Research Synthesis Methods **WILEY**

The orchard plot: Cultivating a forest plot for use in ecology, evolution, and beyond

Shinichi Nakagawa[1] | **Malgorzata Lagisz**[1] | **Rose E. O'Dea**[1] | **Joanna Rutkowska**[2] | **Yefeng Yang**[1] | **Daniel W. A. Noble**[3] | **Alistair M. Senior**[4]

[1]Evolution & Ecology Research Centre, School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, New South Wales, Australia

[2]Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland

[3]Division of Ecology and Evolution, Research School of Biology, The Australian National University, Canberra, Australian Capital Territory, Australia

[4]Charles Perkins Centre, School of Life and Environmental Sciences, University of Sydney, Camperdown, New South Wales, Australia

Correspondence
Shinichi Nakagawa, Evolution & Ecology Research Centre and School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, New South Wales 2052, Australia.
Email: s.nakagawa@unsw.edu.au
Alistair M. Senior, Charles Perkins Centre and School of Life and Environmental Sciences, University of Sydney, Camperdown, New South Wales 2006, Australia.
Email: alistair.senior@sydney.edu.au

"Classic" forest plots show the effect sizes from individual studies and the aggregate effect from a meta-analysis. However, in ecology and evolution, meta-analyses routinely contain over 100 effect sizes, making the classic forest plot of limited use. We surveyed 102 meta-analyses in ecology and evolution, finding that only 11% use the classic forest plot. Instead, most used a "forest-like plot," showing point estimates (with 95% confidence intervals [CIs]) from a series of subgroups or categories in a meta-regression. We propose a modification of the forest-like plot, which we name the "orchard plot." Orchard plots, in addition to showing overall mean effects and CIs from meta-analyses/ regressions, also include 95% prediction intervals (PIs), and the individual effect sizes scaled by their precision. The PI allows the user and reader to see the range in which an effect size from a future study may be expected to fall. The PI, therefore, provides an intuitive interpretation of any heterogeneity in the data. Supplementing the PI, the inclusion of underlying effect sizes also allows the user to see any influential or outlying effect sizes. We showcase the orchard plot with example datasets from ecology and evolution, using the R package, *orchard*, including several functions for visualizing meta-analytic data using forest-plot derivatives. We consider the orchard plot as a variant on the classic forest plot, cultivated to the needs of meta-analysts in ecology and evolution. Hopefully, the orchard plot will prove fruitful for visualizing large collections of heterogeneous effect sizes regardless of the field of study.

KEYWORDS
caterpillar plot, credibility interval, credible interval, evidence synthesis, graphical tool, meta-regression, summary forest plot

Malgorzata Lagisz, Daniel W. A. Noble, and Alistair M. Senior contributed equally to this study.

1 | INTRODUCTION

Forest plots, also known as "confidence interval plots" or "blobbograms," visualize results of a meta-analysis elegantly and informatively.[1] A typical forest plot shows

individual point estimates from each study in a meta-analysis, along with their (95%) confidence intervals (CIs), and also, at the bottom, depicts an overall mean and its CI, usually as a diamond[2,3] (Figure 1A); from hereon, we define this as the "classic forest plot." Our definition of the classic forest plot includes a forest plot where point estimates have been sorted according to their size and study-specific labels excluded, which is sometimes known as a "caterpillar plot" (Figure 1B; for more on the caterpillar plot, see Appendix A). Although the forest plot originated in medicine, researchers from many fields have subsequently adopted the classic forest plot.

In the fields of ecology and evolution, however, the use of classic forest plots is limited. Forest plots are often impractical and inelegant because such meta-analyses can include 100+ effect sizes[4,5] (cf. Figure 1B). In ecology and evolution, it is common to use what we term a "forest-like plot." Forest-like plots vary somewhat, but typically consist of a series of estimates from meta-regression categorical moderators (or subset analyses) and may or may not also include an overall mean effect (Figure 1C,D). These forest-like plots are similar to what is sometimes termed "summary forest plot" where individual data points are from a number of meta-analyses (or subset meta-analyses).[1] Forest-like plots suit ecologists and evolutionary biologists, because we are often interested in explaining heterogeneity among different groups (eg, taxa or environmental variables), rather than just the overall mean from a single meta-analysis.[4,5]

Here, we propose a novel information-rich version of a forest-like plot, which we term an "orchard plot." Orchard plots include four notable features that unambiguously display model estimates and the underlying heterogeneity of the data. Those features are: (a) model point estimates, (b) CIs, (c) (95%) prediction intervals (PIs; also known as "credibility intervals"),[6-8] and (d) individual effect sizes scaled by their precision (the inverse of SE or sample size). First, we present results from a survey on the usage of variants on the forest plot in ecology and evolution. Then, we introduce the orchard plot and illustrate its use with example datasets.

