A CONTRAST OF META AND METAFOR PACKAGES FOR META-ANALYSES IN R

Christopher J. Lortie

Abstract There is extensive support and choice in R to support meta-analyses. Two common packages in the natural sciences include meta and metafor. Here, a brief contrast of the strengths of each is described for the synthesis scientist. Meta is a direct, intuitive choice for rapid implementation of general meta-analytical statistics. Metafor is a comprehensive package for analyses if the fit models are more complex. Both packages provide estimates of heterogeneity, excellent visualization tools, and functions to explore publication bias. Preference and critical outcomes can facilitate choice between these two specific options. Nonetheless, metafor has a steeper learning curve but greater rewards.

Introduction

Meta-analyses are common and powerful synthesis tools in science. Typically in the natural sciences, meta-analyses are used as a mechanism to describe and aggregate quantitative evidence from a set of peer-reviewed, primary research publications (Lortie and Bonte, 2016; Nakagawa et al., 2017). A meta-analysis in the natural sciences, i.e. outside the health sciences, is comprised of a formalized systematic review and analysis of effect sizes and is termed a meta-analysis when statistics examining intervention efficacy are included (Lortie, 2014). In other fields, the terms systematic review and meta-analysis are used more interchangeable, and meta-statistics are often done on compiled randomized controlled trials or other relatively large datasets in addition to sets of data derived from peer-reviewed publications. The derived data in the natural sciences (as the intended primary audience here) routinely extracts only the mean values or single point measures from publications (Stewart and Schmid, 2015). The synthesis statistics were commonly done using MetaWin (Rosenberg et al., 2000) or other GUI-based applications for a number of years. More recently however, statistics in the fields of ecology and evolution for instance have increasingly moved to the programming language R (Lai et al., 2019), and synthesis statistics are no exception. At least two R packages have risen to prominence for general meta-analytical statistics in the natural sciences - namely meta (Schwarzer, 2019) and metafor (Viechtbauer, 2017). Given that meta-analyses are also increasingly published in these same fields (Cadotte et al., 2012; Lortie and Bonte, 2016), a brief comment on the ecosystem of analytical choices that R provides is beneficial and timely. We need synthesis to inform evidence-based decisioning, and meta-analyses can be the primary tool if aggregated primary datasets are unavailable. Furthermore even with primary data in hand, data reduction to effect sizes within primary and synthesis studies is a mechanism to illustrate differences and strength of effects. These approaches provide the capacity for higher-order analyses and reuse (Gerstner et al., 2017) suggesting that familiarity with effect sizes is both germane and practical.

The R ecosystem for meta-analyses

Like many fundamental challenges in science, the R developer community provides potential solution sets distributed across multiple packages for synthesis. Broadly speaking, alternative packages in R sometimes examine an issue from different perspectives and provide unique functions. In other instances, packages can be very similar or analogs in terms of functionality and use conceptually aligned functions that differ only in nomenclature or arguments. Scientific synthesists that choose to do a meta-analyses in R have options. A total of 63 packages associated with various aspects of conducting a meta-analysis have been identified in a comprehensive review and typology of options (Polanin et al., 2016). Both meta (Schwarzer, 2019) and metafor (Viechtbauer, 2017) are amongst 11 generic packages identified (Polanin et al., 2016). These two packages are analogs but with different inherent workflows. There is also rmeta for simple fixed and random effects meta-analyses (Lumley, 2018), mada for diagnostics (Doebler, 2017), (Doebler, 2017), netmeta for frequentist network meta statistics (Rucker et al., 2019), and mvmeta for multivariate derived data aggregations (Gasparrini, 2018) to name a few options. The latter three packages listed have distinct and specific niches for analysis whilst meta and metafor overlap considerably. Consequently, a brief contrast in facilitating choice between these two packages for the general analyst is provided here.

