

Guidelines to validating generalized linear mixed models in Template Model Builder using quantile residuals.

Model validation, whether via graphical examination or formal hypothesis tests, is a crucial step in statistical analyses to alert the analyst to potential model misfit. Unlike model selection, where models are compared relative to each other, model validation looks for inadequacies in a single model and helps identify likely causes and thus potential solutions. Generalized linear mixed models (GLMMs) are now ubiquitous in the ecological literature, yet well-established protocols for model validation are lacking compared to generalized linear models. This is partly because Pearson residuals are unreliable for model validation, and the more appropriate quantile residuals are more difficult to calculate and interpret.

Here, we review two distinct statistical approaches for quantile residuals: one-step-ahead (OSA) and simulation residuals via DHARMA, both of which are readily available in the popular TMB package. We review the statistical properties, interpretation, and calculation of each method and their variants, including their application in TMB. We test the calibration of p-values from normality tests of residuals using simulation on three examples: a LMM, time series model, and spatial model. We also provide examples of several different types of common mis-specifications in ecology to demonstrate appropriate model validation statistics and test whether the mis-specified models fail validation. In certain cases, simulation residuals were faster to calculate and had good performance, but OSA residuals were better in the multivariate context. Overall, the flexibility of generalized linear mixed models can affect the power needed to detect model mis-specification.