

# Example Analyses in Statistical Ecology

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## Abstract

This vignette serves as an online appendix for the manuscript [Tamási and Hothorn \(2022\)](#). It presents three example analyses that use mixed-effects additive transformation models to reanalyze datasets from recently published studies in the field of ecology.

## 1 *E. coli* concentrations in streams with different grazing periods

[Hulvey et al. \(2021\)](#) compare the concentration levels of *Escherichia coli* bacteria (most probable number, MPN) in streams under three different rotational grazing regimes. In the additive mixed model specifications they estimated, within-year variability was modeled, as functions of the day of year (DOY), with cubic regression splines and between-year and location-level variability was captured by random intercepts of pasture-specific year effects and separate stream effects. Note that although the cyclic version of the cubic regression splines (`bs = 'cc'` in `mgcv` and `tramME`) would be more appropriate for modeling the within-year trend, the original article used `bs = 'cr'` and hence we also stick with this basis in our reanalysis.

As a first step, we replicate the results of all model variants that they investigated in the original article with the R package `gamm4` ([Wood and Scheipl, 2020](#)). Next, we reproduce the results with additive transformation models assuming conditional normality and, finally, relax the distributional assumption and evaluate how the model fits change. As [Table 1](#) shows, we managed to reproduce the `gamm4` results with `tramME`. Moreover, relaxing the distributional assumption of the normal linear model resulted in stronger model fits in terms of log-likelihood values.

```
R> ## specifications w/o random effects
R> mf <- c(log10(ecoli_MPN) ~ treatment + cattle +
+         s(DOY, bs = 'cr', by = treatment),
+         log10(ecoli_MPN) ~ treatment + cattle + s(DOY, bs = 'cr'),
+         log10(ecoli_MPN) ~ treatment + s(DOY, bs = 'cr', by = treatment),
+         log10(ecoli_MPN) ~ cattle + s(DOY, bs = 'cr'),
+         log10(ecoli_MPN) ~ treatment + s(DOY, bs = 'cr'),
+         log10(ecoli_MPN) ~ s(DOY, bs = 'cr'))
R> names(mf) <- paste("Model", c(1:5, "Null"))
R> ecoli_res <- data.frame(matrix(NA, nrow = length(mf), ncol = 3))
R> colnames(ecoli_res) <- c("gamm", "LmME", "BoxCoxME")
```

```

R> rownames(ecoli_res) <- names(mf)
R> for (i in seq_along(mf)) {
+   m_gamm <- gamm4(mf[[i]], data = ecoli,
+                   random = ~ (1 | year:stream:pasture) + (1 | stream),
+                   REML = FALSE)
+   ecoli_res$gamm[i] <- logLik(m_gamm$mer)
+   mf2 <- update(mf[[i]], . ~ . + (1 | year:stream:pasture) + (1 | stream))
+   m_LmME <- LmME(mf2, data = ecoli)
+   if (m_LmME$opt$convergence == 0) ecoli_res$LmME[i] <- logLik(m_LmME)
+   m_BCME <- BoxCoxME(mf2, data = ecoli)
+   if (m_BCME$opt$convergence == 0) ecoli_res$BoxCoxME[i] <- logLik(m_BCME)
+ }

```

Table 1: Log-likelihood values of the fitted models presented by [Hulvey et al. \(2021, GAMM\)](#), replicated as mixed-effects additive transformation models assuming conditional normality (*Additive normal transformation model*) and extended as flexible (non-normal) mixed-effects additive transformation models (*Additive non-normal transformation model*).

	GAMM	Additive normal transformation model	Additive non-normal transformation model
Model 1	-339.23	-339.23	-320.94
Model 2	-343.66	-343.66	-324.54
Model 3	-368.33	-368.33	-349.10
Model 4	-347.70	-347.70	-328.25
Model 5	-367.15	-367.15	-347.27
Model Null	-373.76	-373.76	-353.50

Let us focus on the most complicated specification, Model 1,

```

R> update(mf[[1]], . ~ . + (1 | year:stream:pasture) + (1 | stream))

log10(ecoli_MPN) ~ treatment + cattle + s(DOY, bs = "cr", by = treatment) +
  (1 | year:stream:pasture) + (1 | stream)

```

and compare the effect estimates from the normal model to its non-parametric counterpart. But first, notice that by changing the transformation from  $h(y) = \vartheta_0 + \vartheta_1 y$  to  $h(y) = \mathbf{a}(y)^\top \boldsymbol{\vartheta}$ , we change the scale on which the coefficients and the smooth terms are interpreted. In the normal additive mixed model, the coefficient of a fixed effect captures the change in the expectation of the outcome when increasing the respective predictor by one unit (keeping everything else unchanged). In the non-normal transformation model with  $\Phi$  as the inverse link, the coefficients capture similar effects but on a latent scale defined by the transformation  $h(Y)$ .

