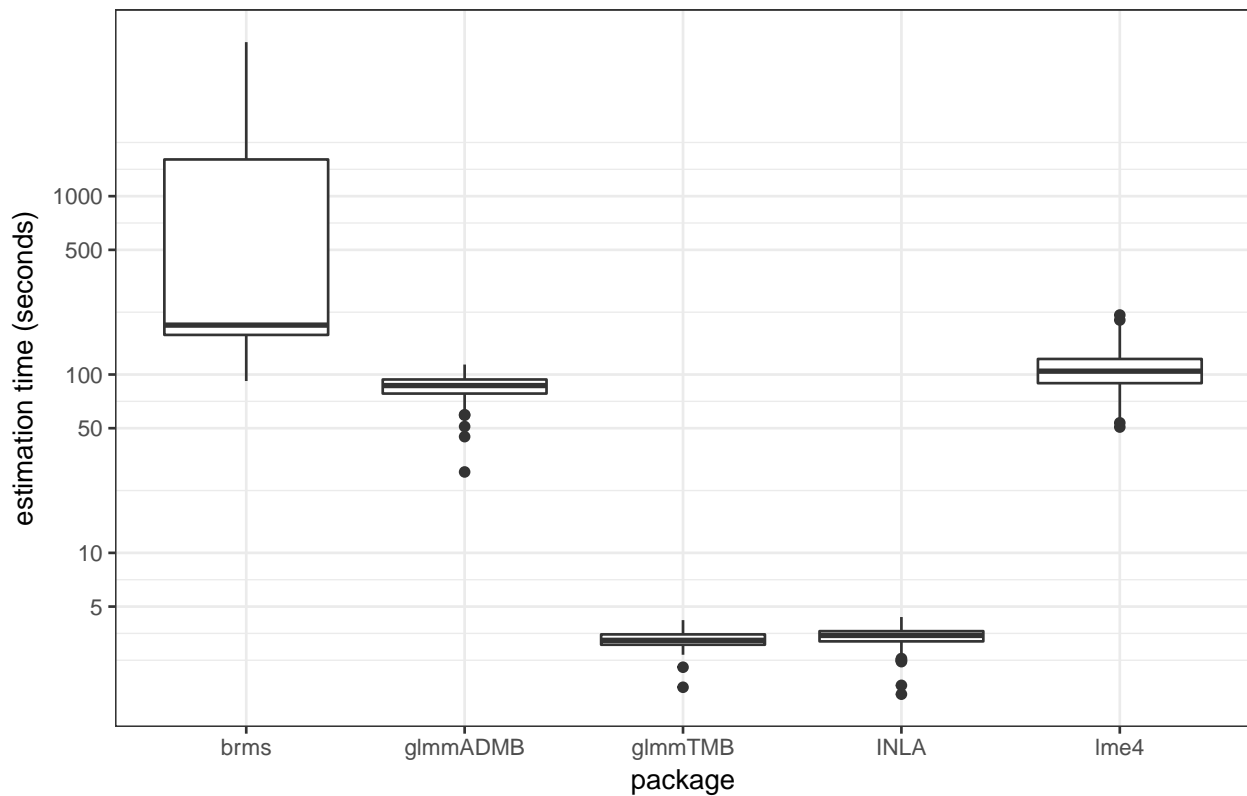


# Appendix A: Speed comparison for negative binomial GLMMs

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These supplementary figures and tables present benchmarking that was done using the Salamander data that was analyzed in appendix A (Price et al. 2016; Price et al. 2015). We compare the timing of functions `glmmTMB`, `glmmadmb`, `glmer.nb`, `brm`, and `inla` (Skaug et al. 2012; Bates et al. 2015; Bürkner in press; Rue, Martino, and Chopin 2009). We used the defaults of each function. However, it would be possible to speed up `brm` by saving the compiled C++ file or using multiple computing cores; it would be possible to speed up `inla` by giving it access to more cores.



