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# A versatile workflow for linear modelling in R

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Linear models are applied widely to analyse empirical data. Modern software allows implementation of linear models with a few clicks or lines of code. While convenient, this increases the risk of ignoring essential assessment steps. Indeed, inappropriate application of linear models is an important source of inaccurate statistical inference. Despite extensive guidance and detailed demonstration of exemplary analyses, many users struggle to implement and assess their own models. To fill this gap, we present a versatile R-workflow template that facilitates (Generalized) Linear (Mixed) Model analyses. The script guides users from data exploration through model formulation, assessment and refinement to the graphical and numerical presentation of results. The workflow accommodates a variety of data types, distribution families, and dependency structures that arise from hierarchical sampling. To apply the routine, minimal coding skills are required for data preparation, naming of variables of interest, linear model formulation, and settings for summary graphs. Beyond that, default functions are provided for visual data exploration and model assessment. Focused on graphs, model assessment offers qualitative feedback and guidance on model refinement, pointing to more detailed or advanced literature where appropriate. With this workflow, we hope to contribute to research transparency, comparability, and reproducibility.

## KEYWORDS

GLMMs, glmmTMB, linear models, model assessment, residual analysis, R-workflow, posterior predictive checks

## 1. Introduction

Complex statistical tools for the analysis of empirical datasets are widely available today. Open-source software such as R provides unrestricted access to such advanced techniques (R Core Team, 2017), where a single line of code often suffices to implement or summarise complex models (Harrison et al., 2018). While this is convenient, it also increases the risk that essential steps of data exploration or model assessment are ignored (Zuur et al., 2010; Zuur and Ieno, 2016). This risk aggravates with lack of time or experience to perform the analysis, and can result in statistical models that insufficiently reflect data dependency structures, commit pseudoreplication, or violate other key model assumptions (Hurlbert, 1984; Quinn and Keough, 2002; Bolker et al., 2009; Zuur and Ieno, 2016; Colegrave and Ruxton, 2018; Harrison et al., 2018; Gelman et al., 2020). Indeed, Bolker et al. (2009) reported that 311 out of 537 (58%) published GLMM analyses in evolution and ecology had used statistical tools inappropriately, a problem that extends beyond the biological sciences (Taper, 2004; Campbell, 2021).

A widely used statistical technique is the linear model. It describes the relationship between one response variable as a function of one or multiple predictors (Montgomery et al., 2021). Basic linear models assume a Gaussian distribution family (LMs: Linear Models). Yet, they can also be implemented with other distributions to analyse skewed, count, or proportional responses (GLMs: Generalized Linear Models), with random effects to deal with repeated or hierarchical sampling designs (LMMs: Linear Mixed Models), or with both (GLMMs: Generalized Linear Mixed Models).

The concepts and applications of linear models have been extensively treated elsewhere (Bolker et al., 2009; Zuur et al., 2009, 2013a; Bolker, 2015; Korner-Nievergelt et al., 2015; Harrison et al., 2018; Gelman et al., 2020; Silk et al., 2020). Previous studies also offer worked examples, best-practice guidelines and troubleshooting advice for data exploration and transformation (Zuur et al., 2010), the specification of fixed and random terms, the implementation of interactions or correlation structures (Bolker et al., 2009; Harrison et al., 2018), model assessment (Harrison et al., 2018), and reporting of results (Zuur and Ieno, 2016). Several R packages such as *performance* (Lüdtke et al., 2020a), *visreg* (Breheny and Burchett, 2017) or *DHARMA* (Hartig and Lohse, 2020) offer convenient support for data exploration and model assessment. However, less experienced data analysts still struggle to gather, read, and correctly apply all these recommendations to produce code tailored to their own analyses, and to draw well-informed conclusions.

We here present a richly commented and user-friendly step-by-step workflow for linear models in R, based on the package *glmmTMB* (Brooks et al., 2017). The template R script provided as an online supplement accommodates a wide variety of data structures and covers data exploration, initial model formulation, thorough model assessment, model refinement, as well as numerical and graphical result summaries. It also points users to advanced literature sources where advisable. In this workflow, coding by users is only required to import the data and check its structure, assign names to relevant variables, formulate the linear model, and specify predictors and grouping variables for model assessment, the extraction of parameter estimates, and the final visualisation of results.

Our routine facilitates the implementation of a comprehensive analysis workflow for model formulation, assessment and reporting, but assumes conceptual understanding of the principles of statistics, and at least basic R coding skills. Note that this workflow cannot mitigate inappropriate experimental designs or non-representative sampling strategies (Gelman et al., 2020), and it should not be mistaken as a comprehensive guidance to all aspects of linear modelling.

## 2. The guided workflow

The workflow requires a data structure where rows represent single observations and columns represent a single response, one or more predictors, and optionally one or more grouping variables that describe the dependency structure of the observations. Prior to analysis, users need to carefully inspect their dataset for typing errors and correct assignment of all variables to numeric, integer, or factor vector classes.

First, users specify the variables (= columns or vectors) of interest (Figure 1). The script then produces default displays that guide users

through graphical data exploration (modified from Zuur et al., 2010). Based on these, users formulate an initial linear model. Next, the script produces graphical output to support model assessment, and eventual refinement (return back to model formulation). Model assessment and refinement continue until users have identified an adequate final model. The script then provides access to model results and parameter estimates. Finally, it produces publication-ready graphs that combine raw data with model predictions for up to two-way predictor interactions. The template script (*Linear modelling workflow\_template.R*) automatically imports all functions needed for the workflow from a second R script (*Linear modelling workflow\_support\_functions.R*).

## 3. Definition of variables

All variables considered for the model must be part of a single R dataframe. Users assign all dataframe columns that might be relevant for their model to any of the labels listed below. Specifying a response variable is compulsory. Labels with no variable assigned should be defined as not available (NA).

### 3.1. One response variable

The first object, *var\_resp*, requires the name of a single response variable of vector class numeric or integer. This can be any quantitative measure, but also a binary response such as presence/absence, dead/alive, or failure/success coded as zeros and ones (examples in Table 1).

### 3.2. Fixed predictor variables

Fixed predictors may include any quantitative (i.e., numerical covariates) or categorical variables (i.e., factors) that are used to predict variation in the response variable (cf. Bolker et al., 2009). They can describe properties of study subjects (e.g., body size) or the experimental design (e.g., treatment groups).

- *var\_num*: Name(s) of quantitative predictor variable(s), assigned to vector classes numeric or integer.
- *var\_fac*: Name(s) of categorical predictor variable(s) with defined grouping levels, assigned to vector class factor.

### 3.3. Random predictor variables

Linear models assume that observations are independent (Hurlbert, 1984), i.e., that the response measure of a given replicate is independent of any other such measurement for the given (combination of) predictor(s). This assumption is usually violated when study subjects are measured repeatedly or datasets contain a spatial or temporal structure, e.g., among replicated experimental blocks or sequential sampling bouts. Ignoring such dependencies among observations in a statistical analysis generates pseudoreplication (Hurlbert, 1984; Zuur and Ieno, 2016; Colegrave and Ruxton, 2018; Harrison et al., 2018), and thus an underestimation of the uncertainty associated with the estimated model parameters (Korner-Nievergelt et al., 2015). Linear models can account



TABLE 1 Recommended response distribution families and link functions for initial model formulation. See Table 2 in section 6 for possible refinements after model assessment.

