

Figure 1. Residual diagnostic plots for the GLMM model predicting beetle species richness. The plots assess model assumptions including linearity, homoscedasticity, and normality of residuals. The residuals appear approximately normally distributed with no strong patterns, suggesting the model assumptions are reasonably met.

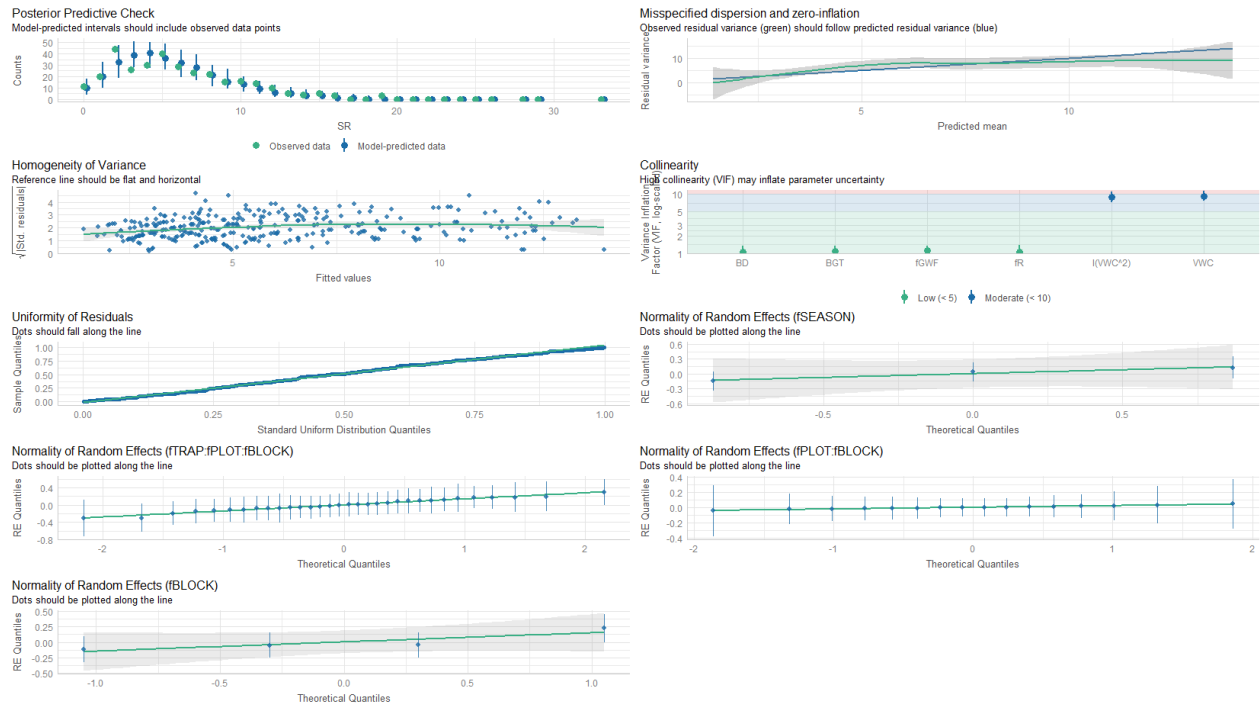


Figure 2. Residual diagnostic plots for the GLMM model predicting beetle abundance. The plots assess model assumptions including linearity, homoscedasticity, and normality of residuals. The residuals appear approximately normally distributed with no strong patterns, suggesting the model assumptions are reasonably met.

