

# Post-model-fitting procedures with `glmmTMB` models: diagnostics, inference, and model output

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The purpose of this vignette is to describe (and test) the functions in various downstream packages that are available for summarizing and otherwise interpreting `glmmTMB` fits. Some of the packages/functions discussed below may not be suitable for inference on parameters of the zero-inflation or dispersion models, but will be restricted to the conditional-mean model.

```
library(glmmTMB)
library(car)
library(emmeans)
library(effects)
library(multcomp)
library(MuMIn)
library(DHARMa)
library(broom)
library(broom.mixed)
library(dotwhisker)
library(ggplot2); theme_set(theme_bw())
library(texreg)
library(xtable)
library(huxtable)
## retrieve slow stuff
L <- load(system.file("vignette_data", "model_evaluation.rda",
                      package="glmmTMB"))
```

A couple of example models:

```
owls_nb1 <- glmmTMB(SiblingNegotiation ~ FoodTreatment*SexParent +  
                    (1|Nest)+offset(log(BroodSize)),  
                    contrasts=list(FoodTreatment="contr.sum",  
                                   SexParent="contr.sum"),  
                    family = nbinom1,  
                    zi = ~1, data=owls)
```

```
data("cbpp",package="lme4")  
cbpp_b1 <- glmmTMB(incidence/size~period+(1|herd),  
                  weights=size,family=binomial,  
                  data=cbpp)  
## simulated three-term Beta example  
set.seed(1001)  
dd <- data.frame(z=rbeta(1000,shape1=2,shape2=3),  
                 a=rnorm(1000),b=rnorm(1000),c=rnorm(1000))  
simex_b1 <- glmmTMB(z~a*b*c,family=beta_family,data=dd)
```

## 1 model checking and diagnostics

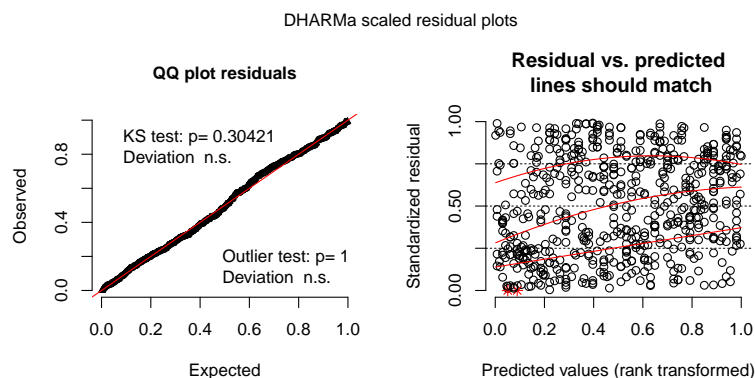
### 1.1 DHARMA

The DHARMA package provides diagnostics for hierarchical models. After running

```
owls_nb1_simres <- simulateResiduals(owls_nb1)
```

you can plot the results:

```
plot(owls_nb1_simres)
```



### 1.1.1 issues

- When you run `simulateResiduals()` you'll notice a long warning (actually a *message*: “It seems you are diagnosing a `glmmTMB` model ...” that explains some issues with `glmmTMB` fits in `DHARMa`
- `DHARMa` will only work for models using families for which a `simulate` method has been implemented (in `TMB` , and appropriately reflected in `glmmTMB` )

## 2 Inference

### 2.1 `car::Anova`

We can use `car::Anova()` to get traditional ANOVA-style tables from `glmmTMB` fits. A few limitations/reminders:

- these tables use Wald  $\chi^2$  statistics for comparisons (neither likelihood ratio tests nor  $F$  tests)
- they apply to the fixed effects of the conditional component of the model only (other components *might* work, but haven't been tested at all)
- as always, if you want to do type 3 tests, you should probably set sum-to-zero contrasts on factors and center numerical covariates (see `contrasts` argument above)

```
Anova(owls_nb1) ## default type II
```