Response variable	Response features	Distribution family	Family indicator in glmmTMB	Link	Options for offsets and weights
Continuous measure	Real, symmetrical	Normal	gaussian	identity	
Continuous measure	Real $\geq 0$ , right skew	Gamma	Gamma	log	
Continuous measure	Real $\geq 0$ , right skew	Tweedie	tweedie	log	
Discrete counts	Integer $\geq 0$	Poisson	poisson	log	Offset to model count densities or rates (detail in section 5.2.1)
Proportions from trials <sup>a</sup>	$0 \leq \text{real} \leq 1$	Binomial	binomial	logit	Weight needed to specify the number of trials (detail in section 5.2.1)
Bounded measure	$0 < \text{real} < 1$	Beta	Beta_family	logit	

<sup>a</sup>This is identical to specifying a two-column integer matrix with counts of successes and failures as response variable. The workflow performs best when the response is a one-column vector with proportions, combined with a weight term that specifies the number of trials.

(2) Adding random predictors does not automatically remove every source of pseudoreplication – it is essential that the (combination of) random predictors correctly reflects the dependency structure in the data. (3) When the model contains at least two random predictors, we recommend defining each level with a unique label to avoid misspecification of nested random predictors. For example, five replicate study sites for each experimental block (from A to G) should be labeled from 1 to 5 in block A, from 6 to 10 in block B, etc., and not as repetitive labels 1 to 5 in each block.

### 3.4. Temporal and spatial data structure

In this step, users optionally can specify variables that describe temporal or spatial structure in their data. These variables will be used to assess temporal or spatial autocorrelation in model residuals (see section 6.3), a potential source of non-independence that usually generates overly narrow precision estimates. Note that autocorrelation can arise even if the spatial or temporal variables are also specified as fixed predictors in the model.

- *var\_time*: Name of one numeric vector that specifies temporal information (e.g., sampling year, date, or time).
- *var\_time\_groups* (optional): Name of one factor vector that structures *var\_time* for multiple independent time series.
- *var\_space*: Names of two numeric vectors that specify spatial information on sampling locations as x- and y-coordinates. Both coordinates should be expressed in the same units, and preferably derive from a (roughly) equidistant projection (such as UTM or Gauss-Krueger).

### 3.5. Missing values

Missing values are dataframe entries with no available value (i.e., NA). Because NAs are problematic for model computation, the script excludes by default rows with a missing value for any of the variables specified in the previous steps. Missing values should not occur disproportionately often in particular data subgroups (e.g., a higher fraction of NAs for a particular sex, life-stage, species or study site).

The script generates a separate dataframe that contains all excluded data rows, which allows users to check this assumption.

## 4. Raw data exploration

The script guides users to screen raw data for any pattern that may affect model formulation. We focus on graphical over numerical exploration in accordance with common practice in the field (Gelman et al., 2002; Quinn and Keough, 2002; Läärä, 2009; Zuur et al., 2010; Ieno and Zuur, 2015; Montgomery et al., 2021).

### 4.1. Extreme values

Extremes are values that are clearly smaller or larger than most other observations. Such values deserve specific attention because they may strongly influence model parameter estimates (Zuur et al., 2013a).

#### 4.1.1. Extremes in numerical variables

We use dotplots (Cleveland, 1993) to reveal extremes in quantitative variables, i.e., the response variable and all numeric or integer predictor variables. Dotplots display the row number of each observation ( $y_i$ ) against its value ( $x_i$ ). Points that clearly isolate left or right of the core distribution deserve attention. Implausible extremes that can be objectively explained by an erroneous measurement or a typing error should be corrected or deleted. All other extremes must be kept (Zuur et al., 2010). To model such remaining extremes in the response variable without transforming the data, we recommend consulting Table 1 to select an (initial) distribution family (Zuur et al., 2010). For predictor variables, the unwanted influence of extremes on model estimation can be mitigated with data transformation, e.g.,  $\log(x + 1)$ . Note, however, that data transformation inevitably changes the meaning – and thus interpretation – of model coefficients (Zuur et al., 2010).

#### 4.1.2. Extremes in factor variables

For all factor predictors and random effects, we produce bar charts to reveal striking imbalances in sample sizes among factor levels. Users can reduce such imbalances by pooling factor levels with

few replicates, where meaningful, or accept that effect estimates for factors with small sample sizes will associate with increased uncertainty, i.e., wide standard errors.

## 4.2. Predictor collinearity

Predictor values are often correlated, particularly in observational studies. This complicates the interpretation of the (partial) effects of these predictors and can substantially increase the uncertainty associated with effect estimates (Korner-Nievergelt et al., 2015). We provide graphical (4.2.1) and numerical (4.2.2) support to assess the degree of predictor collinearity.

### 4.2.1. Graphical inspection

The script generates default plots that allow graphical inspection of predictor collinearity with scatterplots, swarm-plots and mosaic plots for all pairwise combinations of the numeric and factor predictor variables defined in section 3. Predictor independence can be identified when datapoints spread homogeneously across the value ranges (or factor levels) of both predictors. Clear deviations indicate collinearity.

### 4.2.2. Variance inflation factors

Variance Inflation Factors (VIF, implementation based on Zuur et al. (2010)) quantify the inflating effect of collinearity on the standard errors of parameter estimates. Entirely independent predictors yield  $VIF = 1$ , while larger VIF values indicate increasing predictor collinearity. The treatment of collinear predictors should not solely depend on arbitrary VIF thresholds, but also on the intended interpretation of model parameters.

First, correlated predictors might represent proxies of a 'core predictor' that we cannot measure directly. For example, we may be interested in effects of 'body size', and measure weight and length to capture two of its main components. Here, users may prefer to select one of their original predictors, or to combine both using a Principal Component Analysis PCA (James and McCulloch, 1990). The first Principal Component (PC1) can then serve as a single model predictor that captures variation in 'body size' (Harrison et al., 2018).

Second, users may be explicitly interested in partial effects, e.g., the added effect of weight on the response variable after taking the

effect of length into account. In that case, correlated predictors should be kept in the model. Note that the inclusion of correlated predictors affects model interpretation and may generate situations where models predict for (combinations of) predictor values that are beyond those present in the studied population (Morrissey and Ruxton, 2018; Gelman et al., 2020).

## 4.3. Predictor-response relationships

In this step, the script produces graphs of pairwise raw data relationships between the response and each potential predictor defined in section 3. These plots may reveal patterns in the raw data such as non-linear relationships and are helpful for initial model formulation and refinement in sections 5.2.1 and 5.2.2.

## 4.4. Response distribution

Users can "force" their response variables to approach normality with transformations (O'Hara and Kotze, 2010). However, transformations can change the relationship between response and predictor variables (Zuur et al., 2009; Duncan and Kefford, 2021) and may fail to improve model fit (O'Hara and Kotze, 2010; Warton and Hui, 2011). We therefore encourage users to rather choose the most appropriate residual distribution family for their model (Bolker, 2008; O'Hara and Kotze, 2010; Fox, 2015; Warton et al., 2016; Dunn and Smyth, 2018; Harrison et al., 2018). Users can identify a suitable initial distribution family based on (1) general considerations on the expected distribution for their type of response measure (guidance in Table 1) and (2) the distribution of the sample, provided it is sufficiently large and representative. The script displays such distribution as a raw data histogram to visually reveal skew or excess of zeroes.