To cast the effect estimates from the two models to a common scale, we can calculate the *probabilistic indices* (PI, [Thas et al., 2012](#)). To simplify the notation, without loss of generality, we will now focus on the simple, fixed effects-only case:

$$\mathbb{P}(Y \leq y \mid \mathbf{X} = \mathbf{x}) = \Phi(h(y) - \mathbf{x}^\top \boldsymbol{\beta})$$

The PI is the probability that one outcome ( $Y^*$ ) is larger than the other ( $Y$ ), given the same covariate values ( $\mathbf{X}$ ) except for one, which is larger with one unit ( $\mathbf{X}^*$ )

$$\begin{aligned}\mathbb{P}(Y < Y^* \mid \mathbf{X}, \mathbf{X}^*) &= \mathbb{P}(h(Y) < h(Y^*) \mid \mathbf{X}, \mathbf{X}^*) \\ &= \mathbb{P}\left(\frac{h(Y) - h(Y^*) + \beta}{\sqrt{2}} < \frac{\beta}{\sqrt{2}} \mid \mathbf{X}, \mathbf{X}^*\right) \\ &= \Phi\left(\frac{\beta}{\sqrt{2}}\right),\end{aligned}$$

where  $\beta$  is the coefficient of the covariate that is different with one unit. The third line is true, because  $h(Y)$  and  $h(Y^*)$  are independent, normally distributed random variables, with unit variance and a mean difference of  $\beta$ . Notice that the PI does not depend on the transformation function. When random effects are present in the model, the PI is conditional on the cluster.

By casting the effect estimates to the probability scale, Figure 1 compares the smooth terms from the normal and non-normal versions of Model 1, while the first two blocks of Table 2 the fixed effects estimates. The results are very close to each other, which suggests that the original log-normal model is actually appropriate. As a built-in visual normality check, we can compare the fitted transformation functions of the normal and non-normal transformation models. The linear function corresponds to normal conditional distribution in Figure 2. This result further confirms the appropriateness of the normal additive model in this specific example.

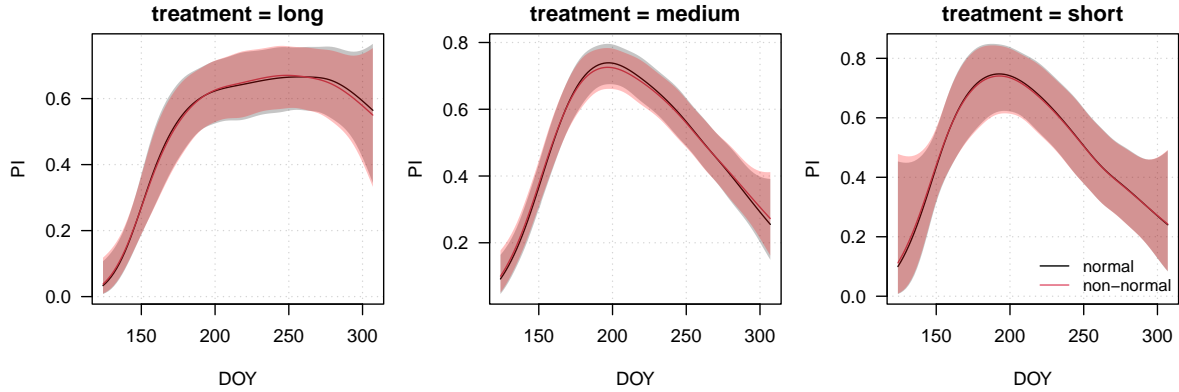


Figure 1: The comparison of the smooth terms from the normal and non-normal (probit link) mixed-effects additive transformation models (specification Model 1).

The outcome variable (MPN per 100 ml) was measured with the Quanti-Tray System, which can detect *E. coli* concentrations up to a maximum of 2,419.6 MPN without dilution. This means that there is an effective upper detection limit on the outcome, i.e., the 25 observations with the value of 2,419.6 are *right censored*. The authors of the original article mention this fact, but they do not take into account in the subsequent analyses. Because censoring can be easily handled in `tramME`, we will rerun the model taking the upper limit into account.

```
R> fm1c <- update(fm1, Surv(log10(ecoli_MPN), event = ecoli_MPN < 2419.6) ~ .)
R> ecoli_m1_cens <- BoxCoxME(fm1c, data = ecoli)
R> summary(ecoli_m1_cens)
```

Non-Normal (Box-Cox-Type) Linear Additive Mixed-Effects Regression Model

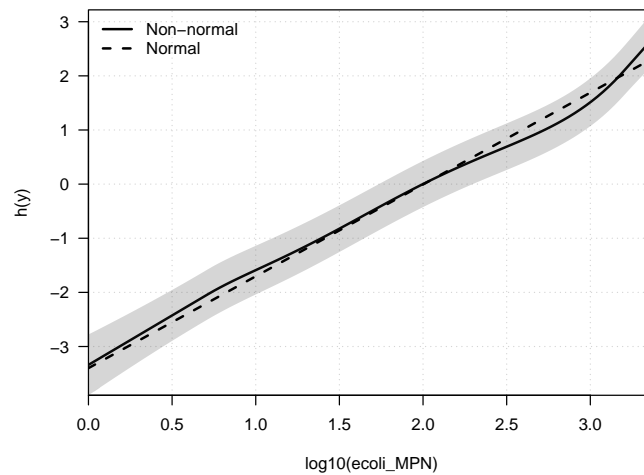


Figure 2: Baseline transformation functions from the normal and non-normal mixed-effects additive transformation models.

```
Formula: Surv(log10(ecoli_MPN), event = ecoli_MPN < 2419.6) ~ treatment +
  cattle + s(DOY, bs = "cr", by = treatment) + (1 | year:stream:pasture) +
  (1 | stream)
```