Contrast of meta versus metafor

Meta is a well-maintained, recently updated CRAN R package (Version 4.9-4 updated on January 3, 2019) with 31 unique functions, 7 sample datasets, and a reference manual. There is also an exceptional textbook devoted to meta-analysis in R that focuses primarily on this package (Schwarzer et al., 2015). It is highly capable of resolving most general meta-analytical challenges that an analyst will face including the capacity to include Empirical Bayes estimators as arguments in some functions, predictive meta-statistics, interaction terms, meta-regression, and modifiers. Note that for some of these methods, the rma.uni function is sourced internally from the package metafor. This is intriguing but mostly opaque and inconsequential to the user if she prefers the structure of the arguments within functions, the semantics, or the workflow of the meta package. The primary strengths include its direct and straightforward implementation with minimal (source) lines of code to do an analysis. Provided one has secured the derived data from the studies and organized into a dataframe with vectors as each key argument within the main meta-model fitting functions, statistics are simple. The type of response variable such as mean, continuous, or rate is matched to a specific function call such as metamean, metacont, or metarate. This is semantically intuitive and encourages good thinking before statistics because it engenders consideration of the data. The effect size calculation is included in this main function and defaults return the most prevalent effect size measure typically associated with those data, but it can also be specified as an argument. The primary workflow is thus a single step if the user elects to rely on the internal calculations provided in this package. Exploration of the model is well articulated with funnel, radial, and forest plots. Z-scores, significance tests, and heterogeneity statistics are printed in the model summary. Publication bias is also provided as a more in-depth function entitled metabias within this package. There are two standout functions in this package. The first is a function entitled metagen, and it is a backup, multipurpose tool so to speak that fits a generic inverse variance meta-analysis. This a handy tool for user-calculated effect size measures or for exploration of statistical trends with reduced data assumptions. In some fields, there are specific effect size estimates that this function provides a robust, easy-to-fit capacity for statistics. The second standout function is bubble.metareg for a quick, visual exploration of the outcome of a meta-regression. It is useful in contemporary data science to use visualization as a means to understand data (Lortie, 2017), but statistical packages do not always provide the means to easily iterate between statistics or model fitting and visualization. In summary, excepting unique data or statistical issues, this package is directly implemented and effective.

Metafor is a more comprehensive package in many respects. This package includes 74 functions, 35 datasets, a vignette (Viechtbauer, 2010), function flowchart as secondary vignette, and website. The package was last updated on CRAN in June of 2017 (Version 2.0-0). The text 'Meta-analysis with R' also describes implementation of this package (Schwarzer et al., 2015) but to a lesser extent than meta. The depth of the package metafor provides greater capacities relative to the meta package but does come at the expense of a steeper initial learning curve. Completing a meta-analysis using this package requires an additional step, i.e. effect sizes must be calculated a priori, not within the model fitting process. This is facilitated with the standalone function escalc, and it can return a wide range of effect sizes measures. Thus, the two-step process begins with firstly compiling and aggregating the derived dataframe to an effect size table then secondly fitting a model. The data structure is also a bit more fixed for the model fitting, and the nomenclature for this subset of functions is written to parallel more traditional general linear model fitting from conventional statistics. This is both a strength and limitation because one must plan the model to fit in advance and learn the function and arguments but it is also an advantage as well because model specification uses the familiar notation of tilde. Model fitting is based on the type of model in the call such a random or fixed effects and not on the type of the response data as in meta package. Here, it is more akin to conventional general linear model fitting for those familiar with these functions in R. If the model is more complex with moderators, then this can be directly included in the model fit here via a mods argument whereas in the meta package the model is updated with moderators in a subsequent step. This suggests that if moderators or covariates in the main model are likely relevant to the analyses, then metafor is a strong starting point. The model summary also prints z-scores, significance tests, and two sets of heterogeneity estimates. Forest and radial plots are also provided as additional functions. Publication bias statistical estimator functions include trimfill and ranktest. Standout elements of this package are primarily associated with enhanced model fitting capacities such as the function fitstats that provides log-likelihood estimates and AIC or BIC scores on meta-analysis objects. This package requires a focus on model fitting, and while there is additional effort in specifying the data at the onset of the workflow, the rewards in subsequent tools to handle models are significant.

Summary

Statistics are sometimes about preferences and thinking styles Hector (2017), and scientific synthesis is both an art and a science Lortie and Bonte (2016). Trade-offs are also common in adopting one ecosystem, analysis tool, or specific package for data wrangling and analyses. If more rapid, less specified, general meta-analyses are the goal – the package meta is a direct means to an end. Moderators are added post hoc in additional, update model steps, but the first model fit is a single, intuitive process. Meta-regression is viable and interaction terms can be included. The generic meta-analysis function is a superb tool. Metafor requires the effect size compilation a priori and is thus a bit more coding to prepare for the meta-model. However, deeper and more complex model fits are inherent in the semantics of these functions. If the synthesist does have not effect size measure in hand or wishes to calculate effect sizes measures but not for meta-models, the escalc function is invaluable in this package. In summary, both packages provide the capacity for basic and advanced meta-analyses but more advanced modelling is likely worth the commitment to metafor.