For example, users may initially select a Gaussian distribution for continuous measures with a roughly symmetrical distribution (e.g., acceleration, weight, or temperature). A Poisson distribution is a reasonable start for counts, and a binomial distribution for presence-absence data or proportions derived from counts (Harrison et al., 2018; Douma and Weedon, 2019; Table 1). Users

TABLE 2 Alternative distribution families to account for issues with dispersion or zero-inflation.

Initial distribution family	Issue	Alternative response distribution	Family indicator in glmmTMB	Link	Zero inflation formula?
Poisson	Dispersion	Negative binomial	nbinom1, nbinom2	log	No
		Composite Poisson	compois	log	No
		Generalised Poisson	genpois	log	No
Binomial	Dispersion	Beta binomial	beta_binomial	logit	No
Poisson	Zero-inflation	Hurdle Poisson	truncated_poisson	log	Yes
		Zero inflated Poisson	poisson	log	Yes
Negative binomial	Zero-inflation	Zero inflated negative binomial	nbinom1, nbinom2	log	Yes
		Hurdle negative binomial	truncated_nbinom1, truncated_nbinom2,	log	Yes
Gamma	Zero values occur	Zero inflated gamma	ziGamma	log	Yes

The formulation of a zero-inflation formula is explained in section 5.2.2 - Model refinement.

assess (section 6) and—if needed—refine this initial choice with a new distribution in an iteration of section 5.

For each distribution family, users must specify a link function (e.g., log, logit, or identity links; Buckley, 2015). Link functions assure that model predictions for asymptotic predictor-response relationships on the raw data scale (e.g., bounded by zero for counts, and by zero and one for proportions) become linear on the link scale where the linear model coefficients are estimated (Harrison et al., 2018; Corlatti, 2021). Each response distribution has a default link function (Table 1), but other links are possible (Bolker, 2008).

## 5. Model formulation

In this workflow, we recommend informing initial model formulation from the biological question of interest. First, all predictors involved in a researcher's hypothesis or study goal *must* be integrated as fixed predictors, including relevant interaction or polynomial terms. Second, where prior knowledge indicates that relevant variation in the response variable may associate with covariates (e.g., body size), interactions (e.g., the association of a main study predictor with the response likely varies with sex, age, or habitat) or polynomials (e.g., the association with size may possibly be quadratic instead of linear), these additional predictors *should* be included in the model. Third, any variable that describes dependency structures of the data *must* be integrated as random predictor in the model.

An alternative approach selects from a broad range of models or combines models for multi-model inference (Hooten and Hobbs, 2015). However, there is evidence that such 'test-qualified pooling' can generate overly confident effect estimates (Burnham and Anderson, 2007; Colegrave and Ruxton, 2017), and we therefore refrained from integrating model selection and multi-model inference in our workflow. Yet, indicators for model performance based on information theory (e.g., AIC) and multi-model inference can be instrumental when models primarily serve for prediction rather than inference (e.g., Tredennick et al., 2021).

### 5.1. Standardization of numeric predictors

We recommend standardizing numeric predictors before initial model formulation. Standardization often mitigates problems with model convergence, facilitates comparisons of coefficient estimates between predictors measured in different units, and assures that covariate intercepts are estimated at their population mean value (Gelman and Hill, 2007; Schielzeth, 2010; Korner-Nievergelt et al., 2015; Harrison et al., 2018). The script offers the option to z-transform all quantitative predictor variables (`var_num`, 3.2), where predictor means are subtracted from observed values and divided by the predictor's standard deviation. Such z-transformed numeric predictors are expressed in units of standard deviations. Users must yet be aware that model coefficients will then be expressed as regression slopes per unit change in predictor standard deviation (rather than per original measurement unit), and that predictions for new covariate values need to be standardised with the original population mean and SD.

## 5.2. Model implementation

### 5.2.1. Initial linear model formulation

Users can now formulate their initial model. We briefly explain how to code some essential terms in `glmmTMB` but recommend consultation of Brooks et al. (2017) for in-depth guidance.

Our basic linear model example has two additive **fixed predictors**, `pred.1`, and `pred.2`:

$$\text{glmmTMB}(\text{response} \sim \text{pred.1} + \text{pred.2}, \text{data} = \text{df}) \quad (1)$$

**Interaction terms for fixed predictors** are specified with colons, here exemplified for a two-way interaction. We recommend restricting initial models to interaction terms that are relevant for the biological question investigated or required by study design (see above). Model assessment (Section 6) will reveal whether adding more interaction terms should be considered:

$$\text{glmmTMB}\left(\begin{array}{l} \text{response} \sim \text{pred.1} + \text{pred.2} + \\ \text{pred.1} : \text{pred.2}, \text{data} = \text{df} \end{array}\right) \quad (2)$$

Note that when interactions are added, all lower-level interaction terms (present when interactions of higher level than two-way interactions are specified) and main predictors must be part of the model.

**Random predictors** can be included as random intercepts only, or as random intercepts with random slopes (Gelman and Hill, 2007; Harrison, 2015; Harrison et al., 2018). *Random intercepts* estimate differences between the overall response mean and the mean values of each random level (e.g., study site ID, individual ID). A random intercept effect (e.g., `rand.1`) is added to the model as follows:

$$\text{glmmTMB}\left(\begin{array}{l} \text{response} \sim \text{pred.1} + \text{pred.2} + \\ (1 | \text{rand.1}), \text{data} = \text{df} \end{array}\right) \quad (3)$$

Random intercepts assume that the fixed predictors' effects (i.e., regression slopes or differences in group means) are consistent among random predictor levels. However, if such effects vary between random levels, models must specify *random slope* terms to integrate the variation in model coefficients among random levels (Korner-Nievergelt et al., 2015; Harrison et al., 2018; Silk et al., 2020). Ignoring random slopes otherwise produces overly confident effect size estimates (Schielzeth and Forstmeier, 2009; Barr et al., 2013; Aarts et al., 2015). We thus recommend initial models to specify random slopes in such situations. Note that models may fail to converge when the sample size per random level is very low (below 3) or unbalanced, which reflects the need for experimental designs with a higher number of replications per random level (Silk et al., 2020). Random slopes for a fixed predictor (e.g., `pred.1`) for each level of a random predictor (e.g., `rand.1`) are coded as follows:

$$\text{glmmTMB}\left(\begin{array}{l} \text{response} \sim \text{pred.1} + \text{pred.2} + \\ (\text{pred.1} | \text{rand.1}), \text{data} = \text{df} \end{array}\right) \quad (4)$$

**Response distribution and link function** are specified using the *family* argument, as exemplified for a Gamma response distribution with a log-link scale:

$$\text{glmmTMB} \left( \begin{array}{l} \text{response} \sim \text{pred.1} + \text{pred.2}, \\ \text{family} = \text{Gamma}(\text{link} = " \log "), \text{data} = \text{df} \end{array} \right) \quad (5)$$