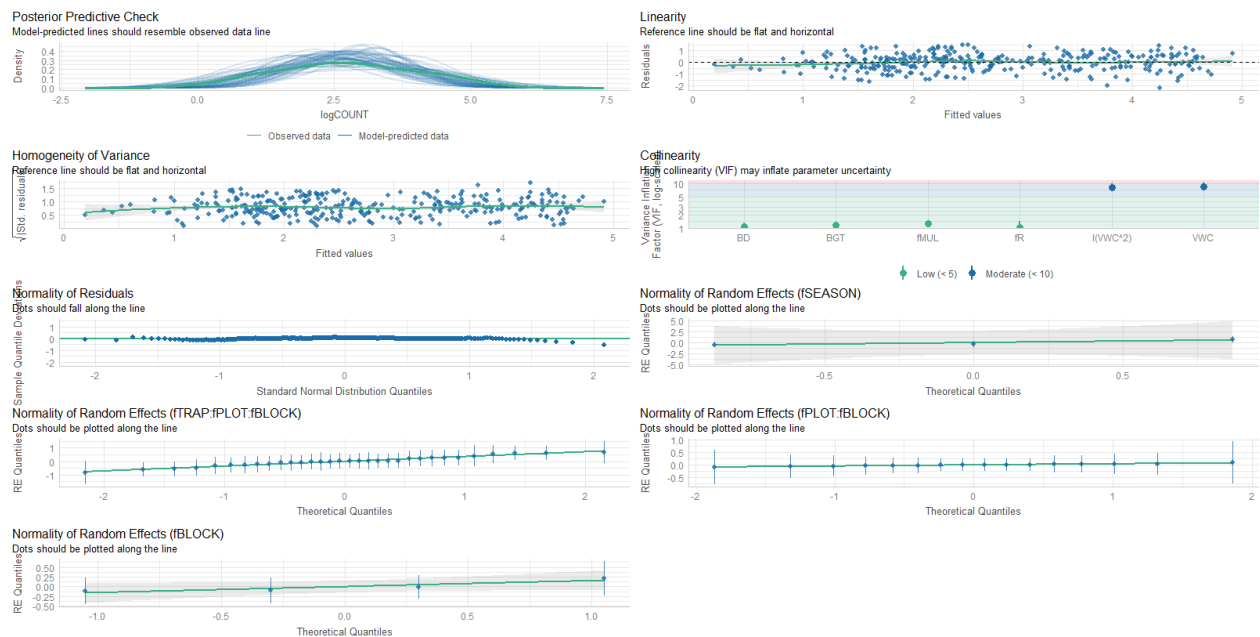


Figure 3. Residual diagnostic plots for the Poisson GLLVM indicated moderate deviation from normality and a slight fan-shaped pattern in the residuals, suggesting violations of model assumptions and inadequate handling of overdispersion in the data.

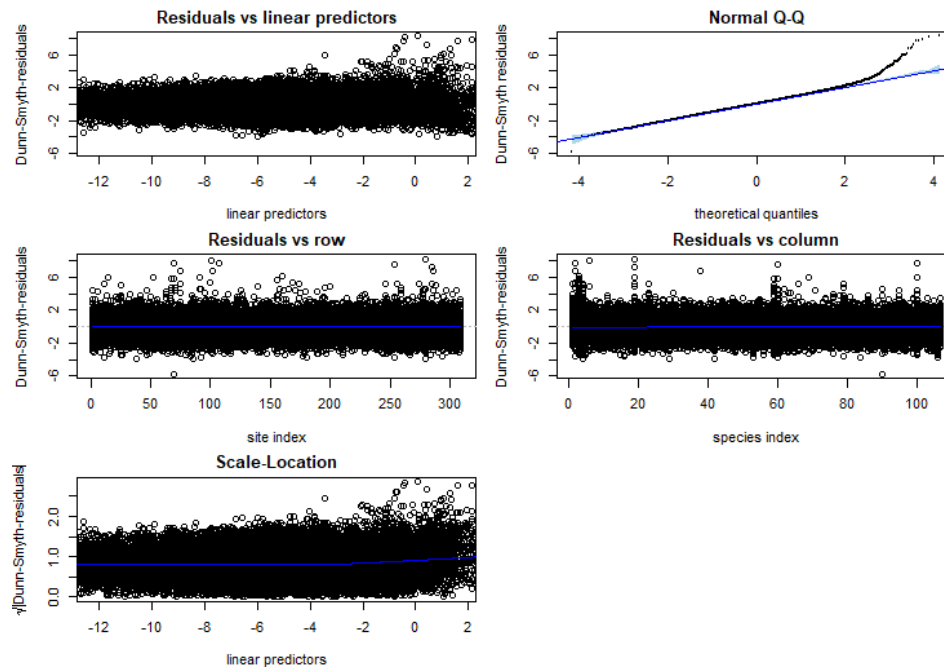


Figure 4. Residual diagnostic plots for the negative binomial GLLVM showed residuals approximately normally distributed with no clear patterns or heteroscedasticity. These results suggest that the model adequately accounts for overdispersion in the data, supporting the suitability of the negative binomial family.

