

BRIEF METHOD NOTE

**The Orchard Plot: Cultivating a Forest Plot for Use in Ecology,
Evolution and Beyond**

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19 **Abstract**

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

37

38 **KEYWORDS**

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

41

42 1 | INTRODUCTION

43 Forest plots, also known as ‘confidence interval plots’ or ‘blobbograms’, visualize results of a meta-
44 analysis elegantly and informatively¹. A typical forest plot shows individual point estimates from
45 each study in a meta-analysis, along with their (95%) confidence intervals (CIs), and also, at the
46 bottom, depicts an overall mean and its CI, usually as a diamond^{2,3} (Figure 1a); from hereon we
47 define this as the ‘classic forest plot’. Our definition of the classic forest plot includes a forest plot
48 where point estimates have been sorted according to their size and study-specific labels excluded,
49 which is sometimes known as a ‘caterpillar plot’ (Figure 1b; for more on the caterpillar plot, see
50 Appendix A). Although the forest plot originated in medicine, researchers from many fields have
51 subsequently adopted the classic forest plot.

52 In the fields of ecology and evolution, however, the use of classic forest plots is limited. Forest
53 plots are often impractical and inelegant because such meta-analyses can include 100+ effect
54 sizes^{4,5} (cf. Figure 1b). In ecology and evolution, it is common to use what we term a ‘forest-like
55 plot’. Forest-like plots vary somewhat, but typically consist of a series of estimates from meta-
56 regression categorical moderators (or subset analyses) and may or may not also include an overall
57 mean effect (Figures 1c & d). These forest-like plots are similar to what is sometimes termed
58 ‘summary forest plot’ where individual data points are from a number of meta-analyses (or subset
59 meta-analyses)¹. Forest-like plots suit ecologists and evolutionary biologists, because we are often
60 interested in explaining heterogeneity among different groups (e.g., taxa, or environmental
61 variables), rather than just the overall mean from a single meta-analysis^{4,5}.

62 Here, we propose a novel information-rich version of a forest-like plot, which we term an ‘orchard
63 plot’. Orchard plots include four notable features that unambiguously display model estimates and
64 the underlying heterogeneity of the data. Those features are: 1) model point estimates, 2) CIs, 3)
65 (95%) prediction intervals (PIs; also known as ‘credibility intervals’)⁶⁻⁸, and 4) individual effect
66 sizes scaled by their precision (the inverse of standard error or sample size). First, we present results

67 from a survey on the usage of variants on the forest plot in ecology and evolution. Then, we
68 introduce the orchard plot and illustrate its use with example datasets.

69 **2 | SURVEY**

70 We examined 102 ecological and evolutionary meta-analyses (studies) published since 2010⁹. In
71 brief, we arrived at these 102 studies by screening 298 articles; they were obtained via a systematic
72 search for studies, including meta-analyses, published between 1 January 2010 and 25 March 2019
73 in the ‘Ecology’ and ‘Evolutionary Biology’ journals classified under the *InCites Journal Citation*
74 *Reports* (Clarivate Analytics); for a full description see⁹.

75 In our survey, we collected information on what types of error bars (whiskers) were used (e.g.,
76 standard errors, confidence/credible intervals, or prediction intervals); whether estimates (or data
77 points) were presented with dots, boxes or bars; and if individual effect sizes were included. For
78 further details of article and data collection procedures and a list of assessed studies and results, see
79 Supporting Material A.

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

85 Note that what we considered a forest-like plot included plots that presented subgroup meta-
86 analyses and meta-regressions, regardless of whether they used dots, bars or boxes to represent
87 point estimates (for differences between forest-like plots using subgroup meta-analyses, and meta-
88 regression with a categorical moderator, see Appendix B). As in the classic forest plot², most of
89 studies employed dots and CIs (as whiskers; Figure 1f & g). Finally, only one paper¹⁰ reported
90 prediction intervals, and notably this figure did not have corresponding CIs. Merely 3 studies¹¹⁻¹³

91 had forest-like plots with individual effects sizes overlaid. None of the figures we examined had all
92 the features of our proposed orchard plot.