Fitted to dataset ecoli

Fixed effects parameters:

=====

	Estimate	Std. Error	z value	Pr(> z )	
treatmentmedium	-0.680	0.230	-2.95	0.0032	**
treatmentshort	-0.772	0.317	-2.44	0.0148	*
cattlePresent	1.108	0.149	7.42	1.2e-13	***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Smooth shift terms:

=====

	edf
s(DOY):treatmentlong	4.38
s(DOY):treatmentmedium	4.55
s(DOY):treatmentshort	4.30

Random effects:

=====

Grouping factor: year:stream:pasture (32 levels)

Standard deviation:

(Intercept)

0.431

Grouping factor: stream (12 levels)

Standard deviation:

(Intercept)

0.000204

Log-likelihood: -358 (npars = 18)

The fitted non-linear terms are compared to the original (normal linear) estimates in Figure 3 and the fixed effects are presented in the third block of Table 2.

Table 2: Estimates of the parametric fixed-effects terms on the *probability scale* (PI: probabilistic index) from the normal, non-normal and non-normal (with censoring taken into account) models, respectively.

	Normal		Non-normal		Non-normal, censored	
	PI	95% CI	PI	95% CI	PI	95% CI
treatment = medium	0.32	0.22—0.44	0.33	0.22—0.45	0.32	0.21—0.44
treatment = short	0.29	0.16—0.45	0.30	0.17—0.46	0.29	0.16—0.46
cattle = present	0.79	0.72—0.84	0.78	0.72—0.84	0.78	0.72—0.84

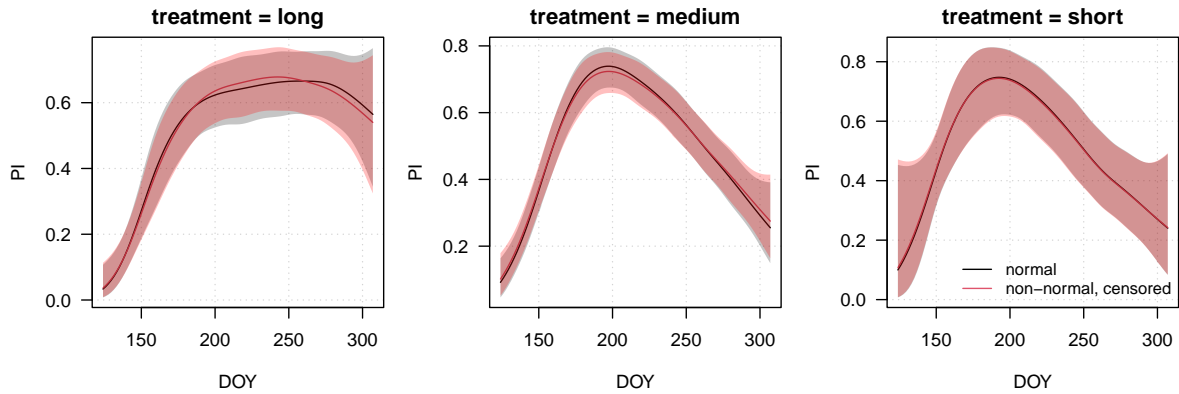


Figure 3: The comparison of the smooth terms from the original model (normal linear) and the non-normal (probit link) extension where censoring is also taken into account.

Because the transformation model approximates the conditional distribution of the outcome, in theory, we do not even have to take the base 10 logarithm of the *Ecoli* most probable numbers (MPN) on the left-hand side of the model formula. `tramME` should be able to approximate the *most likely transformation*.

```
R> f_nontr <- update(fm1, Surv(ecoli_MPN, event = ecoli_MPN < 2419.6) ~ .)
R> ecoli_nontr <- BoxCoxME(f_nontr, data = ecoli, log_first = TRUE)
R> summary(ecoli_nontr)
```

```

Non-Normal (Box-Cox-Type) Linear Additive Mixed-Effects Regression Model

Formula: Surv(ecoli_MPN, event = ecoli_MPN < 2419.6) ~ treatment + cattle +
  s(DOY, bs = "cr", by = treatment) + (1 | year:stream:pasture) +
  (1 | stream)

Fitted to dataset ecoli

Fixed effects parameters:
=====

              Estimate Std. Error z value Pr(>|z|)
treatmentmedium  -0.680      0.230   -2.95  0.0032 **
treatmentshort   -0.772      0.317   -2.44  0.0148 *
cattlePresent      1.108      0.149    7.42 1.2e-13 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Smooth shift terms:
=====

              edf
s(DOY):treatmentlong  4.38
s(DOY):treatmentmedium 4.55
s(DOY):treatmentshort 4.30

Random effects:
=====

Grouping factor: year:stream:pasture (32 levels)
Standard deviation:
(Intercept)
  0.431

Grouping factor: stream (12 levels)
Standard deviation:
(Intercept)
  0.000394

Log-likelihood: -2027 (npar = 18)

```

Notice that we set `log_first = TRUE` in the function call, to take the natural logarithm of the outcome before setting up the Bernstein bases. This usually helps the approximation in the case of positive right-skewed outcomes. With this, we basically estimate the same model as the original, but with the natural logarithm instead of base-ten. Because of this, the log-likelihood values are different,

but the fixed effects and variance components parameter estimates, as well as the smooth terms are essentially the same as in the case of the model `ecoli.m1.cens`.