**Offsets** are predictors whose coefficients (= slopes) are set to 1. Hence, they are constrained to a 1 to 1 relationship with the response variable. Offsets are used to model densities or rates when the response variable represents counts. The offset variable transforms counts into densities (e.g., when the offset specifies areas or volumes) or rates (e.g., when the offset specifies transect lengths, exposure durations, or numbers of replicate surveys; [Korner-Nievergelt et al., 2015](#)). Offset terms do not need to be z-transformed as the numeric predictors, but need to be transformed with a function that is identical to the model link function. This is the logarithm in the above example scenarios, where models would use a Poisson or negative-binomial distribution family. The offset term should be specified as a separate term in the model formula as exemplified for a negative binomial model:

$$\text{glmmTMB} \left( \begin{array}{l} \text{response} \sim \text{pred.1} + \text{pred.2}, \\ \text{family} = \text{nbinom2}(\text{link} = " \log "), \\ \text{offset} = \log(\text{offset.1}), \text{data} = \text{df} \end{array} \right) \quad (6)$$

**Weights** modulate how much each observation contributes to the model. Weighting is appropriate when response values (1) are derived measures such as proportions coming from different sample sizes, or (2) vary in measurement precision. A common example for (1) is proportions of successes per individual from a variable number of replicated trials. In *glmmTMB*, the number of trials can be added as a weight to the binomial model ([Table 1](#)). An example for (2) is species mean sizes that have been calculated from a variable number of individuals per species and thus vary in measurement precision. This is typically accounted for by adding the inverse of the observed, squared standard error per observation as a weight ([Brooks et al., 2017](#)). As with offsets, for our routine weights should be added as separate term in the model formula as follows:

$$\text{glmmTMB} \left( \begin{array}{l} \text{response} \sim \text{pred.1} + \text{pred.2}, \\ \text{family} = \text{gaussian}(\text{link} = " \text{identity} "), \\ \text{weight} = \text{weight.1}, \text{data} = \text{df} \end{array} \right) \quad (7)$$

If users encounter warnings or errors while running the model, they can look for detailed guidance from the troubleshooting article that comes with *glmmTMB*<sup>1</sup>.

### 5.2.2. Model refinement

After assessing model fit (see section 6), the initial model formulation may need refinement. This may require additional model components as described in the following section.

**Zero inflation** describes an excess of zero values in the response variable beyond those expected by the distribution family [[Zuur et al. \(2013b\)](#) for more information]. When posterior predictive checks in

model assessment (6.2.2) reveal zero inflation, users should consider adding a *ziformula* argument to the model. If the excess of zeroes distributes homogeneously across predictor values, it suffices to implement *ziformula* = ~ 1. Otherwise, the *ziformula* argument can contain (combinations of) fixed or random effects to model heterogeneity in the zero distribution across predictors. The following example models an access of zeroes that varies across values of pred.1:

$$\text{glmmTMB} \left( \begin{array}{l} \text{response} \sim \text{pred.1} + \text{pred.2}, \\ \text{ziformula} = \sim \text{pred.1}, \text{data} = \text{df} \end{array} \right) \quad (8)$$

**Dispersion formulas** can be added when model assessment indicates heterogeneous residual dispersion across predictor values (6.1) that cannot be resolved by selecting a different model distribution family. *Dispformula* can be added to the model in a similar way as described for the *ziformula* above, except that it can only contain fixed effects. The example allows dispersion to vary across the values of pred.1:

$$\text{glmmTMB} \left( \begin{array}{l} \text{response} \sim \text{pred.1} + \text{pred.2}, \\ \text{dispformula} = \sim \text{pred.1}, \text{data} = \text{df} \end{array} \right) \quad (9)$$

**Correlation (or covariance) structures** offer solutions when assessment step 6.3 reveals temporal or spatial autocorrelation in model residuals. Temporal autocorrelation is often captured well by an Ornstein-Uhlenbeck (*ou*) covariance structure, which accommodates time series with irregularly or regularly spaced time points. The *glmmTMB* formulation *ou(time + 0|group)* requires two novel elements: “*time*” is a matrix of Euclidean distances that users can calculate from *var\_time* using the function *numFactor*. “*group*” is either the vector already specified in *var\_time\_groups*, or, in case of single time series, a new factor vector with a single grouping level.

$$\text{glmmTMB} \left( \begin{array}{l} \text{response} \sim \text{pred.1} + \text{pred.2} + \\ \text{ou}(\text{time} + 0 | \text{group}), \text{data} = \text{df} \end{array} \right) \quad (10)$$

Treatment of spatial autocorrelation is a very complex topic ([Banerjee et al., 2014](#)) that faces limitations concerning computational abilities ([Simpson et al., 2012](#)) and the stability of fixed effect estimates ([Hodges and Reich, 2010](#)) that are beyond the scope of this overview. Note that, in some cases, the addition of covariates (e.g., habitat types) can already efficiently deal with spatial autocorrelation. Beyond that, users should consult the article on covariance structures that comes with the *glmmTMB* vignette ([Brooks et al., 2017](#)) and more advanced literature on spatial autocorrelation (e.g., [Dupont et al., 2022](#)).

## 6. Model assessment

Before inspecting model coefficients and effect sizes, users should assess how well the model captures patterns in the raw data and fulfills model assumptions ([Freckleton, 2009](#); [Gelman et al., 2013, 2020](#); [Zuur and Ieno, 2016](#)). The script guides users through graphical inspection with residual checks (6.1), posterior predictive checks (6.2), and variograms to assess residual independence across temporal or spatial scales (6.3).

<sup>1</sup> <https://glmmTMB.github.io/glmmTMB/articles/troubleshooting.html>

Model assessment may often call for a refined model that contains other interaction or polynomial terms, or additional predictors (back to section 5). These newly added terms can increase the reliability of model estimates for the predictors specified in the initial model, but their (unexpected) effects should not be used to test new hypotheses. This would cause selection bias and increase the risk of drawing false conclusions (Forstmeier et al., 2017). Users should therefore explicitly name all terms that have been added to the model after model assessment.

## 6.1. Residual checks

Linear models assume that residuals are independent of predicted mean values and distribute homogeneously across all (combinations of) predictor variables. Conformity to these assumptions is visible as an absence of patterns in residual plots, and is a fundamental step of linear modelling to avoid systematic bias in parameter and uncertainty estimates (Gelman and Hill, 2007; Zuur et al., 2009; Zuur and Ieno, 2016; Gelman et al., 2020). The script displays randomised quantile residuals (Dunn and Smyth, 1996; Gelman and Hill, 2007; Dunn and Smyth, 2018) computed using the R package DHARMA (Hartig and Lohse, 2020). These residuals distribute uniformly between 0 and 1, and thus allow to evaluate residuals plots irrespective of the chosen distribution family (Hartig and Lohse, 2020).

### 6.1.1. Distribution of residuals

The script first produces two residual plots. The first is a quantile-quantile (Q-Q) plot (Figures 2A,B), where residuals match the expected distribution when they follow the diagonal line closely (Figure 2B). The second displays residuals against model-predicted values (Figures 2C,D), where points should scatter homogeneously without pattern (Figure 2D) (Korner-Nievergelt et al., 2015; Corlatti, 2021). Heterogeneity in residuals typically shows as a curvature or s-shape in Q-Q plots (Figure 2A), or as a change in residual spread along model predictions on the *x*-axis in residuals vs. fitted values plots (Figure 2C). Such models can produce biased parameter estimates and usually have overly narrow standard errors (Quinn and Keough, 2002; Fox, 2015; Zuur and Ieno, 2016). Issues are often resolved by using a more appropriate distribution family or link function (Tables 1, 2), but other possible solutions are listed in the R script (Korner-Nievergelt et al., 2015; Harrison et al., 2018).