2 | SURVEY

We examined 102 ecological and evolutionary meta-analyses (studies) published since 2010.[9] In brief, we arrived at these 102 studies by screening 298 articles; they were obtained via a systematic search for studies, including meta-analyses, published between 1 January 2010 and 25 March 2019 in the "Ecology" and "Evolutionary Biology" journals classified under the *InCites Journal Citation Reports* (Clarivate Analytics); for a full description, see Reference 9.

In our survey, we collected information on what types of error bars (whiskers) were used (eg, standard errors,

confidence/credible intervals, or PIs); whether estimates (or data points) were presented with dots, boxes, or bars; and if individual effect sizes were included. For further details of article and data collection procedures and a list of assessed studies and results, see Supporting Information A.

Many studies used plots to visualize meta-analysis results (82%, 84 studies). As predicted, the use of classic forest plots (as defined in the Section 1) was limited to only 12 out of 102 papers/studies (12%); among these 12 studies, 4 had the plots that could be further classified as caterpillar plots (see Appendix A). Conversely, forest-like plots were prevalent (71%, 72 papers; Figure 1E).

Note that what we considered a forest-like plot included plots that presented subgroup meta-analyses and meta-regressions, regardless of whether they used dots, bars, or boxes to represent point estimates (for differences between forest-like plots using subgroup meta-analyses, and meta-regression with a categorical moderator, see Appendix B). As in the classic forest plot,[2] most of studies employed dots and CIs (as whiskers; Figure 1F,G). Finally, only one paper[10] reported PIs, and notably this figure did not have corresponding CIs. Merely three studies[11-13] had forest-like plots with individual effects sizes overlaid. None of the figures we examined had all the features of our proposed orchard plot.

3 | ORCHARD PLOT

Clearly, forest-like plots are widely used to visualize the results of meta-analytic models in ecology and evolution. These plots display point estimates (trunks) and CIs (branches). We propose that alongside these features one should include PIs (twigs) and scaled individual effect size points (pieces of fruit) to give a fully formed and information-rich "orchard plot" (Figure 2A). Orchard plots are a type of scatterplot where position on the x-axis corresponds to effect size value (where individual effects are scaled by some measure of precision; eg, sample size). Position in the y-dimension is determined by: (a) grouping within a categorical moderator variable if any such variable is of interest and then (b) using the principles of a "bee swarm plot"[14,15] to make any overlaying individual effect sizes within the same category visible (ie, spreading them within the y-axis based on quasi-random noise; van der Corput sequence[16]).