93 **3 | ORCHARD PLOT**

94 Clearly, forest-like plots are widely used to visualize the results of meta-analytic models in ecology
95 and evolution. These plots display point estimates (trunks) and CIs (branches). We propose that
96 alongside these features one should include PIs (twigs) and scaled individual effect size points
97 (pieces of fruit) to give a fully formed and information-rich ‘orchard plot’ (Figure 2a). Orchard
98 plots are a type of scatterplot where position on the x -axis corresponds to effect size value (where
99 individual effects are scaled by some measure of precision; e.g. sample size). Position in the y -
100 dimension is determined by: 1) grouping within a categorical moderator variable if any such
101 variable is of interest and then 2) using the principles of a ‘bee swarm plot’^{14,15} to make any
102 overlaying individual effect sizes within the same category visible (i.e. spreading them within the y -
103 axis based on quasi-random noise; van der Corput sequence¹⁶).

104 A PI displays a range of plausible effect size values for a new study (assuming an average sample
105 size). In meta-analysis, PIs help the user interpret the extent of heterogeneity (i.e., variation among
106 effect sizes not due to sampling errors) and the associated statistics (e.g., τ^2)⁶⁻⁸. The value of PIs has
107 been noted in the medical literature^{8,17}; PIs can be easily incorporated into a classic forest plot
108 although, in practice, they rarely are. PIs are particularly relevant for ecology and evolution where
109 meta-analyses typically contain very high heterogeneity (typically $I^2 = 90\%$ ⁵), yet reporting and
110 interpretation of such statistics (e.g., I^2 , Q or τ^2) remains poor⁵.

111 It is both informative and insightful to plot individual effect sizes scaled by their precision (or
112 sample size), allowing one to see influential effect sizes and potential outliers. Such an addition is
113 akin to more widely used bubble plots, where effect sizes are plotted as a function of a continuous

114 moderator^{18,19}. Our suggestion also aligns with more general recommendations for the analysis of
115 experimental studies, which call for the inclusion of raw data, rather than bar graphs^{20,21}.

116 To facilitate the implementation of orchard plots we have developed a function using the *R* package
117 *metafor*²² and *ggplot2* graphics²³. The function (*orchard_plot*) and vignette are available through
118 the *orchaRd* package (github.com/itchyshin/orchard_plot). Below, we illustrate the use of orchard
119 plots using three examples from ecology and evolution (details of the implementation are given in
120 the *orchaRd* vignette).

121 **3.1 | Example 1: Dietary Restriction and Lifespan**

122 English and Uller²⁴ meta-analyzed the effects of early-life dietary restriction on lifespan, using the
123 standardised mean difference, SMD (often called Cohen's *d* or Hedges' *g*)²⁵. They found that,
124 across the whole dataset, there was little evidence for an effect of dietary restriction on lifespan. The
125 orchard plot in Figure 2b shows the overall estimate from a random-effects meta-analysis of 77
126 effect sizes centred on zero, with a 95% CI that spans the line of no effect. The PIs clearly depict
127 high levels of heterogeneity. We also visualise the results of a random effects meta-regression,
128 showing the results were consistent for restrictions of dietary quantity (total calories), and dietary
129 'quality' (typically protein restriction; Figure 2c), although again the PIs are wide even within
130 categories.

131 Senior and colleagues²⁶ re-analysed this dataset for effects of dietary restriction on among-
132 individual variation in longevity using the log coefficient of variation ratio, *lnCVR*²⁷. While
133 restrictions of dietary quality and quantity did not affect average lifespan, among-individual
134 variation appeared to be altered by lower diet quality in early life (Figure 2d, which shows one
135 negative effect size far from other points). Variation in the control group was lower than the
136 treatment group, however, the effect was heterogeneous; a substantial number of positive effects
137 were still predicted.