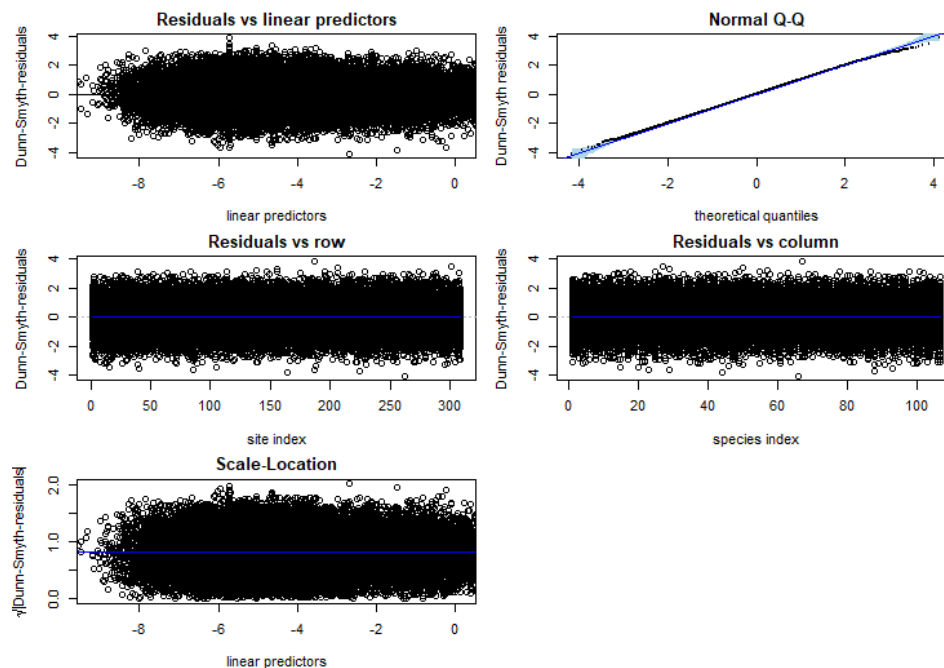


Figure 5. Residual diagnostic plots for `num.1v`

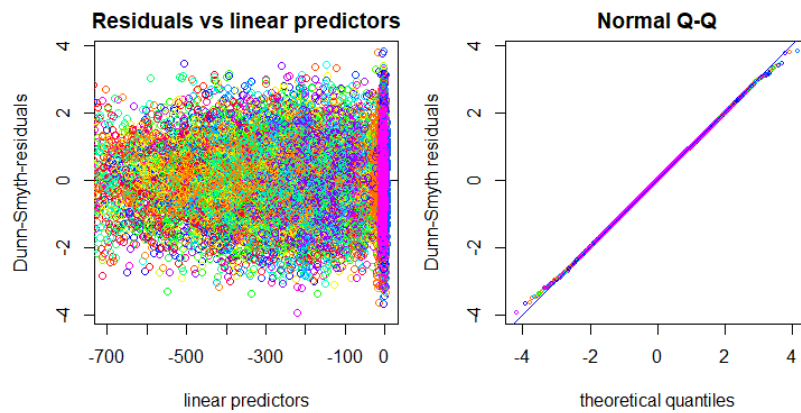


Figure 6. Residual diagnostic plots for the negative binomial GLLVM for the best model showed residuals approximately normally distributed with no clear patterns or heteroscedasticity. These results suggest that the model adequately accounts for overdispersion in the data, supporting the suitability of the negative binomial family.