A PI displays a range of plausible effect size values for a new study (assuming an average sample size). In meta-analysis, PIs help the user interpret the extent of heterogeneity (ie, variation among effect sizes not due to sampling errors) and the associated statistics (eg, τ^2).[6-8] The value of PIs has been noted in the medical
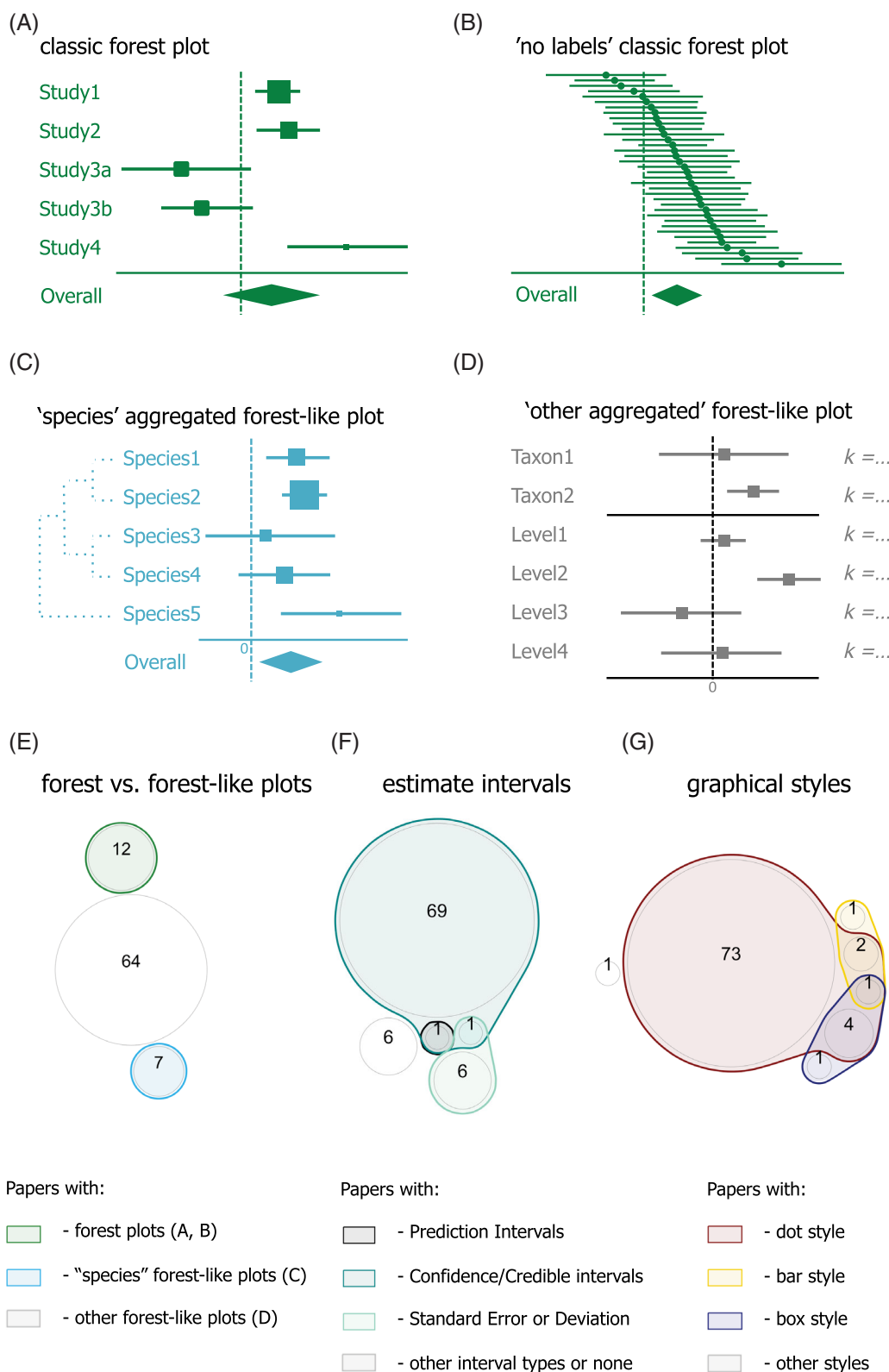
FIGURE 1 Use of classic forest plots and forest-like plots in 102 meta-analytic papers in ecology and evolution: A, a schematic representation of a classic forest plot presenting the individual effect sizes within the analysis and the overall effect estimated by the meta-analysis, or; B, its variant without labels where effect sizes are sorted by size (sometimes referred to as a caterpillar plot; see Appendix A); C, forest-like plots can present effect sizes aggregated at the species level; D, higher level taxonomic groups or moderator categories (*k* represents the number of effect sizes per estimate); E, out of 102 assessed papers, 84 presented at least one plot that can be classified as a forest plot or some form of forest-like plot, including its "species" format; F, numbers of papers that have at least one forest/forest-like plot with a given type of intervals; and G, numbers of papers that have at least one plot in a classic "dot" plot style, or in other less common plot styles [Colour figure can be viewed at wileyonlinelibrary.com]
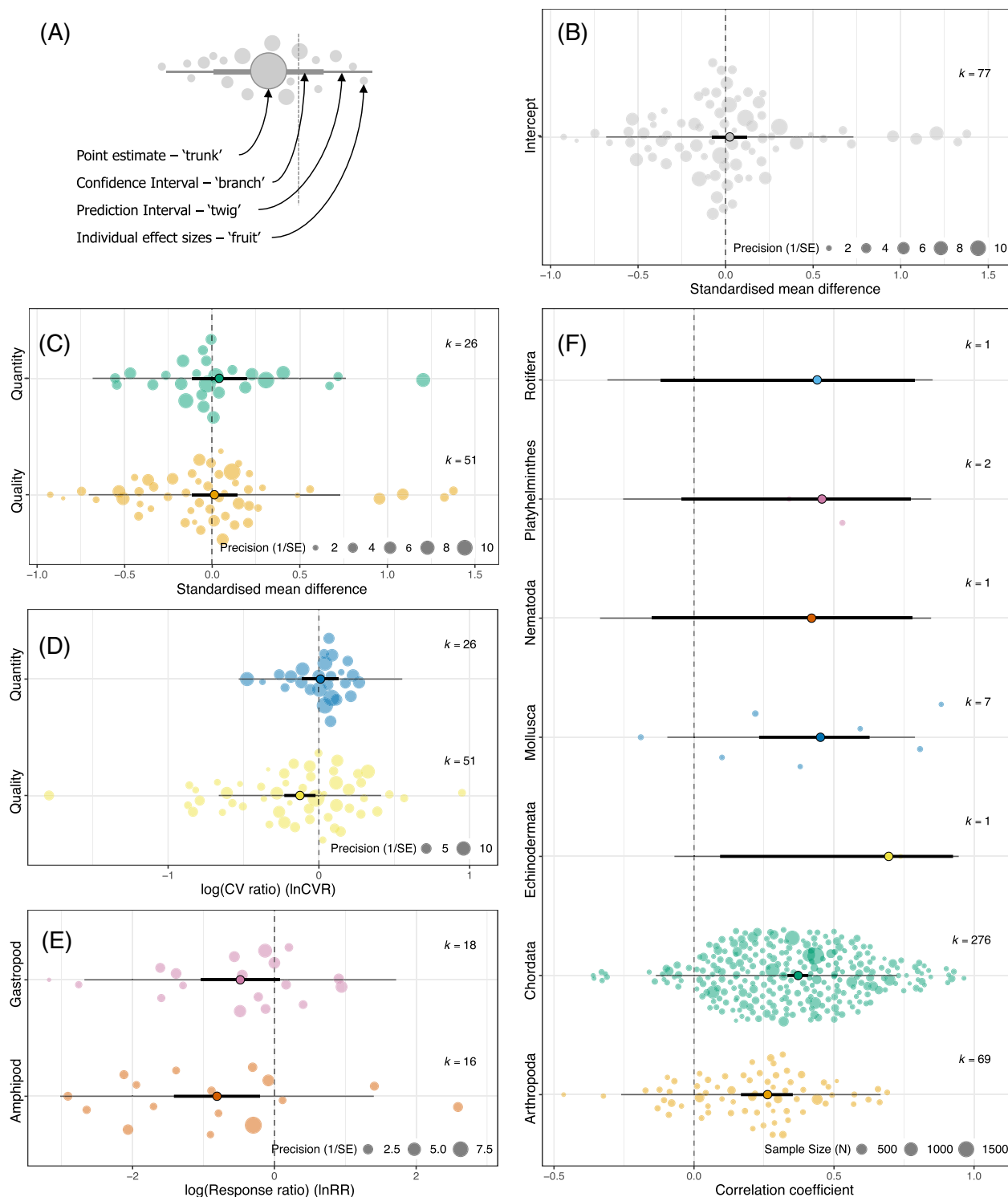
FIGURE 2 Examples of orchard plots: A, a schematic of what is visualized for an orchard plot with some analogies; B, a meta-analytic result of Example 1 in SMD; C, meta-regression results of Example 1 in SMD; D, those in coefficient of variation ratio on log (lnCVR); E, meta-regression results of Example 2 in response ratio on log (lnRR); and F, meta-regression results of Example 3 in correlation coefficients. SMD, standardized mean difference [Colour figure can be viewed at wileyonlinelibrary.com]