If the model contains random predictors, this function also generates a Q-Q plot for each predictor to check if the estimated intercepts are normally distributed (Figures 2E,F; Korner-Nievergelt et al., 2015; Harrison et al., 2018). Note that linear models are rather robust against moderate violations of normality for random intercepts (Schielzeth et al., 2020), at least as long as they are used to estimate between-group variation and are not used to make predictions for unobserved random levels.

### 6.1.2. Residuals against possible predictors

In this section, the script produces plots of model residuals against all fixed predictors specified in Section 3. We recommend checking residuals against *all* variables in the dataset, including those that are not part of the current model. Any predictor that shows residual patterns (as detailed in 6.1.1) requires further attention.

Predictors already in the model may require the addition of a curvilinear (polynomial) term, which should be added up to the desired degree using the *poly* function in R (Korner-Nievergelt et al., 2015). Note that high-order polynomial terms can perform poorly in regions of a dataset where data is sparse (Wood, 2017) and should thus be used with care (Gelman et al., 2020). If the dataset features more complex non-linear patterns, we recommend resorting to dedicated R packages such as *mgcv* (Wood, 2017) to implement more appropriate models.

Predictors not yet included in the model that show residual patterns should be added to help explaining variation in the response variable (see above).

### 6.1.3. Residuals against possible two-way interactions among predictors

The script produces residual plots for all two-way combinations of fixed predictors. Heterogeneous residual patterns beyond those already seen above identify predictor combinations that may need addition as an interaction term to the refined model formulation, provided the original question being asked is not altered.

### 6.1.4. Residuals against predictors split by random factor levels

Finally, the script helps users to evaluate if a random intercept needs the addition of random slopes over a specific fixed predictor (Korner-Nievergelt et al., 2015). This residual check is relevant only for fixed predictors with 3 or more observations per random level. The plots generated by the script show the distribution of model residuals across the selected predictors, split by the levels of the specified random intercept predictor(s). If panels show diverging slopes for numeric predictors or inconsistent effect directions for categorical predictors, the model requires the addition of random slopes for that predictor (Schielzeth and Forstmeier, 2009; Silk et al., 2020) to avoid overly confident coefficient estimates (Schielzeth and Forstmeier, 2009). Note that residual mean values per random level do not need to be zero: Due to the shrinkage estimation of mean values per random effect level, average residuals can be positive for levels with low means, and negative for levels with high means.

## 6.2. Posterior predictive checks

Even careful residual assessment may leave several important aspects of model fit unexplored (Faraway, 2016; Pekár and Brabec, 2016). Therefore, we assess model performance also with posterior predictive checks, which compare the observed data with the distribution of many (e.g., 2000) replicated datasets simulated from the model (Gelman and Hill, 2007; Gelman et al., 2013; Zuur and Ieno, 2016). The script guides users to graphically evaluate dispersion (6.2.1), zero-inflation (6.2.2) and overall model fit (6.2.3; Figure 3). These plots display observed parameters as blue lines when they are within the central 90% of the simulated distribution (labeled as 'optimal fit'), orange lines when between the central 90% and 99% boundaries ('sub-optimal fit'), and red lines when outside the central 99% boundaries ('poor fit'). These boundaries are set arbitrarily to provide qualitative guidance. We recommend seeking an optimal fit while

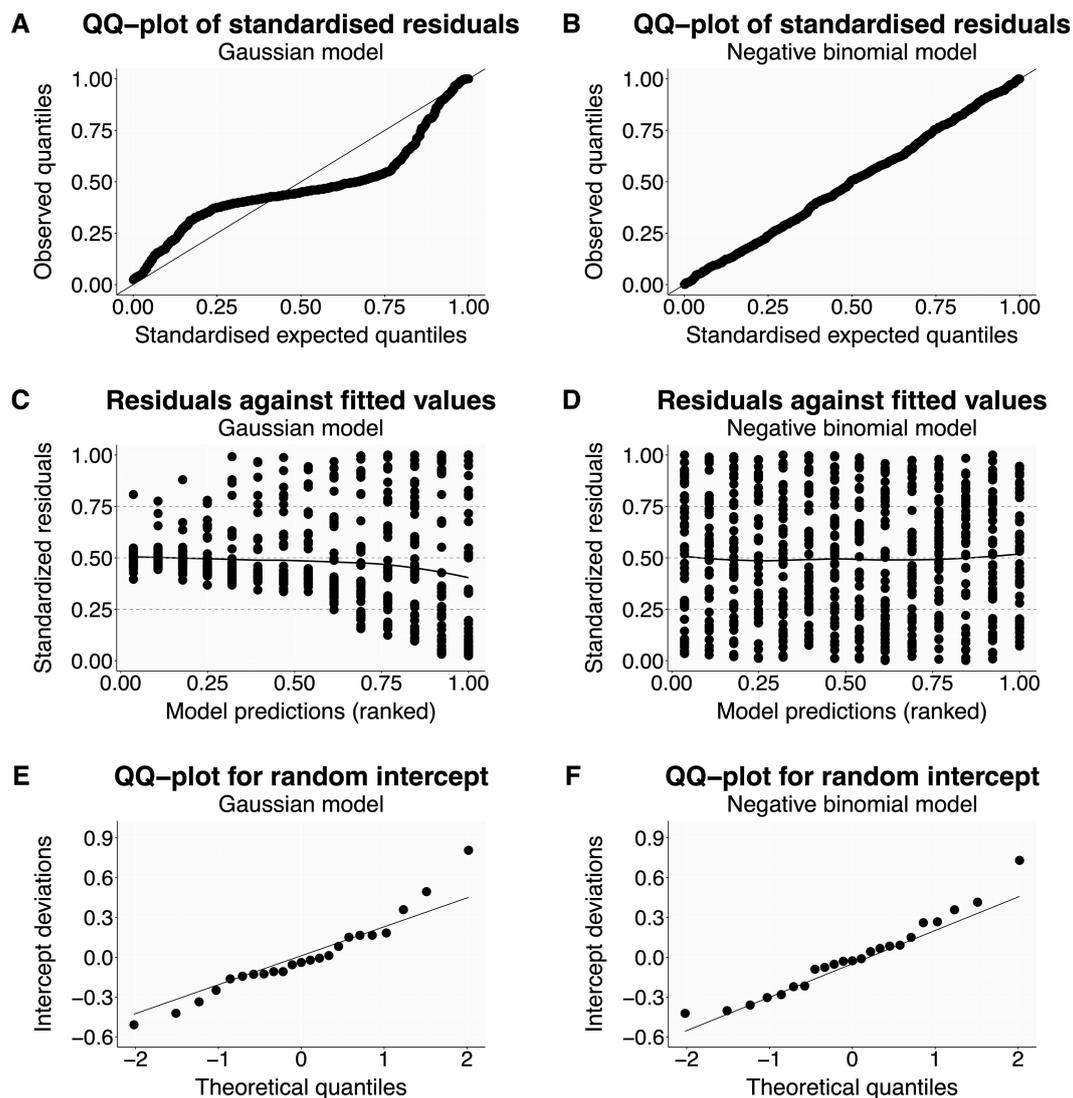


FIGURE 2

Distribution of residuals—examples. The left column shows residual plots for a Gaussian model with clear violations of model assumptions (A,C,E). The right column shows the same residuals plots—now without issues after changing the distribution family to negative binomial (B,D,F). The dataset from Price et al. (2016) is available with the R package glmmTMB (Brooks et al., 2017).

bearing in mind that model performance is seldom perfect for all parameters at once.