In summary, after bringing the estimates to the same scale, the results of the additive mixed effects model did not change much in this specific example by switching to the transformation model approach. The originally applied base 10 logarithm falls very close to the fitted “most likely transformation”, i.e., taking the logarithm of the outcome was sufficient to achieve (close) conditional normality. This could be verified through comparing the baseline transformation functions of the normal and non-normal models, which can also serve as a visual check on conditional normality. Moreover, the number of censored outcomes was relatively small in the sample, so taking the censoring properly into account did not result in large differences, either. However, as the example demonstrated, transformation models are flexible enough to accommodate these properties of the response of interest (non-normality and censoring) automatically, without the need to apply ad hoc transformations or to implement new estimation procedures.

## 2 Sea urchin removal experiment

[Andrew and Underwood \(1993\)](#) analyzed the percentage cover of filamentous algae under four sea urchin removal treatments (Control/33%/66%/Removal). The algae colonization was measured on five quadrants located on several larger patches, so there is a clear grouped structure in the data. [Douma and Weedon \(2019\)](#) reanalyzed the data as a demonstration for the usage of mixed-effects models for zero-inflated beta regression models. Here we fit mixed-effects transformation models to the data, and compare the results to zero-inflated mixed-model estimates obtained from `glmmTMB` ([Brooks et al., 2017](#)). Figure 4 presents the empirical cumulative distribution functions of the outcome under the four treatments. Note the large number of zeros, especially in the control group.

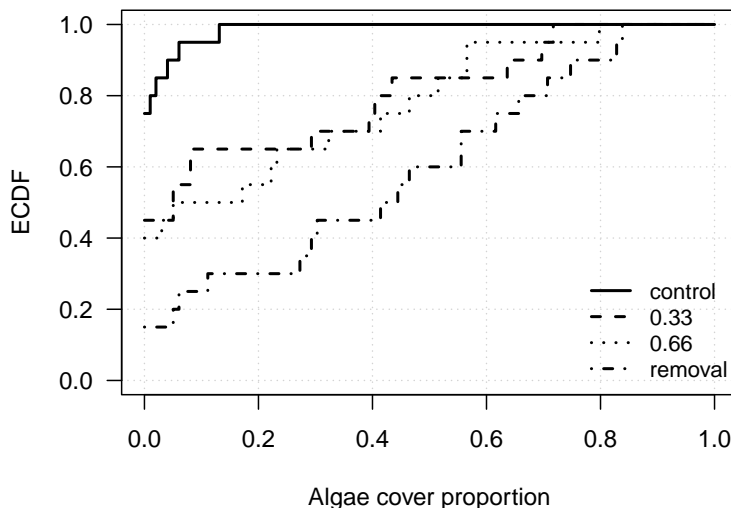


Figure 4: Empirical CDFs of the algae cover proportions under the four treatments.

First we fit a zero-inflated beta regression model with random intercepts for the patches. The probability of observing zero values depends is allowed to vary with the treatment.

```

R> urchin_zib <- glmmTMB(pALGAE ~ TREAT + (1 | PATCH), ziformula = ~ TREAT,
+                        data = andrew, family = beta_family())
R> summary(urchin_zib)

Family: beta (logit)
Formula:          pALGAE ~ TREAT + (1 | PATCH)
Zero inflation:    ~TREAT
Data: andrew

      AIC      BIC   logLik deviance df.resid
    87.2    111.0   -33.6    67.2      70

Random effects:

Conditional model:
Groups Name      Variance Std.Dev.
PATCH (Intercept) 0.124    0.352
Number of obs: 80, groups: PATCH, 16

Dispersion parameter for beta family (): 4.06

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -2.060      0.530   -3.89  0.0001 ***
TREAT0.33      1.280      0.614    2.08  0.0372 *
TREAT0.66      1.374      0.602    2.28  0.0223 *
TREATremoval    1.783      0.585    3.05  0.0023 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Zero-inflation model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    1.099      0.516    2.13  0.03338 *
TREAT0.33     -1.299      0.685   -1.90  0.05772 .
TREAT0.66     -1.504      0.689   -2.18  0.02908 *
TREATremoval  -2.833      0.812   -3.49  0.00048 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

As an alternative to the traditional beta regression approach, we estimate a mixed-effects continuous outcome logistic regression.