Chisq	Df	Pr(>Chisq)
44.2	1	3e-11
0.032	1	0.858
2.29	1	0.13

```
Anova(owls_nb1, type="III")

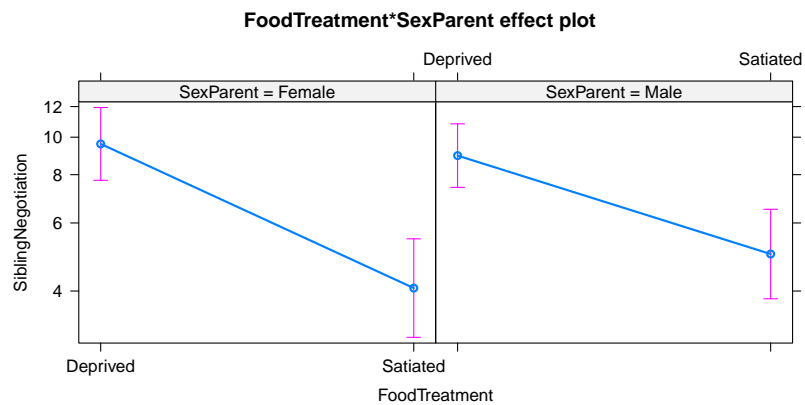
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: SiblingNegotiation
##
##               Chisq Df Pr(>Chisq)
## (Intercept)    21.4354  1  3.66e-06 ***
## FoodTreatment    46.1411  1  1.10e-11 ***
## SexParent        0.5117  1    0.4744
## FoodTreatment:SexParent  2.2900  1    0.1302
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## 2.2 effects

```
(ae <- allEffects(owls_nb1))

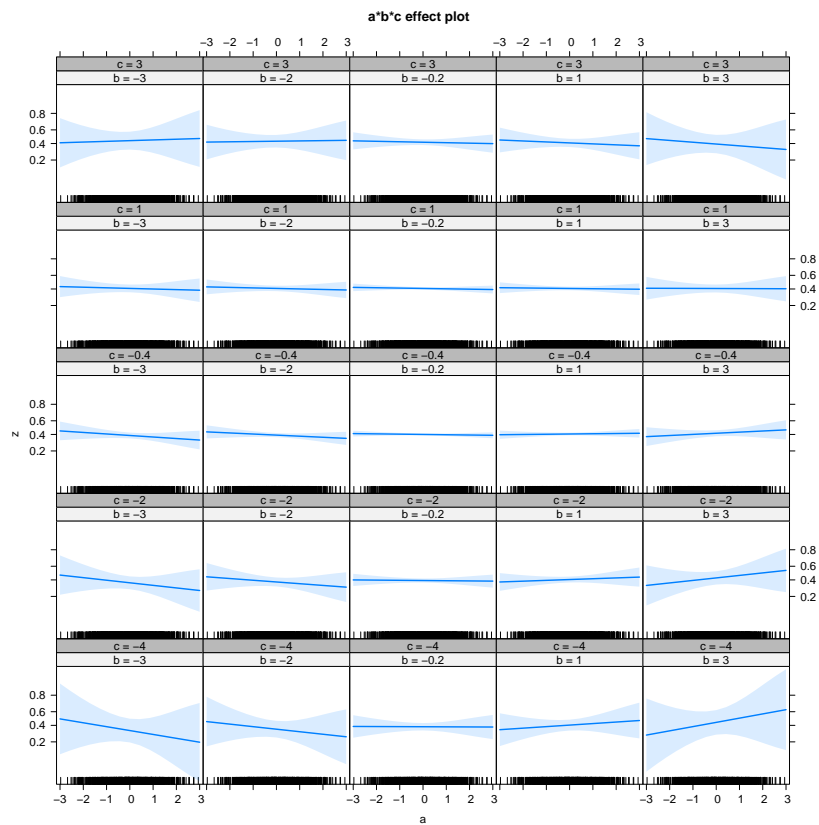
## Warning in Effect.glmmTMB(predictors, mod, vcov. = vcov., ...):
## overriding variance function for effects:  computed variances may
## be incorrect
##
## model: SiblingNegotiation ~ FoodTreatment * SexParent + offset(log(BroodSize))
##
## FoodTreatment*SexParent effect
##
```

