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| Variable | Example | Type of Regression | R function / R function for mixed models |
| Continuous | Quality of Life, linear scales | linear | lm() |
| lmer(), glmmTMB() |
| Binary | Success yes/no | binary logistic | glm(family=binomial) |
| glmer(\*), glmmTMB(\*) |
| Trials (or proportion of *counts*) | 20 successes out of 30 trials | logistic1 | glm(cbind(trial,success), family=binomial) |
| glmer(\*), glmmTMB(\*) |
| Count data | Number of usage, counts of events | Poisson | glm(family=poisson) |
| glmer(\*), glmmTMB(\*) |
| Count data, with excess zeros or overdispersion | Number of usage, counts of events (with higher variance than mean of response) | negative binomial | glm.nb() |
| glmer.nb(), glmmTMB(family=nbinom) |
| Count data with very many zeros (inflation) | see count data, but response is modelled as mixture of Bernoulli & Poisson (two sources of zeros) | zero-inflated | zeroinfl() |
| glmmTMB(ziformula, family=poisson) |
| 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 | zeroinfl(dist="negbin") |
| glmmTMB(ziformula, family=nbinom) |
| Count data, zero-truncated | see count data, but only for positive counts (hurdle component models zero-counts) | hurdle (Poisson) | hurdle() |
| glmmTMB(family=truncated\_poisson) |
| Count data, zero-truncated and overdispersion | see “Count data, zero-truncated”, but with higher variance than mean of response | hurdle (neg. binomial) | vglm(family=posnegbinomial) |
| glmmTMB(family=truncated\_nbinom) |
| Proportion / Ratio (without zero and one) | Percentages, proportions of *continuous* data | Beta1 | betareg() |
| glmmTMB(family=beta) |
| Proportion / Ratio (including zero and one) | Percentages, proportions of *continuous* data | Beta-Binomial, zero-inflated Beta | BBreg(), betabin(), vglm(family=betabinomial) |
| glmmTMB(ziformula, family=beta\_family/ betabinomial) |
| Ordinal | Likert scale, worse/ok/better | ordinal, pro-portional odds | polr(), clm() |
| clmm(), mixor(), MCMCglmm() |
| Cumulative, multinomial | No natural order of categories, like red/green/blue | cumulative link, multinomial | multinom(), clm(),bracl(), brmultinom() |
| clmm(), mixor(), MCMCglmm() |
| Continuous, right-skewed | Financial data, reaction times | Gamma | glm(family=Gamma) |
| glmer(\*), glmmTMB(\*) |
| (Semi-)Continuous, (right) skewed, probably spike at zero (zero-inflation) | Financial data, probably exponential dispersion of variance | Tweedie | glm(family=tweedie), cpglm() |
| cpglmm(),glmmTMB(family=tweedie) |
| (Semi-)Continuous, skewed, zero-inflation | Normal distribution, negative values censored and stacked on zero | Tobit | censReg(), tobit() |
| semLme() |
| Continuous, but truncated or outliers |  | truncated | censReg(), tobit(), vglm(family=tobit) |
| Proportion / Ratio with > 2 categories | Biomass partitioning in plants (ratio of leaf, stem and root mass) | Dirichlet | DirichReg() |
| Time-to-Event | Survival-analysis, time until event/death occurs | Cox (proportional hazards) | coxph() |
| coxme() |

\* 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.