file(s) used by the authors".

The "same computational steps" also requires some nuance: for example, it's taken as given in studies evaluating reproducibility that things like the file system paths of input files don't really count as meaningful barriers to computational reproducibility. It doesn't seem "fair" to declare a result as unable to be reproduced purely because the code as written assumes a different file folder structure than exists on the reproducer's computer system.

The above example of file paths seems unambiguous enough (and is very common), but "alterations to the code as supplied" exists on a spectrum: if we agree that altering the computational steps to enable files to be read is at the end of "insubstantial changes", at what point do changes to the code as supplied become substantial, and we agree that we are no longer taking the same computational steps?

Examples from this study include typos in code that once corrected produce matching results. Correcting the (perhaps obvious) typo is making an act of interpretation: we're intuiting what the original authors intended, even though it is not literally what they have written in code.

This particular example also feeds back to the "same code" issue: if an analysis script contains a typo/syntax error that does not produce the results reported in the paper, can it be "the same" code run by the authors? If it was, they would have obtained an error message instead of a result, and so could not have reported that result in the paper. This makes it clear that the shared code file is not literally the code that was run to obtain the original results.

Beneath all this, there is some notion that when we refer to computational steps, we are referring to the computational steps that "really matter" to the calculation of the result.

Same conditions of analysis Should we take this to mean the same computing and software environment? In the context of this study and its results, it seems that the conditions of analysis mostly concerns software packages and perhaps their versions—the fact that meta-analysis results were typically only reported to the third decimal place at most, as well as the observed success rate at the target result level indicates that information about computer hardware (e.g., architecture, processors) is wholly unnecessary, as is information about operating and file systems. This would not be universal across research disciplines, but it seems reasonable for meta-analysis.

As found in this study, study authors often reported the software tools they used for analysis, even when code was not shared. Not all mentions of software were accompanied by information about versions, but this study shows that a lack of version information was not fatal to reproduction attempts, although software version differences may be contributing to the discrepancies between original and reproduced values.

One condition of analysis that clearly stood out as an issue was the lack of specification of random seeds for procedures which involved pseudo-random number generation. Without random seeds, such procedures become an inescapable source of discrepancy between original and reproduced values. Specifying a random seed can nullify this problem, however.