literature[8,17]; PIs can be easily incorporated into a classic forest plot although, in practice, they rarely are. PIs are particularly relevant for ecology and evolution where meta-analyses typically contain very high heterogeneity (typically $I^2 = 90\%$[5]), yet reporting and interpretation of such statistics (eg, I^2, Q, or τ^2) remains poor.[5]

It is both informative and insightful to plot individual effect sizes scaled by their precision (or sample size), allowing one to see influential effect sizes and potential outliers. Such an addition is akin to more widely used bubble plots, where effect sizes are plotted as a function of a continuous moderator.[18,19] Our suggestion also aligns with more general recommendations for the analysis of experimental studies, which call for the inclusion of raw data, rather than bar graphs.[20,21]

To facilitate the implementation of orchard plots, we have developed a function using the *R* package *metafor*[22] and *ggplot2* graphics.[23] The function (*orchard_plot*) and vignette are available through the *orchaRd* package (github.com/itchyshin/orchard_plot). Below, we illustrate the use of orchard plots using three examples from ecology and evolution (details of the implementation are given in the *orchaRd* vignette).

3.1 | Example 1. Dietary restriction and lifespan

English and Uller[24] meta-analyzed the effects of early-life dietary restriction on lifespan, using the standardized mean difference (often called Cohen's *d* or Hedges' *g*).[25] They found that, across the whole dataset, there was little evidence for an effect of dietary restriction on lifespan. The orchard plot in Figure 2B shows the overall estimate from a random-effects meta-analysis of 77 effect sizes centered on zero, with a 95% CI that spans the line of no effect. The PIs clearly depict high levels of heterogeneity. We also visualize the results of a random effects meta-regression, showing the results were consistent for restrictions of dietary quantity (total calories) and dietary "quality" (typically protein restriction; Figure 2C), although again the PIs are wide even within categories.