```
## offset = 1.439028
##
##           SexParent
## FoodTreatment  Female    Male
##      Deprived 9.607085 8.961150
##      Satiated 4.070916 4.986572
plot(ae)
```



(the error can probably be ignored)

```
plot(allEffects(simex_b1))
```



## 2.3 emmeans

```
emmeans(owls_nb1, poly ~ FoodTreatment | SexParent)

## $emmeans
## SexParent = Female:
## FoodTreatment emmean      SE   df lower.CL upper.CL
## Deprived      2.30 0.1104 592      2.09      2.52
## Satiated       1.44 0.1493 592      1.15      1.74
##
## SexParent = Male:
## FoodTreatment emmean      SE   df lower.CL upper.CL
## Deprived      2.23 0.0964 592      2.04      2.42
## Satiated       1.65 0.1357 592      1.38      1.91
```

```
##
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $contrasts
## SexParent = Female:
## contrast estimate      SE  df t.ratio p.value
## linear      -0.859 0.149 592 -5.776  <.0001
##
## SexParent = Male:
## contrast estimate      SE  df t.ratio p.value
## linear      -0.586 0.129 592 -4.531  <.0001
##
## Results are given on the log (not the response) scale.
```

## 2.4 drop1

`stats::drop1` is a built-in R function that refits the model with various terms dropped. In its default mode it respects marginality (i.e., it will only drop the top-level interactions, not the main effects):

```
system.time(owls_nb1_d1 <- drop1(owls_nb1, test="Chisq"))
```

```
##      user  system elapsed
##    2.656    0.008    2.912
```

```
print(owls_nb1_d1)
```

```
## Single term deletions
##
## Model:
## SiblingNegotiation ~ FoodTreatment * SexParent + (1 | Nest) +
##   offset(log(BroodSize))
##              Df      AIC      LRT Pr(>Chi)
## <none>              3383.6
## FoodTreatment:SexParent  1 3383.9 2.2766  0.1313
```

In principle, using `scope = . ~ . - (1|Nest)` should work to execute a “type-3-like” series of tests, dropping the main effects one at a time while leaving the interaction in (we have to use `-(1|Nest)` to exclude the random effects because `drop1` can’t handle them). However, due to the way that R handles formulas, dropping main effects from an interaction of *\*factors\** has no effect on the overall model. (It would work if we were testing the interaction of continuous variables.)

### 2.4.1 issues

The `mixed` package implements a true “type-3-like” parameter-dropping mechanism for `[g]lmer` models. Something like that could in principle be applied here.

## 2.5 Model selection and averaging with MuMIn

We can run `MuMIn::dredge(owls_nb1)` on the model to fit all possible submodels. Since this takes a little while (45 seconds or so), we’ve instead loaded some previously computed results:

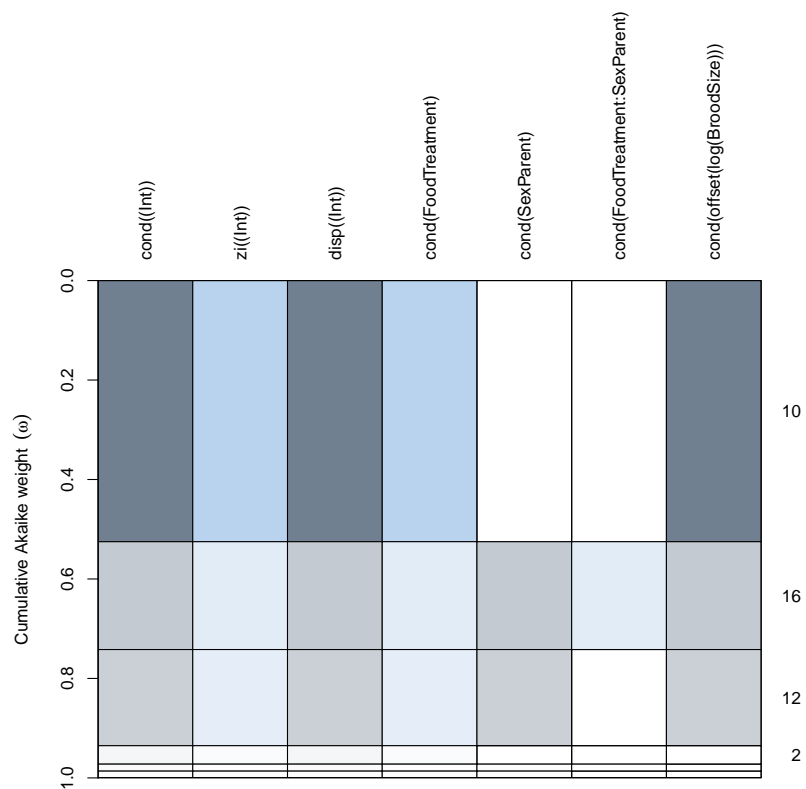
```
owls_nb1_dredge