*Figure A.1* - Estimation times for fitting models to 100 simulated data sets using functions `glmmTMB`, `glmmadmb`, `glmer.nb`, `brm`, and `inla`. The estimated model was identical to the model used for simulation and can be represented as `glmmTMB(count ~ spp * mined + (1|site), Salamanders, family="nbinom2")`.

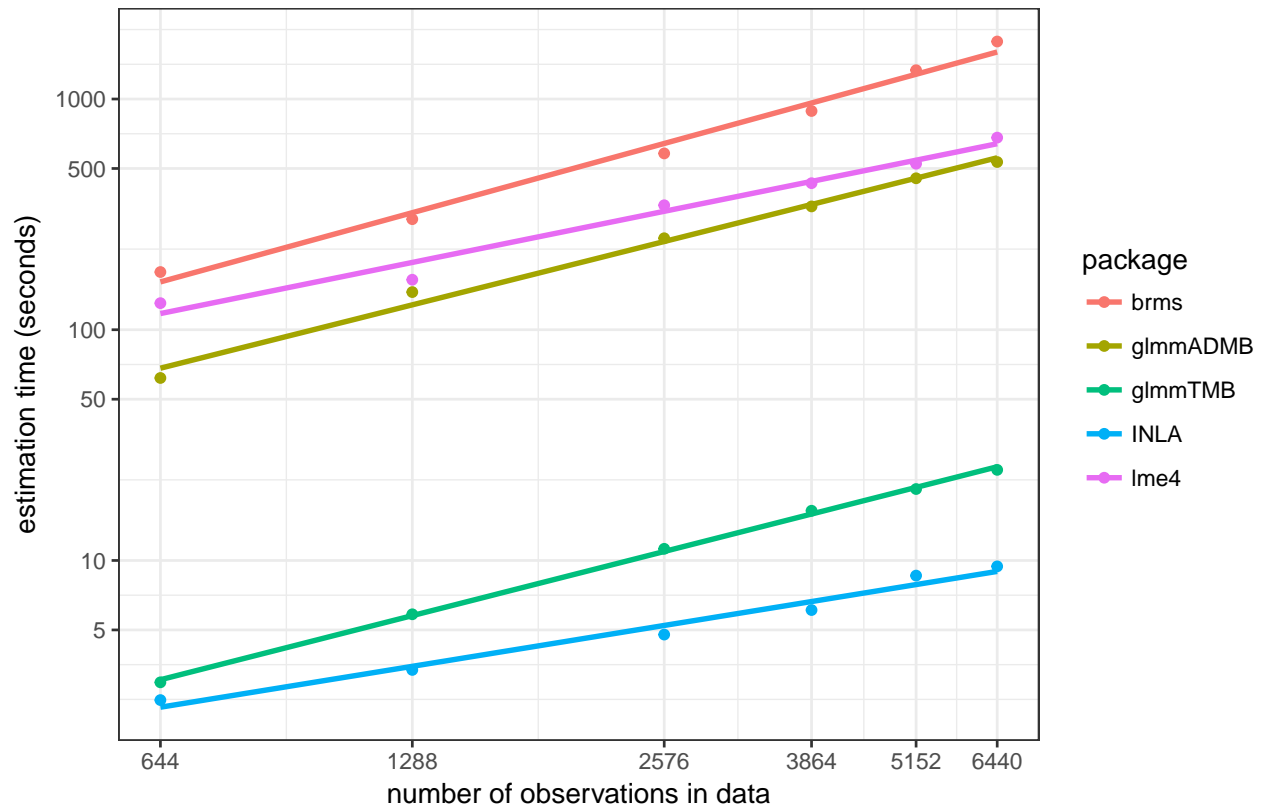


Figure A.2 - The Salamander data set was replicated by 1, 2, 4, 6, 8, and 10 times to create larger data sets. The time required to fit the same model using functions `glmmTMB`, `glmmadmb`, `glmer.nb`, `brm`, and `inla` was recorded. That model can be represented as `glmmTMB(count ~ spp * mined + (1|site), Salamanders, family="nbinom2")`. All models had the same number of parameters including random effect levels.

