Appendix S1: Survey of publication bias tests reported in ecology and evolution meta-analyses

## X.1 | Survey method

The main objective of the literature survey was to capture the types of publication bias methods recently used in the field of ecology and evolution. The survey reported here was conducted alongside a larger survey on reporting standards from the PRISMA-EcoEvo project (Preferred Reporting Items for Systematic reviews and Meta-Analyses in Ecology and Evolutionary Biology; full details and materials provided in {O’Dea, 2019 #28}). The survey was based on 102 meta-analysis papers published between 1 January 2010 and 25 March 2019. We aimed for the sample of 102 meta-analyses to be representative of recently published meta-analyses in ecology and evolutionary biology journals.

### Representative Sample

To select the representative sample of meta-analysis publications, we first searched the Scopus database for papers with (“meta-analy\*” OR “metaanaly\*” OR “meta-regression”) in the title, abstract, or keywords (where the asterisk allows for any ending to the word, such as “meta-analyses” or “meta-analysis”), restricted the date to papers published after 2009, and restricted the ISSN (International Standard Serial Number) to journals classified as ‘Ecology’ and/or ‘Evolutionary Biology’ by the 2017 rankings of the ISI InCites Journal Citation Reports. On 25 March 2019 this search returned 1,668 papers from 134 journals.

Second, the returned papers were categorised as being from journals listed as ‘Ecology’, ‘Evolution’, or ‘Both’, and we reduced the number of journals and papers. To reduce the number of journals we arranged journals in descending order of frequency (i.e. to indicate which journals published the most meta-analyses). After removing journals in more applied sub-fields (such as ecology economics), we retained the top 10 journals classified as ecology, the top 10 journals classified as evolutionary biology, and the top 11 journals classified as both ecology and evolutionary biology. The list of 31 retained journals is shown in Table S1. Next, we selected 297 studies to be screened for inclusion in the sample, by using the ‘sample’ function in *R* (v. 3.5.1; R Core Team, 2018) to randomly select up to 17 studies from the journals classified as ‘Evolutionary Biology’ (57 studies total) or ‘Both’ (150 studies total), and up to 9 studies from journals classified as ‘Ecology’ (90 studies total).

## Table S1

Journals screened in our search for a representative sample of meta-analyses published in ecology and evolutionary biology. ISI Classification is based on the 2017 ISI InCites Journal Citation Reports. The number of papers returned from the Scopus database search is described by ‘N hits’, while the number of studies selected for screening is described by ‘N screened’.

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| --- | --- | --- | --- |
| **ISI Classification** | **Full Journal Title** | **N hits** | **N screened** |
| Both | Proceedings of the Royal Society of London B: Biological Sciences | 47 | 17 |
| Both | Ecology and Evolution | 43 | 17 |
| Both | Molecular Ecology | 35 | 17 |
| Both | Journal of Evolutionary Biology | 32 | 17 |
| Both | Evolution | 25 | 17 |
| Both | American Naturalist | 20 | 17 |
| Both | Biology Letters | 17 | 17 |
| Both | Evolutionary Ecology | 14 | 14 |
| Both | Nature Ecology & Evolution | 7 | 7 |
| Both | Heredity | 5 | 5 |
| Both | Molecular Ecology Resources | 5 | 5 |
| Ecology | Global Change Biology | 135 | 9 |
| Ecology | Ecology Letters | 98 | 9 |
| Ecology | Oikos | 65 | 9 |
| Ecology | Global Ecology and Biogeography | 51 | 9 |
| Ecology | Biological Conservation | 49 | 9 |
| Ecology | Oecologia | 47 | 9 |
| Ecology | Conservation Biology | 43 | 9 |
| Ecology | Journal of Applied Ecology | 42 | 9 |
| Ecology | Journal of Ecology | 35 | 9 |
| Ecology | Marine Ecology Progress Series | 35 | 9 |
| Evolution | BMC Evolutionary Biology | 12 | 12 |
| Evolution | Evolutionary Applications | 10 | 10 |
| Evolution | Biological Journal of the Linnean Society | 9 | 9 |
| Evolution | Molecular Biology and Evolution | 7 | 7 |
| Evolution | Genome Biology and Evolution | 4 | 4 |
| Evolution | Molecular Phylogenetics and Evolution | 4 | 4 |
| Evolution | Evolutionary Bioinformatics | 3 | 3 |
| Evolution | Evolutionary Biology | 3 | 3 |
| Evolution | Journal of Heredity | 3 | 3 |
| Evolution | Systematic Biology | 2 | 2 |