### 6.2.1. Dispersion

Some response distributions (e.g., Poisson and binomial) assume tight coupling between mean and variance, an assumption that is often violated (Cox, 1983; Yang et al., 2010). Over- or underdispersion arises when the data (and residual) variation is higher or lower than predicted from the population mean. Both can lead to biased parameter estimates and inappropriately small (or large) standard errors (Hilbe, 2011; Zuur and Ieno, 2016; Campbell, 2021). The script graphically compares the variance of the observed data with the variance distribution of model-simulated datasets (Figures 3A,B). We recommend users to split this plot by the levels of each categorical predictor used in the model, because dispersion should also be checked within each factor level.

Dispersion issues can originate from an inappropriate distribution family, a wider spread of the data than expected by the observed mean, or an excess of zero values (Harrison, 2014). Dispersion checks should therefore always go along with zero-inflation checks (6.2.2). Potential solutions include a distribution family that better captures the observed data dispersion (Table 2; Hilbe, 2011; Harrison, 2015; Harrison et al., 2018) or that adequately integrates the excess of zeroes (Yang et al., 2010).

### 6.2.2. Zero-inflation

Here, the script visualises the observed number of zero values against the zero-distribution derived from model-simulated datasets (Figures 2C,D). Users should split displays by factor levels as described for dispersion (6.2.1). If deviations are detected, users may choose a distribution family that better captures the observed zero frequencies (Table 2) or add a zero-inflation formula to the model (5.2.2).

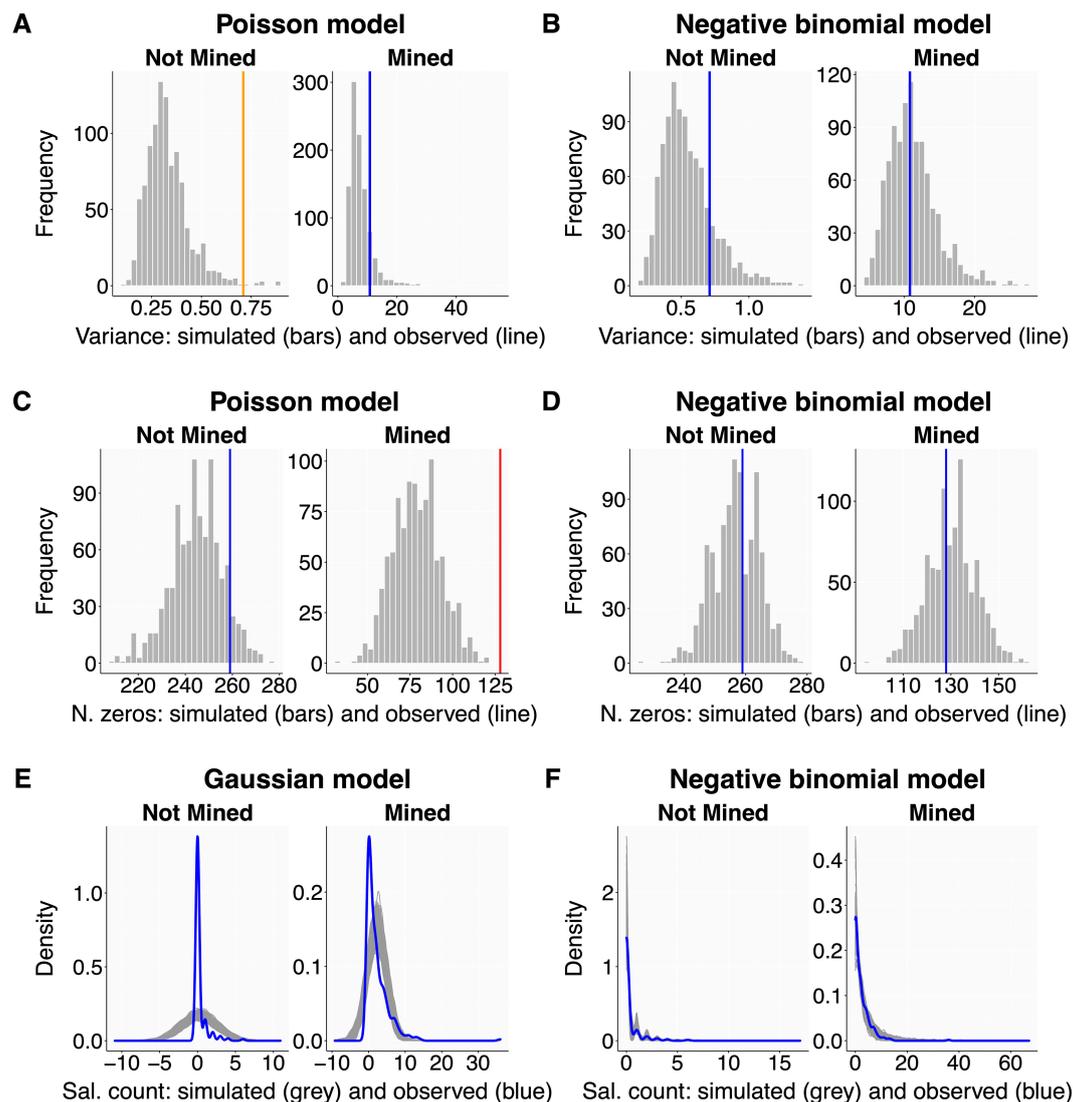


FIGURE 3

Posterior predictive checks - examples. All plots show observed values or data distributions (thick colored lines) in relation to those obtained from 10,000 simulations of raw datasets from the model. Each panel is split by a categorical predictor with two levels (sites without and with mining activity). The left column shows clear deviations between observed and simulated data for dispersion (A), number of zeros (C), and overall data distribution (E). The right column has all issues solved by changing distribution family from Poisson to negative binomial for (B) and (D), and from Gaussian to negative binomial for (F). A Gaussian distribution was here chosen only to create a clear deviation for display purposes. Dataset as in Figure 2.

### 6.2.3. Data distribution

This final posterior predictive check evaluates overall model fit (Gelman et al., 2013; Zuur and Ieno, 2016). The script plots the density of the observed data distribution (blue line) against that of model-simulated datasets (gray lines; Figures 3E,F), ideally split by the levels of each factor predictor as before. The observed (blue) line should be central within the gray background pattern of simulated data. If this is clearly not the case, users should carefully re-evaluate all preceding steps of model assessment and reformulate their model accordingly (back to section 5).

### 6.3. Autocorrelation checks

Ecological sampling often has a temporal or spatial component. This may introduce dependency structures in the response variable

where observations closer in time or space are more similar (Zuur et al., 2010; Korner-Nievergelt et al., 2015), leading to pseudoreplication. To assess whether such temporal or spatial autocorrelation is present in the data, the script produces graphical autocorrelation checks for temporal (based on *var\_time* and *var\_time\_groups* from 3.4) or spatial data structures (based on *var\_space* from 3.4) using semivariograms (Schabenberger and Pierce, 2002). Semivariograms display how the 'standardised semivariance' (i.e., standardised, half squared differences in model residuals between all observation pairs) changes with the spatial or temporal distance between sample pairs (Hengl, 2007; Korner-Nievergelt et al., 2015). Standardised semivariances of fully independent observations fluctuate around 1. Smaller semivariance values identify observations that are more similar than expected at random, and thus autocorrelated. Observed semivariances are

calculated using the *variog* function of the *geoR* package (Ribeiro and Diggle, 2001). To aid interpretation, we plot these (blue line) against the distribution of semivariances expected in the absence of autocorrelation, as derived from many (e.g., 2000) permuted model residuals (Figure 4). Observed standardised semivariances that clearly fall below the gray permuted pattern indicate autocorrelation. In such cases, users should consider adding a covariance structure to the model (5.2.2).