138 **3.2 | Example 2: Predation and Invertebrate Community**

139 Eklöf and colleagues²⁸ evaluated the effects of predation on benthic invertebrate communities.
140 Using the log response ratio ($\ln RR$)²⁹, they quantified differences in abundance and/or biomass of
141 gastropods and amphipods in groups with and without predation in an experimental setting (Figure
142 2e). The effects were negative for both gastropods and amphipods, suggesting that mean
143 abundance/biomass in the control group was lower than in the treatment group, although the effect
144 was the largest, and is statistically significant, for amphipods. In both cases the PIs reveal the extent
145 of heterogeneity and predict not only negative but also positive effects.

146 **3.3 | Example 3: Maternal-Offspring Morphological Correlations**

147 Lim and colleagues³⁰ synthesized the strength of correlation between maternal and offspring size
148 within species across a very wide range of taxa. They found a moderate positive correlation
149 between maternal size and offspring size within species (i.e. larger mothers have larger offspring).
150 However, they also found evidence for relatively strong phylogenetic effect (signals)^{31,32},
151 suggesting the strength of the association was dependent on evolutionary lineage.

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

159 **4 | DISCUSSION AND CONCLUSION**

160 Our survey shows most meta-analyses in ecology and evolution use ‘forest-like plots’. We advocate
161 formalising this approach in the orchard plot. Interestingly, Schild and Voracek’s survey³³ revealed

162 that meta-analyses in medicine almost always have forest plots, but this is not the case for those in
163 psychology and economics. Similarly to ecology and evolution, meta-analyses in psychology and
164 economics often have too many effect sizes (studies)^{34,35} to use the classic forest plot. Therefore, the
165 proposed orchard plot is also likely to be useful in the social sciences.

166 Our examples using orchard plots show how they can provide a comprehensive picture of model
167 results and their underlying data. The inclusion of PIs, in particular, gives an intuitive visualisation
168 of heterogeneity and allows interpretation thereof, something that is badly needed in our field. We
169 should note that this is not the first time researchers proposed improvements to forest plots^{36,37} (e.g.,
170 thick forest plots or rainforest plots³⁸). However, orchard plots fill a fruitful niche, as they can be
171 used to visualize the results of meta-regression analysis with a categorical moderator, as is
172 commonplace in ecology and evolution.

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177 SN and AMS conceived the initial idea and wrote the first draft, REO led the literature search to
178 obtain ecology and evolution meta-analyses. ML led the survey of forest plots with help from SN,
179 JR, REO, and YY. DWAN made the R package with help from SN and AMS. All authors
180 contributed to the design of the study and to editing and commenting on drafts.

181 **CONFLICT OF INTEREST**

182 The author reported no conflict of interest

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191 **HIGHLIGHTS**

- 192 • Forest plots are of limited use when there are a large number of effect sizes, as is common in
193 ecology and evolution.
- 194 • A survey of 102 meta-analyses in the field of ecology and evolution revealed that forest
195 plots are used infrequently.
- 196 • We present the ‘orchard plot’, a modified version of the classic forest plot.
- 197 • Orchard plots are an informative, insightful and intuitive way of representing the results of
198 large meta-analyses.
- 199 • They display underlying data in clear, transparent and fruitful ways by visualizing
200 heterogeneity among effect sizes.

201

202 **APPENDIX A: CATERPILLARS IN AN ORCHARD**

203 A formal definition of the term ‘caterpillar plot’ seems to be missing in the literature, but it appears
204 to have been used when a forest plot 1) excludes the overall mean (often depicted by a diamond; as
205 for a confidence interval plot³⁹) and/or 2) has individual effect sizes ordered from the smallest to the
206 largest (e.g.,⁴⁰). Here, we use the term, caterpillar plot to refer to the latter. Under this definition,
207 around 5% of the 102 studies used caterpillar plots in our survey (Supporting Material A).
208 However, none of these presented results from meta-regression models with categorical moderators.
209 Such models are extremely common in ecology and evolution (see section B.1), and we have
210 designed the orchard plot to present the associated results in an informative manner. One could,
211 however, use caterpillar-type plots to present results from different groups (e.g., a categorical meta-
212 regression model). Therefore, we have created the function named ‘*caterpillars*’ in our *R* package,
213 *orchaRd*. We refer to these types of plots as a ‘caterpillars plot’ (rather than ‘caterpillar plot’),
214 because multiple caterpillars (groups) are displayed on the same plot. Importantly, similarly to the
215 orchard plot described in the main text, our caterpillars plot includes 95% prediction intervals (PIs)
216 as well as confidence intervals (CIs; Figure A1a; see also, ref.⁴¹).