```

R> urchin_tram <- ColrME(
+   Surv(pALGAE, pALGAE > 0, type = "left") ~ TREAT + (1 | PATCH),
+   bounds = c(-0.1, 1), support = c(-0.1, 1), data = andrew,
+   order = 6)
R> summary(urchin_tram)

```

Mixed-Effects Continuous Outcome Logistic Regression Model

Formula: `Surv(pALGAE, pALGAE > 0, type = "left") ~ TREAT + (1 | PATCH)`

Fitted to dataset andrew

Fixed effects parameters:

=====

	Estimate	Std. Error	z value	Pr(> z )
TREAT0.33	-2.04	1.31	-1.56	0.1178
TREAT0.66	-2.49	1.31	-1.90	0.0571 .
TREATremoval	-4.10	1.34	-3.06	0.0022 **

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Random effects:

=====

Grouping factor: PATCH (16 levels)

Standard deviation:

(Intercept)

1.48

Log-likelihood: -26.3 (npar = 11)

To allow for a jump in the CDF of the outcome, we expand its bound and treat the zero observations as left-censored. This way, we can place a point mass on zero, i.e., introduce a jump at 0 (see Figure 5).

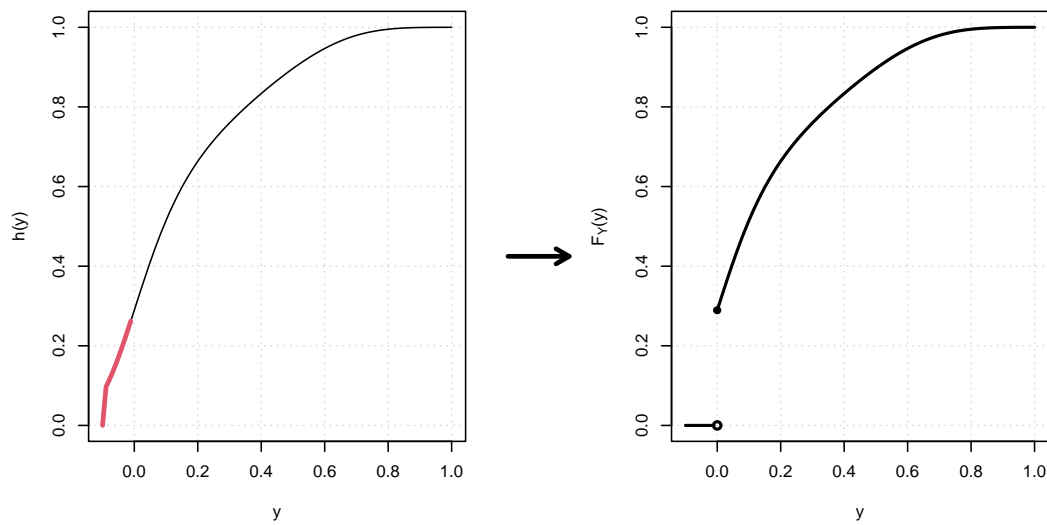


Figure 5: Visual demonstration of how a discrete jump is introduced in the CDF by extending the support and treating the edge cases as censored.

Because the zero-inflated beta model is a mixture of two models, the interpretation of its results is cumbersome. It is not clear which parameters, or combinations of parameters, one needs to inspect to contrast the effects of the various treatments. Moreover, extra steps are needed to calculate the marginal effects of the covariates. In contrast, the mixed-effects transformation model only contains a single set of fixed effects parameters and their interpretation is straightforward: For example, the odds of observing higher proportions of algae cover under the 33% removal treatment is about  $\exp(-\hat{\beta}_{0.33}) = 7.71$  times higher compared to the control group.

To assess the fits of the two models we can marginalize the conditional distributions by integrating over the random effects numerically, and compare against the ECDFs. As Figure 6 shows, both model overestimate the dispersion in the control group.

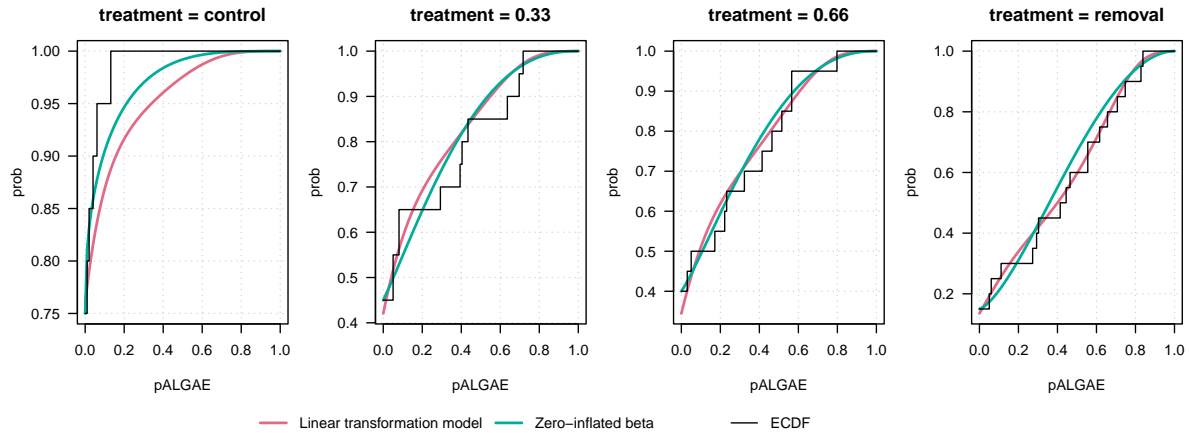


Figure 6: Fitted marginal distributions of algae cover proportion from the zero-inflated beta regression and the mixed-effects transformation model, respectively. The step functions show the empirical cumulative distribution functions in the four treatment groups.

Systematic differences in the outcome variability in the treatment groups occur in many situations (Douma and Weedon, 2019). By modeling the dispersion separately, we can incorporate such differences in the beta regression model.