Senior et al[26] reanalyzed this dataset for effects of dietary restriction on among-individual variation in longevity using the log coefficient of variation ratio, lnCVR.[27] Although restrictions of dietary quality and quantity did not affect average lifespan, among-individual variation appeared to be altered by lower diet quality in early life (Figure 2D, which shows one negative effect size far from other points). Variation in the control group was lower than the treatment group; however, the effect was heterogeneous; a substantial number of positive effects were still predicted.

3.2 | Example 2. Predation and invertebrate community

Eklof et al[28] evaluated the effects of predation on benthic invertebrate communities. Using the log response ratio (lnRR),[29] they quantified differences in abundance and/or biomass of gastropods and amphipods in groups with and without predation in an experimental setting (Figure 2E). The effects were negative for both gastropods and amphipods, suggesting that mean abundance/biomass in the control group was lower than in the treatment group, although the effect was the largest, and is statistically significant, for amphipods. In both cases, the PIs reveal the extent of heterogeneity and predict not only negative but also positive effects.

3.3 | Example 3. Maternal-offspring morphological correlations

Lim et al[30] synthesized the strength of correlation between maternal and offspring size within species across a very wide range of taxa. They found a moderate positive correlation between maternal size and offspring size within species (ie, larger mothers have larger offspring). However, they also found evidence for relatively strong phylogenetic effect (signals),[31,32] suggesting the strength of the association was dependent on evolutionary lineage.

Analyzing the results by phyla, the orchard plot (Figure 2F) clearly shows the analysis was dominated by data from chordates and arthropods, with other phyla poorly represented, although we have PIs for all phyla. Also, there was a difference between the strength of a typical correlation within the two well-represented groups (Chordata and Arthropoda), which might explain the phylogenetic signal (variance) detected by Lim et al. Lastly, there remains a large overlap in predicted range of effect sizes between Chordata and Arthropoda; that is, individual species within these two phyla are still highly variable.

4 | DISCUSSION AND CONCLUSION

Our survey shows most meta-analyses in ecology and evolution use "forest-like plots." We advocate formalizing this approach in the orchard plot. Interestingly, Schild and Voracek's survey[33] revealed that meta-analyses in medicine almost always have forest plots, but this is not the case for those in psychology and economics. Similarly, to ecology and evolution, meta-analyses in psychology and economics often have too many effect sizes (studies)[34,35] to use the classic forest plot. Therefore, the proposed orchard plot is also likely to be useful in the social sciences.

Our examples using orchard plots show how they can provide a comprehensive picture of model results and their underlying data. The inclusion of PIs, in particular, gives an intuitive visualization of heterogeneity and allows interpretation thereof, something that is badly needed in our field. We should note that this is not the first time researchers proposed improvements to forest plots[36,37] (eg, thick forest plots or rainforest plots[38]). However, orchard plots fill a fruitful niche, as they can be used to visualize the results of meta-regression analysis with a categorical moderator, as is commonplace in ecology and evolution.

CONFLICT OF INTEREST
The author reported no conflict of interest.

AUTHOR CONTRIBUTIONS
S.N. and A.M.S. conceived the initial idea and wrote the first draft. R.E.O. led the literature search to obtain ecology and evolution meta-analyses. M.L. led the survey of forest plots with help from S.N., J.R., R.E.O., and Y.Y. D.W.A.N. made the R package with help from S.N. and A.M.S. All authors contributed to the design of the study and to editing and commenting on drafts.

DATA AVAILABILITY STATEMENT
For further details of article and data collection procedures and a list of assessed studies and results, see Supporting information A.

ORCID
Shinichi Nakagawa https://orcid.org/0000-0002-7765-5182
Malgorzata Lagisz https://orcid.org/0000-0002-3993-6127
Rose E. O'Dea https://orcid.org/0000-0001-8177-5075
Joanna Rutkowska https://orcid.org/0000-0003-0396-1790
Yefeng Yang https://orcid.org/0000-0002-8610-4016
Daniel W. A. Noble https://orcid.org/0000-0001-9460-8743
Alistair M. Senior https://orcid.org/0000-0001-9805-7280