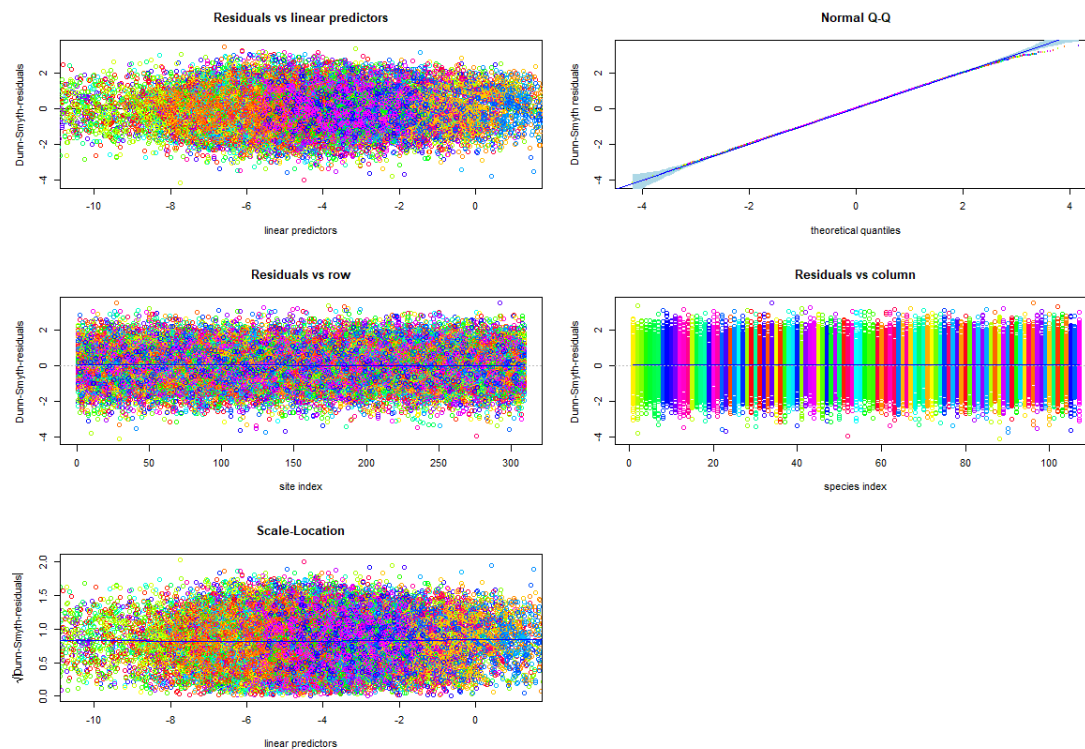


Figure 7. Residual diagnostic plots for the Beta family GLMM predicting FRic.