## Global model call: glmmTMB(formula = SiblingNegotiation ~ FoodTreatment * SexPa
##      (1 | Nest) + offset(log(BroodSize)), data = Owls, family = nbinom1,
##      ziformula = ~1, contrasts = list(FoodTreatment = "contr.sum",
##      SexParent = "contr.sum"), dispformula = ~1)
## ---
## Model selection table
##      cnd((Int))  zi((Int))  dsp((Int))  cnd(FdT)  cnd(SxP)  cnd(FdT:SxP)
## 10      0.4284    -2.094      +          +
## 16      0.4275    -2.055      +          +          +
## 12      0.4257    -2.100      +          +          +
## 2       1.8290    -1.990      +          +
## 8       1.8280    -1.955      +          +          +
## 4       1.8260    -1.996      +          +
## 9       0.6295    -1.373      +
## 1       2.0980    -1.232      +
## 11      0.6220    -1.381      +          +
```



```
## 3      2.0920    -1.236      +      +
##      cnd(off(log(BrS))) df      logLik    AICc delta weight
## 10      + 5 -1685.978 3382.1 0.00 0.525
## 16      + 7 -1684.819 3383.8 1.77 0.217
## 12      + 6 -1685.957 3384.1 2.00 0.193
## 2      5 -1688.628 3387.4 5.30 0.037
## 8      7 -1687.556 3389.3 7.24 0.014
## 4      6 -1688.610 3389.4 7.30 0.014
## 9      + 4 -1708.573 3425.2 43.15 0.000
## 1      4 -1708.672 3425.4 43.35 0.000
## 11      + 5 -1708.420 3426.9 44.88 0.000
## 3      5 -1708.509 3427.1 45.06 0.000
## Models ranked by AICc(x)
## Random terms (all models):
## 'cond(1 | Nest)'
```

```
op <- par(mar=c(2,5,14,3))
plot(owls_nb1_dredge)
```



```
par(op) ## restore graphics parameters
```

Model averaging:

```
model.avg(owls_nb1_dredge)

##
## Call:
## model.avg(object = owls_nb1_dredge)
##
## Component models:
## '14'      '1234'    '124'      '1'        '123'      '12'       '4'        '(Null)'
## '24'      '2'
##
## Coefficients:
```

```
##          cond((Int)) cond(FoodTreatment1) zi((Int)) cond(SexParent1)
## full      0.5183099          0.353877 -2.079432      -0.009556203
## subset    0.5183099          0.353877 -2.079432      -0.021827791
##          cond(FoodTreatment1:SexParent1)
## full              0.01569108
## subset            0.06797533
```

### 2.5.1 issues

- may not work for Beta models because the `family` component ("beta") is not identical to the name of the family function (`beta_family()`)? (Kamil Bartoń, pers. comm.)

## 2.6 multcomp for multiple comparisons and *post hoc* tests