## 7. Model results and parameter estimates

Once the iteration of model assessment and refinement resulted in an adequate model, users can finally inspect model estimates. This workflow refrains from null hypothesis tests because they offer limited information about the magnitude and biological meaning of the observed effects and bear a substantial risk of misinterpretation (Johnson, 1999; Nakagawa and Cuthill, 2007; Cumming, 2008; Halsey et al., 2015; Cumming and Calin-Jageman, 2017; Halsey, 2019). We instead focus on reporting effect sizes with their ‘compatibility intervals’ (Gelman and Greenland, 2019; Halsey, 2019; Berner and Amrhein, 2022), i.e., the central 95% density interval of effect values that are most compatible with the observed data. Berner and Amrhein (2022) offer further guidance on reporting without falling back to ‘null hypothesis testing’ terminology.

### 7.1. Overall coefficient estimates

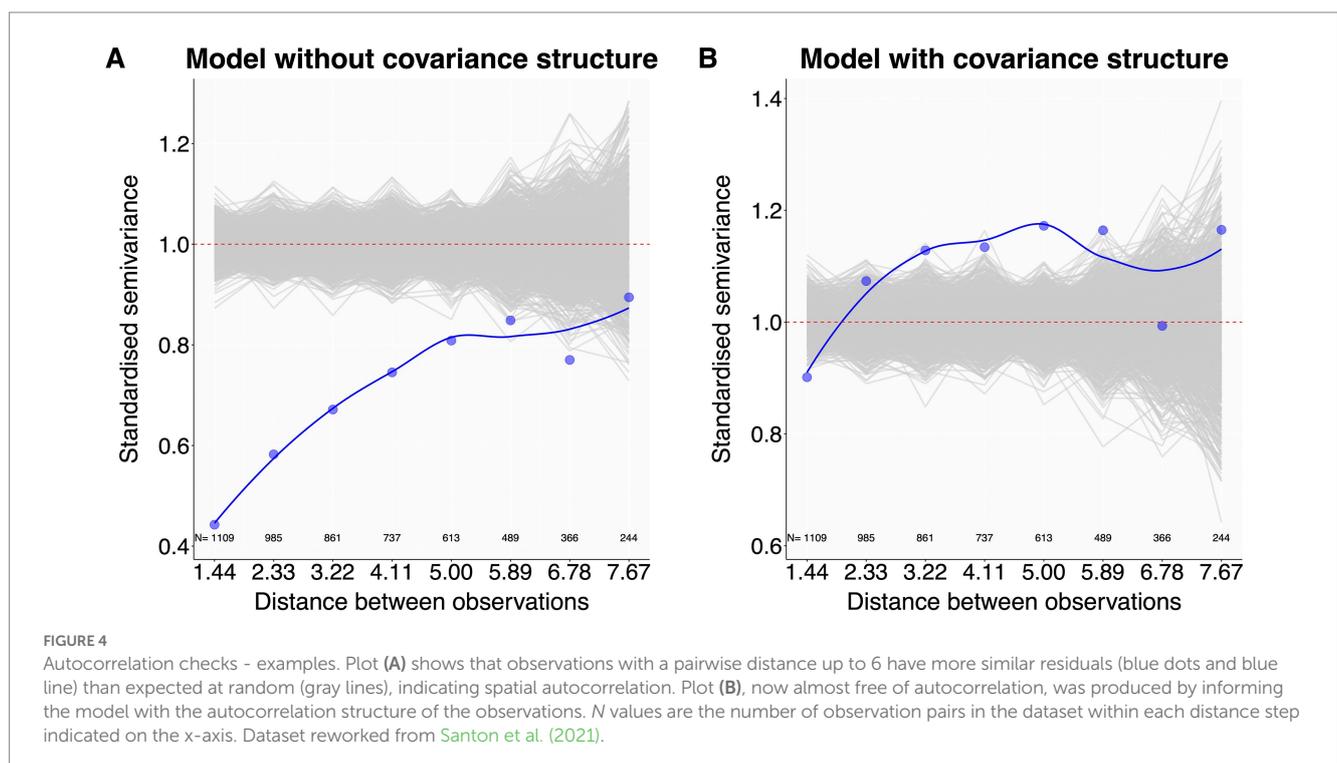
The script displays coefficient estimates for each model parameter, including their 95% compatibility intervals using a

custom function based on the *parameters* package (Lüdtke et al., 2020b). Note that parameter estimates are on the model link scale. As an alternative way of measuring effect sizes, the *r2* function from the *performance* package (Lüdtke et al., 2020a) estimates the variance explained by the model for fixed predictors only (marginal  $R^2$ ), and for fixed plus random predictors (conditional  $R^2$ ; Nakagawa and Schielzeth, 2013; Nakagawa et al., 2017; Harrison et al., 2018).

Users may want to also report estimates of regression slopes within factor levels, or differences in predicted mean values between factor levels. We introduce functions that extract such estimates and their 95% compatibility intervals in the following two sections. We refer users to the extensive guidance provided with the *emmeans* package (Lenth, 2023) to compute estimates beyond the capabilities of the functions presented in the script.

### 7.2. Estimation of regression slopes

This section computes predicted slopes and their 95% CIs for models containing interaction terms between one numeric predictor and up to two factor predictors using a custom function based on the *emmeans* package (Lenth, 2023). Slope estimates per unit increase of the numeric predictor are always given on the model link scale where regression slopes are linear. For log and logit link models, we additionally provide estimates for the resulting response ratios and odds ratios, respectively. For standardised numeric predictors, slope estimates show changes per unit standard deviation of the predictor. The predicted slopes and their 95% CIs can be reported as exemplified in Table 3. Effect size strength increases with the deviation of estimates from zero (for