REFERENCES
1. Anzures-Cabrera J, Higgins JPT. Graphical displays for meta-analysis: an overview with suggestions for practice. *Res Syn Meth*. 2010;1(1):66-80.
2. Lewis S, Clarke M. Forest plots: trying to see the wood and the trees. *Br Med J*. 2001;322(7300):1479-1480.
3. Borman GD, Grigg JA. Visual and narrative interpretation. In: Cooper H, Hedges LV, Valentine JC, eds. *The Handbook of Research Synthesis and Meta-Analysis*. New York, NY: Russell Sage Foundation; 2009:497-519.
4. Gurevitch J, Koricheva J, Nakagawa S, Stewart G. Meta-analysis and the science of research synthesis. *Nature*. 2018;555 (7695):175-182.
5. Senior AM, Grueber CE, Kamiya T, et al. Heterogeneity in ecological and evolutionary meta-analyses: its magnitude and implications. *Ecology*. 2016;97(12):3293-3299.
6. Borenstein M, Higgins JP, Hedges LV, Rothstein HR. Basics of meta-analysis: I2 is not an absolute measure of heterogeneity. *Res Syn Meth*. 2017;8(1):5-18.
7. Higgins JPT. Commentary: heterogeneity in meta-analysis should be expected and appropriately quantified. *Int J Epidemiol*. 2008;37(5):1158-1160.
8. IntHout J, Ioannidis JPA, Rovers MM, Goeman JJ. Plea for routinely presenting prediction intervals in meta-analysis. *BMJ Open*. 2016;6(7):1-6.
9. O'Dea RE, Jennions MD, Koricheva J, et al. *Protocol for assessment of current reporting practices of preferred reporting items for systematic reviews and meta-analyses in ecology and evolution (PRISMA-EcoEvo)*. OSF. 2019 (https://doi.org/10.17605/OSF.IO/2XPFG).
10. Davidson KE, Fowler MS, Skov MW, Doerr SH, Beaumont N, Griffin JN. Livestock grazing alters multiple ecosystem properties and services in salt marshes: a meta-analysis. *J Appl Ecol*. 2017;54(5):1395-1405.
11. Slot M, Kitajima K. General patterns of acclimation of leaf respiration to elevated temperatures across biomes and plant types. *Oecologia*. 2015;177(3):885-900.
12. Moore MP, Riesch R, Martin RA. The predictability and magnitude of life-history divergence to ecological agents of selection: a meta-analysis in livebearing fishes. *Ecol Lett*. 2016;19(4): 435-442.
13. Lehmann A, Zheng WS, Rillig MC. Soil biota contributions to soil aggregation. *Nat Ecol Evol*. 2017;1(12):1828-1835.
14. Eklund A. *Beeswarm: the bee swarm plot, an alternative to stripchart. R Package Version 01*. Vienna, Austria: R Foundation; 2012.
15. Clarke E, Sherrill-Mix S. *ggbeeswarm: categorical scatter (violin point) plots. R package version 0.6.0*. Vienna, Austria: R Foundation; 2017.
16. Sherrill-Mix S, Clarke E. *Plot categorical data using quasirandom noise and density estimates. R package version 0.4.5*. Vienna, Austria: R Foundation; 2017.
17. Riley RD, Higgins JPT, Deeks JJ. Interpretation of random effects meta-analyses. *Br Med J*. 2011;342:d549.
18. Kiran A, Crespillo AP, Rahimi K. Graphics and statistics for cardiology: data visualisation for meta-analysis. *Heart*. 2017; 103(1):19-23.
19. Nakagawa S, Noble DWA, Senior AM, Lagisz M. Meta-evaluation of meta-analysis: ten appraisal questions for biologists. *BMC Biol*. 2017;15:18.
20. Weissgerber TL, Milic NM, Winham SJ, Garovic VD. Beyond Bar and line graphs: time for a new data presentation paradigm. *Plos Biol*. 2015;13(4):1-10.

21. Ho J, Tumkaya T, Aryal S, Choi H, Claridge-Chang A. Moving beyond P values: data analysis with estimation graphics. *Nat Methods*. 2019;16(7):565-566.

22. Viechtbauer W. Conducting meta-analyses in R with the metafor package. *J Stat Softw*. 2010;36(3):1-48.

23. Wickham H. *ggplot2: Elegant Graphics for Data Analysis*. New York: Springer; 2009.

24. English S, Uller T. Does early-life diet affect longevity? A meta-analysis across experimental studies. *Biol Lett*. 2016;12 (9):1-4.

25. Hedges LV, Olkin I. *Statistical Methods for Meta-Analysis*. Orlando: Academic Press; 1985.

26. Senior AM, Nakagawa S, Raubenheimer D, Simpson SJ, Noble DWA. Dietary restriction increases variability in longevity. *Biol Lett*. 2017;13(3):1-4.

27. Nakagawa S, Poulin R, Mengersen K, et al. Meta-analysis of variation: ecological and evolutionary applications and beyond. *Meth Ecol Evol*. 2015;6(2):143-152.

28. Eklof JS, Alsterberg C, Havenhand JN, Sundback K, Wood HL, Gamfeldt L. Experimental climate change weakens the insurance effect of biodiversity. *Ecol Lett*. 2012;15(8): 864-872.

29. Hedges LV, Gurevitch J, Curtis PS. The meta-analysis of response ratios in experimental ecology. *Ecology*. 1999;80(4): 1150-1156.