Bibliography

M. Cadotte, L. Mehrkens, and D. Menge. Gauging the impact of meta-analysis on ecology. *Evolutionary Ecology*, 26:1153–67, 2012. [p1]

P. Doebler. mada. *CRAN*, page Version 0.5.8, 2017. [p1]

A. Gasparrini. mvmeta. *CRAN*, page Version 0.4.11, 2018. [p1]

K. Gerstner, D. Moreno-Mateos, J. Gurevitch, M. Beckmann, S. Kambach, H. P. Jones, and R. Seppelt. Will your paper be used in a meta-analysis? make the reach of your research broader and longer lasting. *Methods in Ecology and Evolution*, 8(6):777–784, 2017. ISSN 2041-210X. doi: 10.1111/2041-210X.12758. URL http://dx.doi.org/10.1111/2041-210X.12758. [p1]

A. Hector. *The New Statistics with R*. Oxford University Press, Oxford, 2017. ISBN 978-0198729051. [p3]

J. Lai, C. J. Lortie, R. A. Muenchen, J. Yang, and K. Ma. Evaluating the popularity of r in ecology. *Ecosphere*, 10(1):e02567, 2019. ISSN 2150-8925. doi: 10.1002/ecs2.2567. URL https://doi.org/10.1002/ecs2.2567. [p1]

C. Lortie. R for data science. *Journal of Statistical Software*, 77:1–3, 2017. doi: 10.18637/jss.v077.b01. URL https://www.jstatsoft.org/index.php/jss/article/view/v077b01. [p2]

C. J. Lortie. Formalized synthesis opportunities for ecology: systematic reviews and meta-analyses. *Oikos*, 123:897–902, 2014. [p1]

C. J. Lortie and D. Bonte. Zen and the art of ecological synthesis. *Oikos*, 125(3):285–287, 2016. ISSN 1600-0706. doi: 10.1111/oik.03161. URL http://dx.doi.org/10.1111/oik.03161. [p1, 3]

T. Lumley. rmeta. *CRAN*, page Version 3.0, 2018. [p1]

S. Nakagawa, D. W. A. Noble, A. M. Senior, and M. Lagisz. Meta-evaluation of meta-analysis: ten appraisal questions for biologists. *BMC Biology*, 15(1):18, 2017. ISSN 1741-7007. doi: 10.1186/s12915-017-0357-7. URL https://doi.org/10.1186/s12915-017-0357-7. [p1]

J. R. Polanin, E. A. Hennessy, and E. E. Tanner-Smith. A review of meta-analysis packages in r. *Journal of Educational and Behavioral Statistics*, 42(2):206–242, 2016. ISSN 1076-9986. doi: 10.3102/1076998616674315. URL https://doi.org/10.3102/1076998616674315. [p1]

M. Rosenberg, D. Adams, and J. Gurevitch. *MetaWin: Statistical software for meta-analysis. Version 2.0*. 2000. [p1]

G. Rucker, U. Krahn, J. Konig, O. Efthimious, and G. Schwarzer. netmeta. *CRAN*, 1.0.1:Version 1.0.1, 2019. [p1]

G. Schwarzer. meta. *CRAN*, page Version 4.94, 2019. [p1]

G. Schwarzer, J. Carpenter, and G. Rücker. *Meta-Analysis with R*. Springer, Switzerland, 2015. ISBN 978-3-319-21416-0. [p2]

G. B. Stewart and C. H. Schmid. Lessons from meta-analysis in ecology and evolution: the need for trans-disciplinary evidence synthesis methodologies. *Research Synthesis Methods*, 6:109–110, 2015. doi: 10.1002/jrsm.1152. URL https://doi.org/10.1002/jrsm.1152. [p1]

W. Viechtbauer. Conducting meta-analyses in r with the metafor package. *J Stat Software*, 36, 2010. doi: 10.18637/jss.v036.i03. URL https://doi.org/10.18637/jss.v036.i03. [p2]

W. Viechtbauer. metafor. *CRAN*, page Version 2.0, 2017. [p1]

Christopher J. Lortie
The National Center for Ecological Analysis and Synthesis, UCSB
735 State St. Santa Barbara
USA
ORCID
chris@christopherlortie.info