```
R> urchin_zib_disp <- glmmTMB(pALGAE ~ TREAT + (1 | PATCH),
+                             ziformula = ~ TREAT, dispformula = ~ TREAT,
+                             data = andrew, family = beta_family())
R> summary(urchin_zib_disp)
```

```
Family: beta (logit)
Formula:      pALGAE ~ TREAT + (1 | PATCH)
Zero inflation: ~TREAT
Dispersion:    ~TREAT
Data: andrew
```

AIC	BIC	logLik	deviance	df.resid
87.9	118.8	-30.9	61.9	67

```
Random effects:
```

```
Conditional model:
Groups Name      Variance Std.Dev.
PATCH (Intercept) 0.198    0.445
Number of obs: 80, groups: PATCH, 16

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -2.908      0.420   -6.92 4.5e-12 ***
TREAT0.33      2.158      0.587    3.68 0.00023 ***
TREAT0.66      2.213      0.559    3.96 7.6e-05 ***
TREATremoval    2.595      0.523    4.96 7.0e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Zero-inflation model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    1.099      0.516    2.13 0.03338 *
TREAT0.33     -1.299      0.685   -1.90 0.05772 .
TREAT0.66     -1.504      0.689   -2.18 0.02908 *
TREATremoval   -2.833      0.812   -3.49 0.00048 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    3.612      0.849    4.26 2.1e-05 ***
TREAT0.33     -2.424      0.925   -2.62 0.0087 **
TREAT0.66     -2.279      0.921   -2.47 0.0134 *
TREATremoval   -2.036      0.870   -2.34 0.0193 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In the mixed-effects linear transformation model, we stratify to the treatment group to allow for separate transformation functions.

```
R> urchin_tram_strat <- ColrME(
+   Surv(pALGAE, pALGAE > 0, type = "left") | 0 + TREAT ~ 1 + (1 | PATCH),
+   bounds = c(-0.1, 1), support = c(-0.1, 1), data = andrew,
+   order = 6, control = optim_control(iter.max = 1e3, eval.max = 1e3,
+                                       rel.tol = 1e-9))
R> summary(urchin_tram_strat)
```

Stratified Mixed-Effects Continuous Outcome Logistic Regression Model

Formula: Surv(pALGAE, pALGAE > 0, type = "left") | 0 + TREAT ~ 1 + (1 | PATCH)

```

Fitted to dataset andrew

Fixed effects parameters:
=====

No estimated shift coefficients.

Random effects:
=====

Grouping factor: PATCH (16 levels)
Standard deviation:
(Intercept)
      1.51

Log-likelihood: -22.9 (npar = 29)

```

As Figure 7 illustrates, the two models fit the data much better. However, the cost of this flexibility is that we cannot reduce the group comparisons to inference of a small set of parameters anymore.

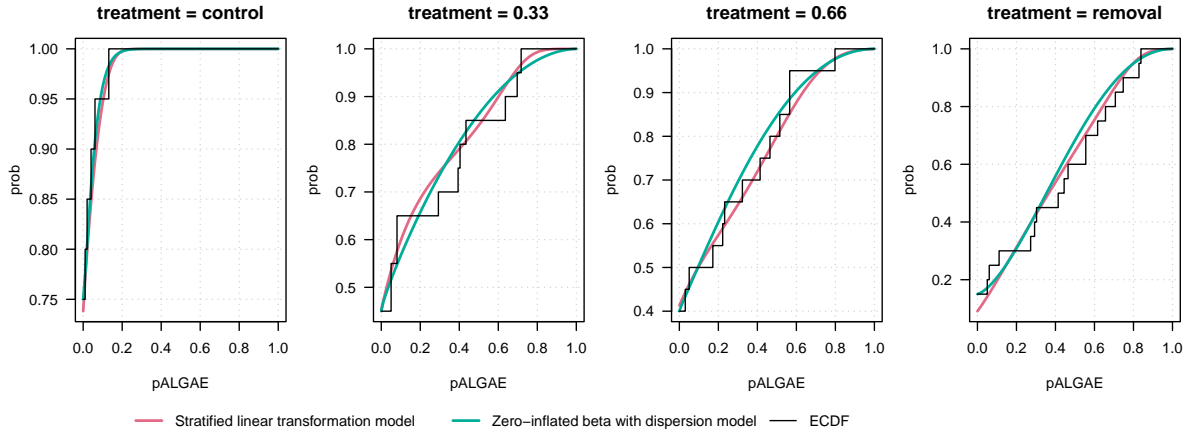


Figure 7: Fitted marginal distributions of algae cover proportion from the zero-inflated beta regression with dispersion model and the stratified mixed-effects transformation model, respectively. The step functions show the empirical cumulative distribution functions in the four treatment groups.

Figures 6 and 7 demonstrate the flexibility of the distribution-free approach of transformation models compared to the parametric alternative. This is also reflected in the log-likelihood values (Table 3).

### 3 Mosquito control trial

Juarez et al. (2021) presented the results of a cluster randomized crossover trial that assessed the efficacy of Autocidal Gravid Ovitraps (AGO) as a tool for against the mosquito species *Aedes aegypti*. The outcome of interest was the number of female mosquitoes collected on glue boards that were placed

Table 3: Log-likelihood values of the four model specifications for the sea urchin removal experiment.

