Figure 1: The Salamander data set was replicated by 1, 2, 4, 6, 8, and 10 times to create larger data sets. The time required to fit the same model using functions `glmmadmb,glmmTMB,inla, glmer.nb`, and `gam` was recorded. That model can be represented as `glmmTMB(count ~ spp * mined + (1 | site), Salamanders, family="nbinom2")`. All models had the same number of parameters including random effect levels. Lines represent linear models fit on the log-log scale. With increasing numbers of observations (n), estimation times increased as a power-law function (n^x) with exponents (x) reported next to model names.

default number of iterations, burn-in samples, and thinning. In each package, we fit zero-inflated Poisson models with six fixed effects, one random effect; we also accounted for overdispersion, although sometimes (of necessity) in slightly different ways with different packages (e.g., negative binomial vs. log-normal-Poisson models). We allowed zero-inflation to vary with food treatment and vary randomly with nest. See Appendix B for details of these methods, including code.

Estimates and confidence (or credible) intervals (CI) from **brms**, **mgcv**, MCMCglmm, and **INLA** were nearly identical to those of **glmmTMB**, when running the Bayesian models with flat priors (Figures 8 and 9).

Conclusions

We have introduced an R package that can quickly estimate a variety of models including GLMs, GLMMs, zero-inflated GLMMs, and hurdle models. By providing this flexibility in a single package, we reduce the need for researchers to learn multiple packages. Another benefit is that models estimated with a single package can be compared using likelihood-based methods including information criteria. Using information criteria to select a model for the salamander data, we found that (among the models we considered) zero-inflation did not improve the fit; we expect that this will be a common result. While **glmmTMB** allows users to easily fit complicated models, a maximally complex model might not be necessary and might not converge, as we saw here. Other packages have many of the features implemented in **glmmTMB**, but none have the ability to fit Conway-Maxwell-Poisson GLMMs. Overall, **glmmTMB** is a very flexible package for modeling count data with zero-inflated GLMMs while still ranking highly in speed comparisons.

Acknowledgements