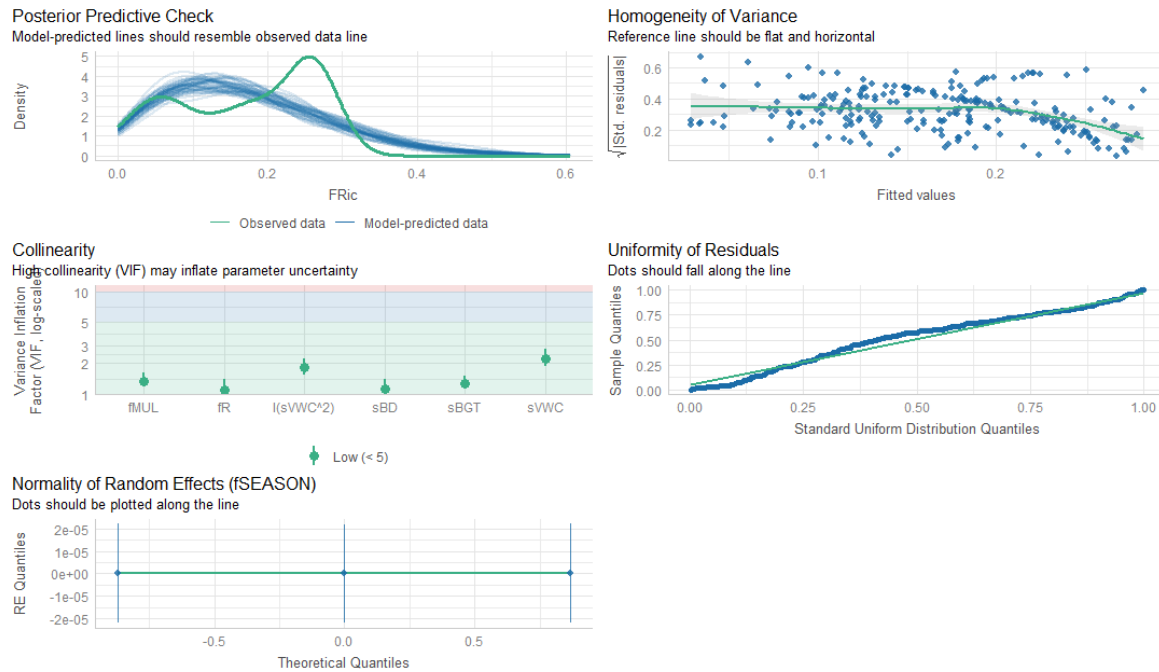


Figure 8. Residual diagnostic plots for the Beta family GLMM predicting FEve.

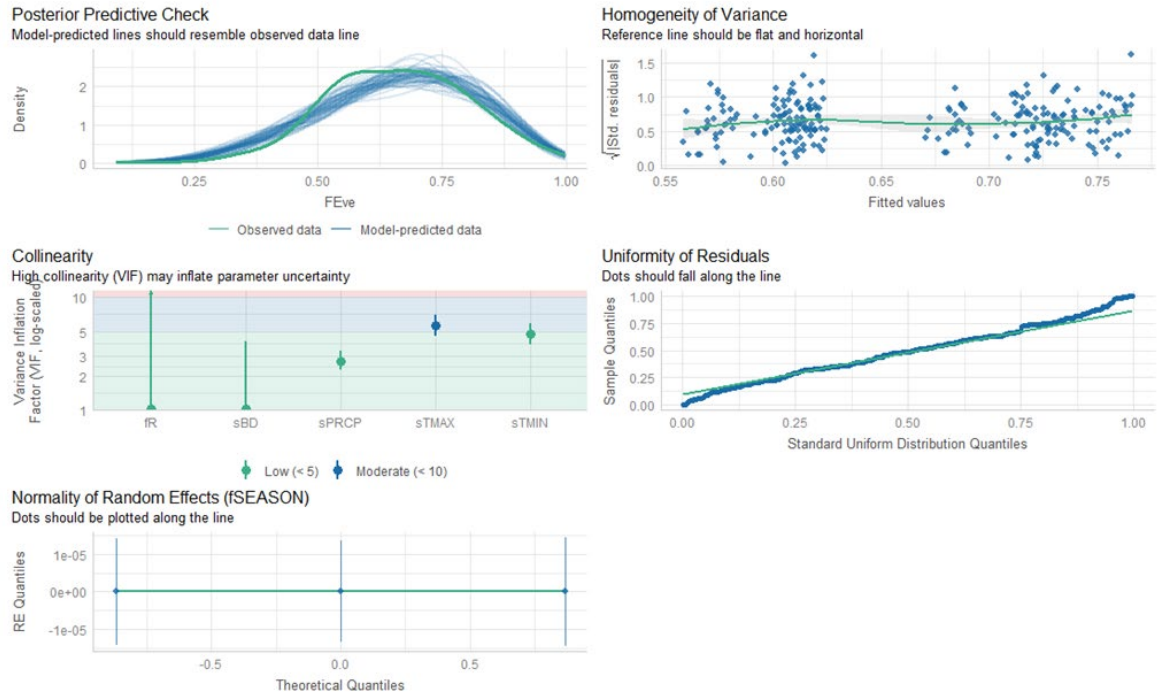


Figure 9. Residual diagnostic plots for the Beta family GLMM predicting FDiv