	$\log \mathcal{L}$
Zero-inflated beta w/o dispersion model	-33.60
Linear transformation model	-26.27
Zero-inflated beta w/ dispersion model	-30.93
Stratified linear transformation model	-22.86

either inside or outside the selected houses in various neighborhoods. Within-year patterns in mosquito counts as well as coverage of the treatment in different areas were modeled with non-linear smooths, while unobserved household and community level effects were captured by nested random effects. The original article presented the results of a conditional Poisson and a negative binomial model. We reproduce these results with `gamm4`, and also estimate a mixed-effects additive transformation model for count data with “expt” inverse link function. Detailed exposition of count transformation models is given by [Siegfried and Hothorn \(2020\)](#). For this, we will use the following custom-made ‘CotramME’ model class, which is currently not part of the `tramME` package.

```
R> ## additive count transformation model
R> CotramME <- function(formula, data,
+                       method = c("logit", "cloglog", "loglog", "probit"),
+                       log_first = TRUE, plus_one = log_first, prob = 0.9,
+                       ...) {
+   method <- match.arg(method)
+   rv <- all.vars(formula)[1]
+   stopifnot(is.integer(data[[rv]]), all(data[[rv]] >= 0))
+   data[[rv]] <- data[[rv]] + as.integer(plus_one)
+   sup <- c(-0.5 + log_first, quantile(data[[rv]], prob = prob))
+   bou <- c(-0.9 + log_first, Inf)
+   data[[rv]] <- as.Surv(R(data[[rv]], bounds = bou))
+   fc <- match.call()
+   fc[[1L]] <- switch(method, logit = quote(ColrME), cloglog = quote(CoxphME),
+                      loglog = quote(LehmannME), probit = quote(BoxCoxME))
+   fc$method <- NULL
+   fc$plus_one <- NULL
+   fc$prob <- NULL
+   fc$log_first <- log_first
+   fc$bounds <- bou
+   fc$support <- sup
+   fc$data <- data
+   out <- eval(fc, parent.frame())
+   out$call$data <- match.call()$data
+   class(out) <- c("CotramME", class(out))
+   out
+ }
R> mosquito_tram <- CotramME(AEAfemale ~ Year + Income*Placement
```

```

+   + s(Week) + s(CovRate200) + (1|HouseID)
+   + (1|Community), offset = -log(daystrapping), data = AGO,
+   method = "logit", order = 5, log_first = TRUE, prob = 0.9)

```

Table 4 compares the log-likelihood values of the three model versions. In terms of in-sample model fit, as measured by the log-likelihood value, both the negative binomial and the transformation model perform much better than the Poisson GAMM. The results suggest slight improvement in the model fit when we relax the conditional distribution assumption of the negative-binomial GAMM and follow the distribution-free transformation model approach.

Table 4: Log-likelihood values of the fitted Poisson and negative binomial GAMMs reproduced from [Juarez et al. \(2021\)](#) along with the log-likelihood of an additive transformation model for count data.

	Log-likelihood
Poisson GAMM	-6875.73
Negative binomial GAMM	-4883.26
Additive count transformation model	-4873.07

We will now concentrate on comparing the estimates from the negative binomial and the count transformation models. Note that the scales on which the parameters are interpreted are different in the two models: While, in the negative binomial model, the parametric and smooth terms affect the log of the conditional mean of the outcome, in the transformation model with “logit” link (i.e., “expit” inverse link), they are interpreted on the log-hazard scale. Unlike in the example application of Section 1, we cannot easily transform the negative binomial parameters to the probability scale. Although the magnitudes of the effect estimates of the two models are not directly comparable, their directions, significance and the general patterns of the smooths can be contrasted.

Figure 8 compares the smooth estimates of the GAMM from `gamm4` and the transformation model from `tramME`. Although the within-year time patterns (`s(Week)`) from the two models are almost identical (on different scales), the differences of the smooth estimates of the coverage rate (`s(CovRate200)`) are marked. The general patterns of the smooths are similar, but the negative binomial GAMM penalizes it more, which is also reflected in the EDFs: 2.96 and 17.49 for the negative binomial and count transformation models, respectively.

Because the parametric and smooth terms of the two models are defined on different scales, the magnitudes of the effect estimates are not directly comparable. As Table 5 shows, the directions of the effects match and neither model finds evidence that the main effect of middle income is different from zero.