30. Lim JN, Senior AM, Nakagawa S. Heterogeneity in individual quality and reproductive trade-offs within species. *Evolution*. 2014;68(8):2306-2318.

31. Hadfield J, Nakagawa S. General quantitative genetic methods for comparative biology: phylogenies, taxonomies and multi-trait models for continuous and categorical characters. *J Evol Biol*. 2010;23:494-508.

32. Nakagawa S, Santos ESA. Methodological issues and advances in biological meta-analysis. *Evol Ecol*. 2012;26: 1253-1274.

33. Schild AH, Voracek M. Less is less: a systematic review of graph use in meta-analyses. *Res Syn Meth*. 2013;4(3):209-219.

34. Ioannidis JPA, Stanley TD, Doucouliagos H. The power of bias in economics research. *Econ J*. 2017;127(605):F236-F265.

35. Stanley TD, Carter EC, Doucouliagos H. What meta-analyses reveal about the replicability of psychological research. *Psychol Bull*. 2018;144(12):1325-1346.

36. Jackson CH. Displaying uncertainty with shading. *Am Stat*. 2008;62(4):340-347.

37. Barrowman NJ, Myers RA. Raindrop plots: a new way to display collections of likelihoods and distributions. *Am Stat*. 2003; 57(4):268-274.

38. Schild AHE, Voracek M. Finding your way out of the forest without a trail of bread crumbs: development and evaluation of two novel displays of forest plots. *Res Syn Meth*. 2015;6(1): 74-86.

39. Kossmeier M, Tran US, Voracek M. Charting the landscape of graphical displays for meta-analysis and systematic reviews: a comprehensive review, taxonomy, and feature analysis. *BMC Med Res Methodol*. 2020;20(1):1-24.

40. Spiegelhalter DJ. Funnel plots for comparing institutional performance. *Stat Med*. 2005;24(8):1185-1202.

41. Kossmeier M, Tran US, Voracek M. *Visualizing Meta-Analytic Data with R Package Metaviz*. R Package Version 0.3.1. Vienna, Austria: R Foundation; 2020.

SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of this article.

APPENDIX A: CATERPILLARS IN AN ORCHARD

A formal definition of the term "caterpillar plot" seems to be missing in the literature, but it appears to have been used when a forest plot (1) excludes the overall mean (often depicted by a diamond; as for a confidence interval plot[39]) and/or (2) has individual effect sizes ordered from the smallest to the largest (eg, Reference [40]). Here, we use the term caterpillar plot to refer to the latter. Under this definition, around 5% of the 102 studies used caterpillar plots in our survey (Supporting Information A). However, none of these presented results from meta-regression models with categorial moderators. Such models are extremely common in ecology and evolution (see Section B.1), and we have designed the orchard plot to present the associated results in an informative manner. One could, however, use caterpillar-type plots to present results from different groups (eg, a categorical meta-regression model). Therefore, we have created the function named "*caterpillars*" in our *R* package, *orchaRd*. We refer to these types of plots as a "caterpillars plot" (rather than "caterpillar plot"), because multiple caterpillars (groups) are displayed on the same plot. Importantly, similarly to the orchard plot described in the main text, our caterpillars plot includes 95% prediction intervals (PIs) as well as confidence intervals (CIs; Figure A1A; see also, Reference[41]).

