

Variable	Example	Type of Regression	R function / R function for mixed models
Continuous	Quality of Life, linear scales	linear	<code>lm()</code> <code>lmer()</code> , <code>glmmTMB()</code>
Binary	Success yes/no	binary logistic	<code>glm(family=binomial)</code> <code>glmer(*)</code> , <code>glmmTMB(*)</code>
Trials (or proportion of counts)	20 successes out of 30 trials	logistic ¹	<code>glm(cbind(trials, success), family=binomial)</code> <code>glmer(*)</code> , <code>glmmTMB(*)</code>
Count data	Number of usage, counts of events	Poisson	<code>glm(family=poisson)</code> <code>glmer(*)</code> , <code>glmmTMB(*)</code>
Count data, with excess zeros or overdispersion	Number of usage, counts of events (with higher variance than mean of response)	negative binomial	<code>glm.nb()</code> <code>glmer.nb()</code> , <code>glmmTMB(family=nbinom)</code>
Count data with very many zeros (inflation)	see count data, but response is modelled as mixture of Bernoulli & Poisson distribution (two sources of zeros)	zero-inflated	<code>zeroinfl()</code> <code>glmmTMB(ziformula, family=poisson)</code>
Count data, with very many zeros (inflation) and overdispersion	Number of usage, counts of events (with higher variance than mean of response)	zero-inflated negative binomial	<code>zeroinfl(dist="negbin")</code> <code>glmmTMB(ziformula, family=nbinom)</code>
Count data, zero-truncated	see count data, but only for positive counts (hurdle component models zero-counts)	hurdle (Poisson)	<code>hurdle()</code> <code>glmmTMB(family=truncated_poisson)</code>
Count data, zero-truncated and overdispersion	see "Count data, zero-truncated", but with higher variance than mean of response	hurdle (neg. binomial)	<code>vglm(family=posnegbinomial)</code> <code>glmmTMB(family=truncated_nbinom)</code>
Proportion / Ratio (without zero and one)	Percentages, proportions of <i>continuous</i> data	Beta ¹	<code>betareg()</code> <code>glmmTMB(family=beta)</code>
Proportion / Ratio (including zero and one)	Percentages, proportions of <i>continuous</i> data	Beta-Binomial	<code>BBreg()</code> , <code>betabin()</code> , <code>vglm(family=betabinomial)</code>
Ordinal	Likert scale, worse/ok/better	ordinal, proportional odds	<code>polr()</code> , <code>clm()</code> <code>clmm()</code> , <code>mixor()</code> , <code>MCMCglmm()</code>
Cumulative, multinomial	No natural order of categories, like red/green/blue	cumulative link, multinomial	<code>multinom()</code> , <code>clm()</code> , <code>brmultinom()</code> <code>clmm()</code> , <code>mixor()</code> , <code>MCMCglmm()</code>
Continuous, right-skewed	Financial data, reaction times	Gamma	<code>glm(family=Gamma)</code> <code>glmer(*)</code> , <code>glmmTMB(*)</code>
Continuous, (right) skewed, with excess zeros	Financial data	Tweedie	<code>glm(family=tweedie)</code> , <code>cpglm()</code> <code>cpglm()</code> , <code>glmmTMB(family=tweedie)</code>
Continuous, but truncated or outliers		truncated	<code>censReg()</code> , <code>tobit()</code> , <code>vglm(family=tobit)</code>
Proportion / Ratio with > 2 categories	Biomass partitioning in plants (ratio of leaf, stem and root mass)	Dirichlet	<code>DirichReg()</code>

* Indicates same family-option for mixed models as for their non-multilevel counterparts.

¹ Note that ratios or proportions from count data, like `cbind(trials, success)`, are modelled as logistic regression with `glm(cbind(trials, success), family=binomial())`, while ratios from continuous data where the response ranges from 0 to 1 are modelled using beta-regression.