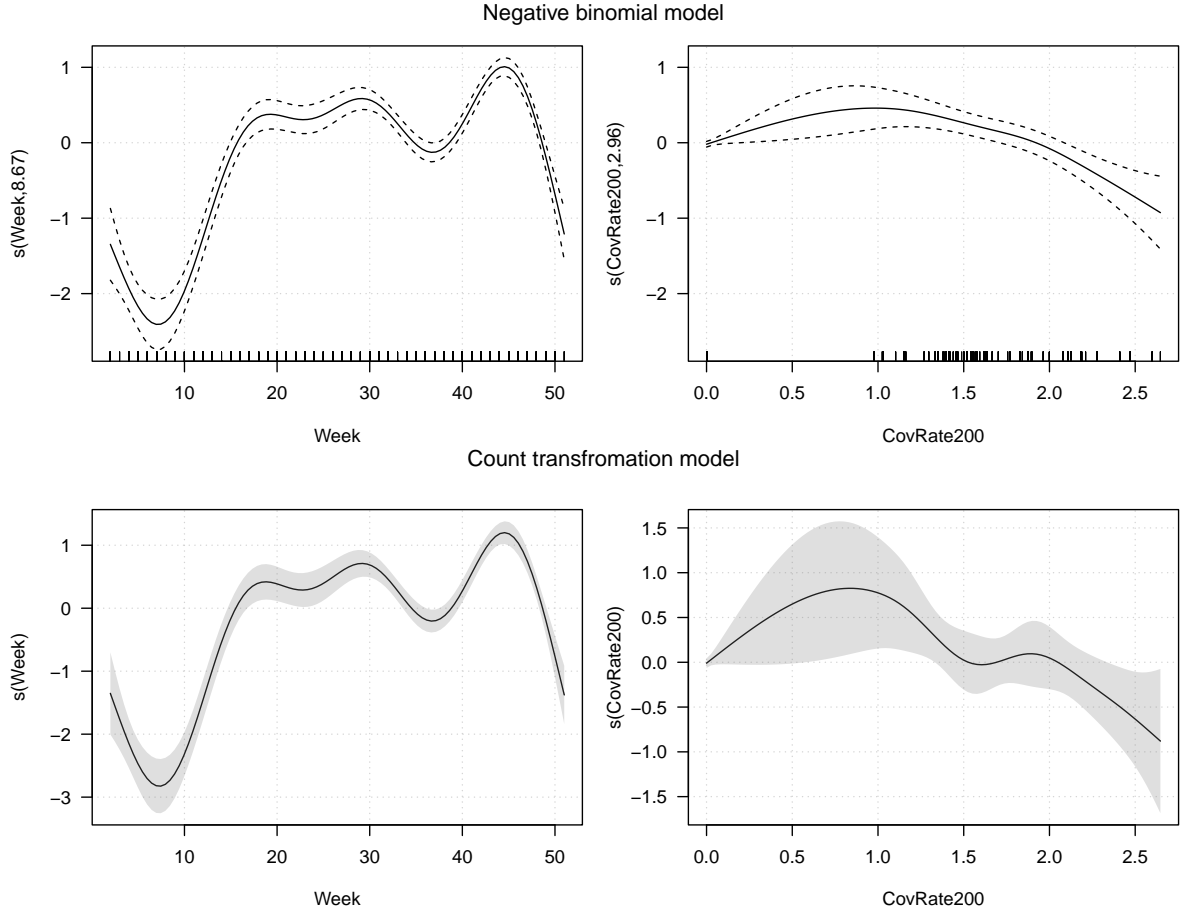


Figure 8: Smooth terms from the negative binomial and transformation models of the *A. aegypti* counts. The dashed lines and the grey areas denote the 95% confidence intervals

Table 5: Point estimates and 95% confidence intervals of the parametric fixed effects terms from the negative binomial and count transformation models of the mosquito control data by [Juarez et al. \(2021\)](#). Note that the scale of the parameters are different and the effect sizes are not directly comparable.

	Negative binomial			Count transformation		
	$\hat{\beta}$	95% CI		$\hat{\beta}$	95% CI	
Year = 2018	-0.20	-0.34	-0.06	-0.35	-0.55	-0.15
Income = middle	-0.78	-1.69	0.13	-0.83	-2.02	0.36
Placement = out	2.37	2.22	2.52	3.01	2.79	3.24
Income = middle & Placement = out	0.38	0.13	0.64	0.51	0.16	0.86

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```

R> sessionInfo()

R version 4.1.2 (2021-11-01)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.4 LTS

Matrix products: default
BLAS:   /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.9.0
LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.9.0

locale:
 [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
 [3] LC_TIME=en_GB.UTF-8      LC_COLLATE=en_US.UTF-8
 [5] LC_MONETARY=en_GB.UTF-8  LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=en_GB.UTF-8     LC_NAME=C
 [9] LC_ADDRESS=C             LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_GB.UTF-8 LC_IDENTIFICATION=C

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base

other attached packages:
 [1] gamm4_0.2-6      lme4_1.1-26      Matrix_1.3-3     xtable_1.8-4
 [5] glmmTMB_1.1.2.3  mgcv_1.8-34      nlme_3.1-152     survival_3.2-13
 [9] tramME_0.1.2.9000 tram_0.6-1       mlt_1.3-2        basefun_1.1-0
[13] variables_1.1-1

loaded via a namespace (and not attached):
 [1] Rcpp_1.0.6      highr_0.8        TMB_1.7.22
 [4] compiler_4.1.2  nloptr_1.2.2.2   tools_4.1.2
 [7] boot_1.3-27     statmod_1.4.35   evaluate_0.14
[10] lattice_0.20-45 polynom_1.4-0     mvtnorm_1.1-1
[13] xfun_0.23       stringr_1.4.0    BB_2019.10-1
[16] knitr_1.36      grid_4.1.2       orthopolynom_1.0-5
[19] multcomp_1.4-17 minqa_1.2.4      TH.data_1.1-0
[22] alabama_2015.3-1 Formula_1.2-4    magrittr_2.0.1
[25] codetools_0.2-18 splines_4.1.2    MASS_7.3-54
[28] numDeriv_2016.8-1.1 quadprog_1.5-8   sandwich_3.0-1
[31] stringi_1.5.3   coneproj_1.14    zoo_1.8-9

```