Comparing caterpillars plots with orchard plots

Figure A1 shows a caterpillar plot and "caterpillars" plot, using some of the same data as in the orchard plots in Figure 2. An advantage of the caterpillar(s) plot is that we can see 95% CIs for all effect sizes. A caterpillar plot (ie, results from a meta-analysis as in Figure A1A) and a caterpillars plot with a small number of groups (as in
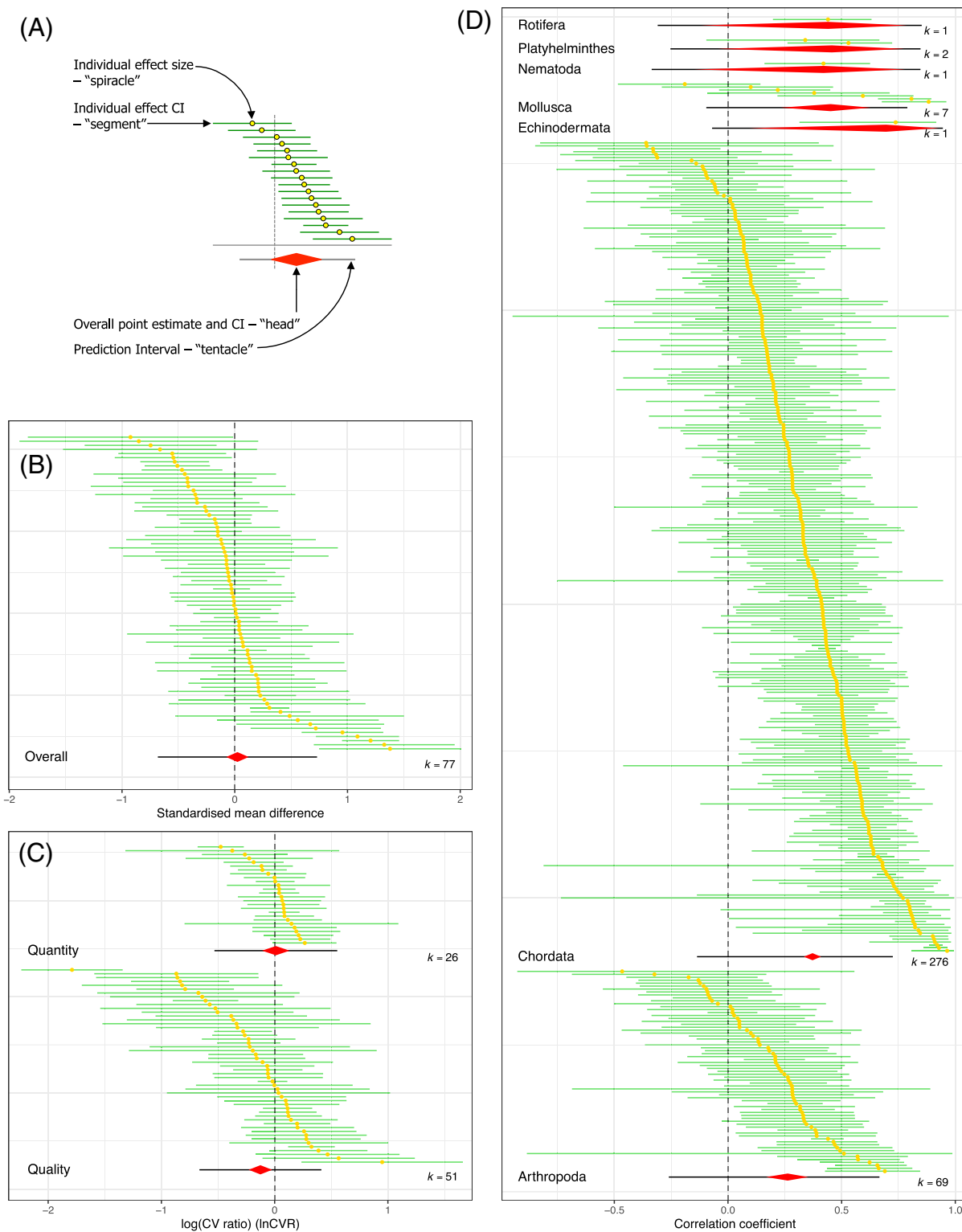
FIGURE A1 Examples of caterpillars plot: A, a schematic of what is visualized for a caterpillars plot with some analogies; B, a meta-analytic result of Example 1 in SMD (cf. Figure 2B); C, meta-regression results of Example 1 in coefficient of variation ratio on log (lnCVR; cf. Figure 2D); and D, meta-regression results of Example 3 in correlation coefficients (cf. Figure 2F). SMD, standardized mean difference [Colour figure can be viewed at wileyonlinelibrary.com]

Figure A1C) are as informative as their orchard-plot counterparts (Figure 2B,D, respectively). However, a caterpillars plot with multiple groups with unequal sample sizes (as in

Figure A1D) is not as visually appealing as its orchard plot counterpart (as in Figure 2F). Additionally, caterpillars plots require more space to convey similar information.

APPENDIX B: MORE DETAILS ON FOREST-LIKE PLOTS

Our definition of a "forest-like plot" included plots presenting results: (1) from meta-regression(s) with a categorical moderator(s) with or without a data point from the main meta-analysis and (2) from a series of subgroup meta-analyses and the main-meta-analysis (sometimes known as "summary forest plots"[1]). The former is much more popular in ecology and evolution (see the next section). The important differences between these two approaches are that: (1) estimates and their CIs and PIs can differ between them and (2) subgroup analyses require at least three data points (effect sizes) to estimate PIs via a meta-analysis fitted to each group, whereas one data point is sufficient to estimate a PI for each category in the meta-regression (as shown in Figure 2F).

Survey results for forest-like plots from meta-analyses or meta-regressions

We examined 607 plots from 80 papers that we identified as having forest-like plots. Among these plots, the majority of forest-like plots were based on results from meta-regression analyses (562 plots, 93%). Also, only 135 plots (22%) presented results from main meta-analyses (Supporting Information A).