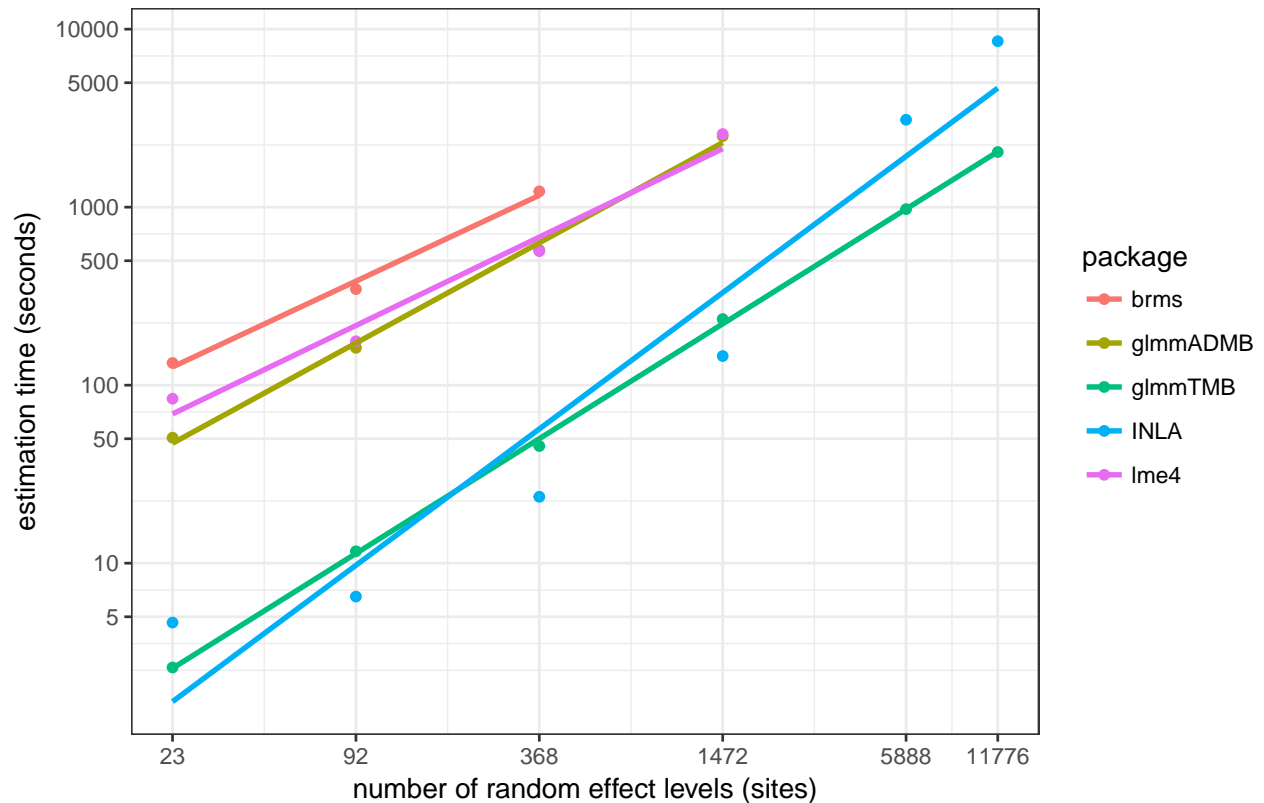


Figure A.3 - Data sets with increasing numbers of levels of the random effect were simulated based on the most parsimonious model fit to the salamander data, `glmmTMB(count ~ spp * mined + (1|site), Salamanders, family="nbinom2")`. The time required to fit the same model using functions `glmmTMB`, `glmmadmb`, `glmer.nb`, `brm`, and `inla` was recorded. Each simulated data set had the same number of observations per random effect level — the same ratio as in the original data.

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