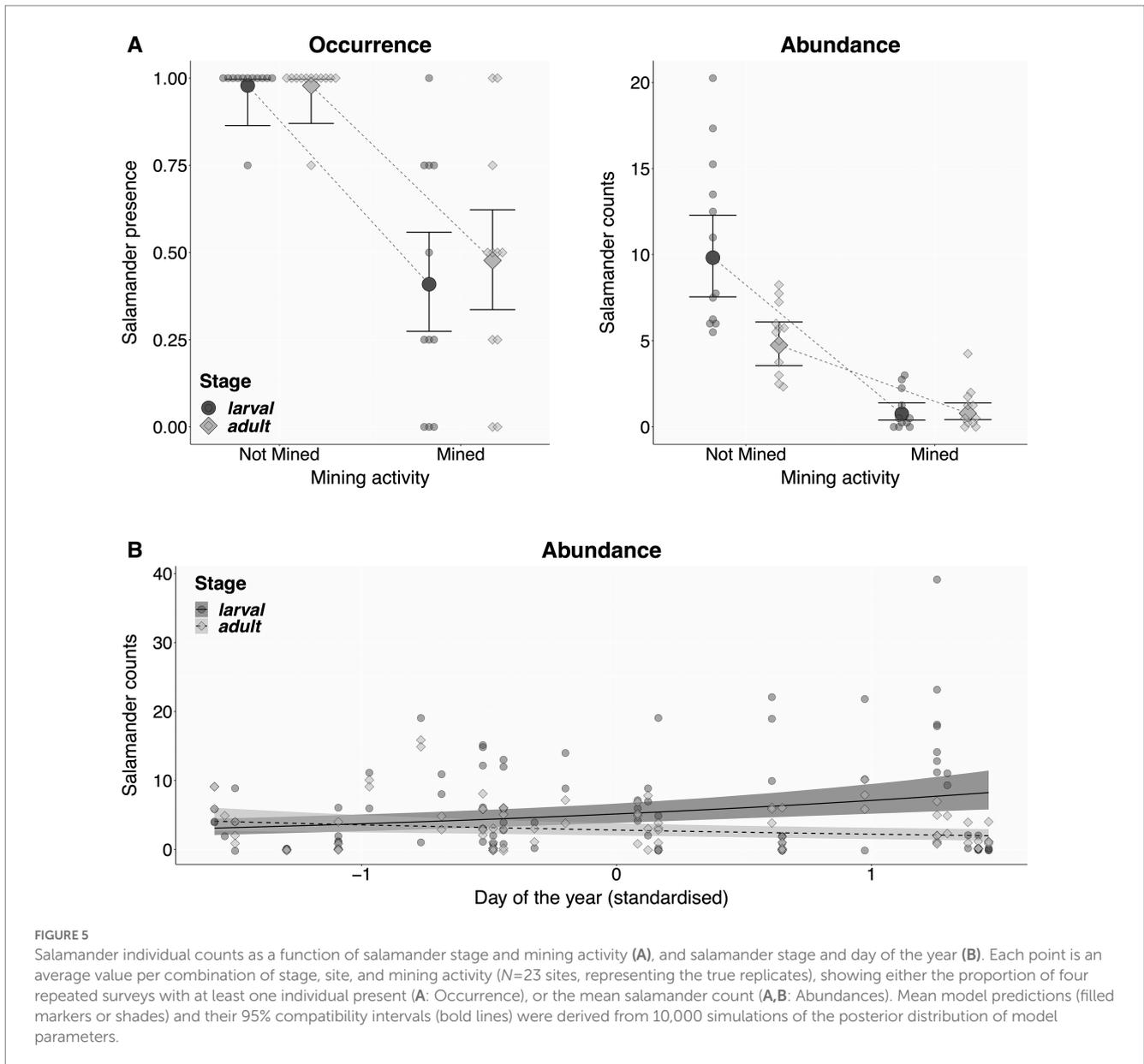


TABLE 3 Example of a numerical presentation of regression slopes.

Stage	Estimates on model link scale: log-ratio of salamander counts			Estimates on response scale: ratio of salamander counts		
	Slope mean	Lower 95% CI	Upper 95% CI	Ratio mean	Lower 95% CI	Upper 95% CI
larvae	0.322	0.172	0.472	1.380	1.188	1.603
adult	-0.237	-0.409	-0.064	0.789	0.664	0.938

Linear change in salamander counts, split between larval and adult stages, along the continuous predictor day of the year (DOY). Since DOY was already z-transformed in the data, slope estimates show changes per unit standard deviation in DOY. Raw data and model predictions are in Figure 5, full model specifications in the final model of the Supplementary file.

Gaussian models, and for changes on the link scale for other model families) or one (for changes expressed as response ratios and odds ratios for log- and logit-link functions, respectively), and the robustness of the result increases the less the 95% Compatibility

Intervals (CIs) overlap with zero or one, respectively. The script additionally produces a graphical output of the effect estimates with their compatibility intervals on the model link scale (examples in the Supplementary file).

TABLE 4 Example for the numerical presentation of differences between factor levels.

Comparison	Mean	Lower 95% CI	Upper 95% CI
<b>1. Occurrence: Binary binomial zi model (logit link)</b>			
Response odds ratios for salamander absence <sup>a</sup> between sites with and without mining.			
<i>Not mined / mined</i> [larval]	0.015	0.002	0.121
<i>Not mined / mined</i> [adult]	0.019	0.002	0.159
<b>2. Abundance: Conditional count model (log link)</b>			
Response ratios of mean counts within occupied sites.			
<i>Not mined / mined</i> [larval]	5.402	3.084	9.465
<i>Not mined / mined</i> [adult]	2.927	1.690	5.071

Differences in salamander occurrence and abundance between sites with and without mining activity, split by larval and adult stages. In the example, we provide estimates and compatibility intervals separately for the zero-inflated (zi) binomial model (as odds ratios for salamander absence<sup>a</sup>) and the negative binomial count model (as response ratios for mean salamander counts per group). Raw data and model predictions are in Figure 5, full model specifications in the final model of the Supplementary file.

<sup>a</sup>Note that zi components estimate odds of absence (= failures), resulting in inverse odds ratios compared to classic binomial models, which express the odds of presence (= successes).

### 7.3. Estimation of differences between factor levels

The script estimates differences in mean values either between all possible combinations of the levels of a user specified selection of factor predictors, or for the levels of one factor predictor *within* the levels of a second one, using a custom function based on the *emmeans* package (Lenth, 2023). The function displays absolute differences in mean values for identity link models, and ratios or odds ratios for log or logit link models, respectively. As above, effect estimates, and their 95% compatibility intervals are reported as a table (exemplified in Table 4) and as a graphical output (examples in the Supplementary file). Effect size and CIs interpretation is the same as described for regression slopes above.

## 8. Graphical display of model predictions

An intuitive and comprehensive way to visualise the relationship between response and predictor variables is a combined display of raw data with model-derived predictions and their 95% compatibility intervals (Best and Wolf, 2013; Halsey, 2019; Ho et al., 2019). The script produces such displays after users specified one or two fixed predictors (Figures 5A,B). First, the script calculates the posterior distribution of fitted values from 10,000 sets of model parameters drawn from a Multivariate Normal Distribution based on the predicted mean and variance of each model coefficient (Brooks et al., 2017). From these, the script extracts model-predicted means and their 95% compatibility intervals per factor level, or along the numeric range of the specified predictor(s) of interest, with all other predictor(s) set to their median values. Finally, the script summarises the raw data at the specified replicate level, and plot them together with predicted means and compatibility intervals (Korner-Nievergelt et al., 2015; Brooks et al., 2017).

### Author's note

The most recent version of the template and support functions R-scripts will be available for download on GitHub: [https://github.com/MSSanton/glmms\\_workflow](https://github.com/MSSanton/glmms_workflow).

## Data availability statement

The original contributions presented in the study are included in the article/supplementary material, further inquiries can be directed to the corresponding author.

## Author contributions

MS and NA conceived the study, coded the R-workflow, and wrote the manuscript. MS analyzed the data. MS, NA, and FK-N tested the R-workflow. FK-N and NM edited the manuscript it. All authors contributed to the article and approved the submitted version.

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## Conflict of interest

FK-N was employed by the company Oikostat GmbH.

The remaining authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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## Supplementary material

The Supplementary material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fevo.2023.1065273/full#supplementary-material>

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