217 **A.1 | Comparing caterpillars plots with orchard plots**

218 Figure A1 shows a caterpillar plot and ‘caterpillars’ plot, using some of the same data as in the
219 orchard plots in Figure 2. An advantage of the caterpillar(s) plot is that we can see 95% CIs for all
220 effect sizes. A caterpillar plot (i.e. results from a meta-analysis as in Figure A1b) and a caterpillars
221 plot with a small number of groups (as in Figure A1c) are as informative as their orchard-plot
222 counterparts (Figure 2b & d, respectively). However, a caterpillars plot with multiple groups with
223 unequal sample sizes (as in Figure A1d) is not as visually appealing as its orchard plot counterpart
224 (as in Figure 2f). Additionally, caterpillars plots require more space to convey similar information.

225 **APPENDIX B: MORE DETAILS ON FOREST-LIKE PLOTS**

226 Our definition of a ‘forest-like plot’ included plots presenting results: 1) from meta-regression(s)
227 with a categorical moderator(s) with or without a data point from the main meta-analysis, and 2)
228 from a series of sub-group meta-analyses and the main-meta-analysis (sometimes known as
229 ‘summary forest plots’¹). The former is much more popular in ecology and evolution (see the next
230 section). The important differences between these two approaches are that: 1) estimates and their
231 CIs and PIs can differ between them, and 2) subgroup analyses require at least 3 data points (effect
232 sizes) to estimate PIs via a meta-analysis fitted to each group, while one data point is sufficient to
233 estimate a PI for each category in the meta-regression (as shown in Figure 2F).

234 **B.1 | Survey results for forest-like plots from meta-analyses or meta-regressions**

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

239

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333

335 **FIGURE LEGENDS**

336 **FIGURE 1.** Use of classic forest plots and forest-like plots in 102 meta-analytic papers in ecology
 337 and evolution: (a) a schematic representation of a classic forest plot presenting the individual effect
 338 sizes within the analysis and the overall effect estimated by the meta-analysis, or; (b) its variant
 339 without labels where effect sizes are sorted by size (sometimes referred to as a caterpillar plot; see
 340 Appendix A); (c) forest-like plots can present effect sizes aggregated at the species level; (d)
 341 higher-level taxonomic groups or moderator categories (k represents the number of effect sizes per
 342 estimate); (e) out of 102 assessed papers, 84 presented at least one plot that can be classified as a
 343 forest plot or some form of forest-like plot, including its ‘species’ format; (f) numbers of papers that
 344 have at least one forest/forest-like plot with a given type of intervals; and (g) numbers of papers that
 345 have at least one plot in a classic ‘dot’ plot style, or in other less common plot styles.

346 **FIGURE 2.** Examples of orchard plots: (a) a schematic of what is visualised for an orchard plot
 347 with some analogies; (b) a meta-analytic result of Example 1 in standardised mean difference
 348 (SMD); (c) meta-regression results of Example 1 in SMD; (d) those in coefficient of variation ratio
 349 on log (lnCVR); (e) meta-regression results of Example 2 in response ratio on log (lnRR); and (f)
 350 meta-regression results of Example 3 in correlation coefficients.

351 **FIGURE A1.** Examples of caterpillars plot: (a) a schematic of what is visualised for a caterpillars
 352 plot with some analogies; (b) a meta-analytic result of Example 1 in standardised mean difference
 353 (SMD; cf. Figure 2b); (c) meta-regression results of Example 1 in coefficient of variation ratio on
 354 log (lnCVR; cf. Figure 2d); and (d) meta-regression results of Example 3 in correlation coefficients
 355 (cf. Figure 2f).