### Inclusion criteria and screening methods

The sample of 102 meta-analysis papers met the following four inclusion criteria: (1) the study addressed a question in the fields of ecology and evolutionary biology; (2) claimed to present results from a meta-analysis; (3) performed a search for, and collected, data from the primary literature; (4) used a statistical model to analyse effect sizes that were collected from multiple studies. Paper screening was conducted in two stages. First, two authors (RO and ML) conducted parallel abstract screening. Conflicting decisions were discussed and resolved. Second, 64% of screened abstracts underwent parallel full-text screening by RO and ML, in consultation with SN.

### Assessing 102 meta-analysis papers

Papers were independently assessed by seven authors (RO, DN, JK, MJ, ML, RO, SN, and TP) as part of a larger, time-consuming survey. The one survey question pertaining to this project was: “*Which publication bias tests are reported in the paper? (Select all that apply)*”. There were 11 possible choices for respondents to select: (A) Funnel plots (including contour-enhanced funnel plots); (B) Normal quantile (QQ) plots (Wang & Bushman); (C) Correlation-based tests (e.g. Begg & Manzumdar rank correlation); (D) Regression-based tests (e.g. Egger regression and its variants); (E) File drawer numbers or fail-safe *N* (Rosenthal, Orwin or Rosenberg method); (F) Trim-and-fill tests; (G) P-curve, P-uniform or its variants; (H) Selection (method) models (e.g. Copas, Hedges or lyengar & Greenhouse model); (I) Time-lag bias tests (e.g., regression or correlation on the relationship between effect sizes and time or cumulative meta-analysis); (J) None reported and (K) ‘Other’ methods. According to Sutton ({, 2009 #17}) (see also {Vevea, 2019 #16}), Methods A-D are tests detecting publication bias, whereas Methods E-F are assessing the impact of publication bias.

## X.2 | Results

Among the 102 assessed papers, 17.8% did not report any tests of publication bias.

Most meta-analysis papers reported one or more tests of publication bias (17.8% of assessed papers did not include any assessment of publication bias). These results suggest tests of publication bias have become more common in recent year in ecology and evolutionary biology, as over half of older meta-analyses assessed by Nakagawa and Santos ({, 2012 #19}) and Koricheva and Gurevitch ({Koricheva, 2014 #18}) did not report any tests of publication bias (although our results are not directly comparable, due to different survey methods). Still, inferential tests of publication bias remain uncommon. By far the most popular test of publication bias were funnel plots (32.4%; Table S2), with all remaining methods represented by fewer than 15% of papers. All methods except ‘selection models’ were present in at least one paper (with ‘other’ being selected for a weighted histogram used by {Loydi, 2013 #70}; Table S2). The absence of selection model methods could be because these methods are comparatively technically challenging, or because ecologists and evolutionary biologists are not yet aware of the benefits of these methods.

## Table S2

Frequency with which publication bias tests were reported in the 102 meta-analysis publications, ranked in order of decreasing popularity. No tests were reported for 17.80% of papers.

|  |  |  |
| --- | --- | --- |
| **Publication Bias Test** | **Number of Papers Reporting Test** | **Percentage of Papers Reporting Test** |
| (A) Funnel plots | 69 | 32.40% |
| (E) Fail-safe N | 30 | 14.10% |
| (D) Regression-based methods | 25 | 11.70% |
| (C) Correlation-based methods | 20 | 9.40% |
| (F) Trim-and-fill tests | 16 | 7.50% |
| (I) Time-lag bias tests | 10 | 4.70% |
| (G) P-value-based methods | 3 | 1.40% |
| (B) Normal quantile (QQ) plots | 1 | 0.50% |
| (K) Other (weighted histogram) | 1 | 0.50% |
| (H) Selection models | 0 | 0.00% |