Bull. Aust. Math. Soc. **114** (2026), 564–565
doi:10.1017/S0004972726101804

NEW STATISTICAL TOOLS FOR META-ANALYSIS IN ECOLOGY AND EVOLUTIONARY BIOLOGY

CORALIE WILLIAMS

(Received 25 June 2026; first published online 3 August 2026 UTC)

2020 *Mathematics subject classification*: primary 62P10; secondary 62-04, 62A01, 62J05, 62J12, 92-08, 92-10.

Keywords and phrases: research synthesis, inverse-variance meta-analysis, phylogenetic comparative analysis, meta-research, reporting practices, Monte Carlo simulation, meta-analysis software.

Meta-analysis is a statistical method that synthesises evidence across primary studies to reveal general patterns and sources of variation. In ecology and evolutionary biology, meta-analysis helps identify trends across broad temporal, spatial scales and across species. However, datasets in these fields often contain multiple, nonindependent effect sizes arising from shared studies, multiple species and their phylogenetic relatedness, or experimental designs, which can violate the assumptions of traditional meta-analytic models.

Mixed-effects models (also called multilevel or hierarchical models) offer a flexible way to account for these dependencies and support more robust inference. Although implementations exist, accessible and fast tools for meta-analytic and phylogenetic applications are limited. The R package glmmTMB is a broad-purpose mixed-effects model software that provides efficient estimation and flexible random effect covariance structures. This thesis evaluates statistical tools across three strands: modelling approaches, software implementation and simulation studies.

First, I propose reporting items for simulation studies used in statistical methods research, expanding on recent recommendations and informed by a survey I carried out of simulation studies in ecology and evolutionary biology [1]. Second, I assess modelling approaches for handling dependent effect size estimates and sampling errors in ecology and evolution meta-analysis [2]. Third, I evaluate an implementation in the glmmTMB package for fitting phylogenetic generalised linear mixed models (GLMMs), comparing speed, convergence and model estimates with existing

Thesis submitted to the University of New South Wales in December 2025; degree approved on 30 March 2026; supervisors Shinichi Nakagawa and David Warton.

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https://doi.org/10.1017/S0004972726101804 Published online by Cambridge University Press

R implementations. Fourth, I develop a covariance structure in glmmTMB to fit meta-analysis by incorporating known sampling variances.

Through this work, I attempt to advance evidence synthesis tools for ecology and evolutionary biology applications by linking developments in statistical modelling with new software implementations and by promoting improved reporting standards for more transparent methodological research.

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CORALIE WILLIAMS, School of Mathematics and Statistics,
University of New South Wales, Sydney, New South Wales 2052, Australia
e-mail: coraliewilliams@outlook.com

https://doi.org/10.1017/S0004972726101804 Published online by Cambridge University Press