```
glht_glmmTMB <- function (model, ..., component="cond") {
  glht(model, ...,
    coef. = function(x) fixef(x)[[component]],
    vcov. = function(x) vcov(x)[[component]],
    df = NULL)
}
modelparm.glmmTMB <- function (model, coef. = function(x) fixef(x)[[component]],
  vcov. = function(x) vcov(x)[[component]],
  df = NULL, component="cond", ...) {
  multcomp::modelparm.default(model, coef. = coef., vcov. = vcov.,
    df = df, ...)
}
```

```
g1 <- glht(cbpp_b1, linfct = mcp(period = "Tukey"))
summary(g1)

##
## Simultaneous Tests for General Linear Hypotheses
```

```
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: glmmTMB(formula = incidence/size ~ period + (1 | herd), data = cbpp,
##             family = binomial, weights = size, ziformula = ~0, dispformula = ~1)
##
## Linear Hypotheses:
##             Estimate Std. Error z value Pr(>|z|)
## 2 - 1 == 0  -0.9923     0.3066  -3.236  0.00635 **
## 3 - 1 == 0  -1.1287     0.3266  -3.455  0.00283 **
## 4 - 1 == 0  -1.5803     0.4274  -3.697  0.00106 **
## 3 - 2 == 0   -0.1363     0.3807   -0.358  0.98368
## 4 - 2 == 0   -0.5880     0.4703   -1.250  0.58571
## 4 - 3 == 0   -0.4516     0.4843   -0.933  0.78116
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

### 2.6.1 issues

It is possible to make `multcomp` work in a way that (1) actually uses the S3 method structure and (2) doesn't need access to private `multcomp` methods (i.e. accessed by `multcomp:::`)? Not sure, but both of the following hacks should work. (The `glht_glmmTMB` solution below is clunky because it isn't a real S3 method; the `model.parm.glmmTMB` solution can't be included in the package source code as-is because `:::` is not allowed in CRAN package code.)

## 3 Extracting coefficients, coefficient plots and tables

### 3.1 broom and friends

The `broom` and `broom.mixed` packages are designed to extract information from a broad range of models in a convenient (tidy) format; the `dotwhisker` package builds on this platform to draw elegant coefficient plots.

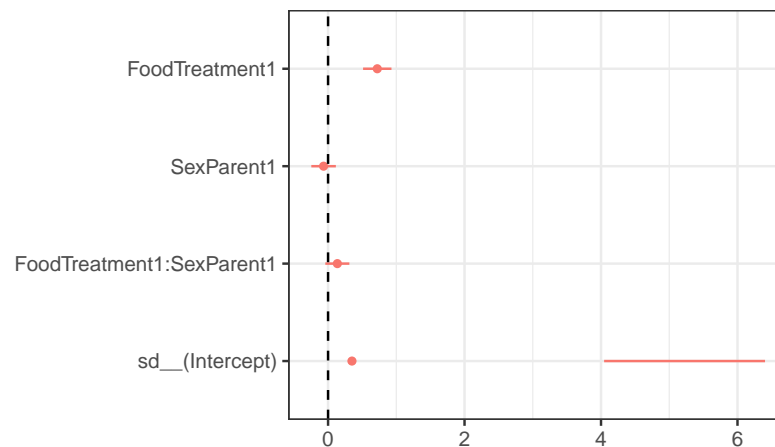
```

(t1 <- broom.mixed::tidy(owls_nb1, conf.int = TRUE))

## # A tibble: 6 x 10
##   effect component group term   estimate std.error statistic    p.value
##   <chr>   <chr>      <chr> <chr>     <dbl>     <dbl>     <dbl>     <dbl>
## 1 fixed   cond        <NA> (Int~    0.427     0.0923      4.63 3.66e- 6
## 2 fixed   cond        <NA> Food~    0.361     0.0532      6.79 1.10e-11
## 3 fixed   cond        <NA> SexP~   -0.0333    0.0466     -0.715 4.74e- 1
## 4 fixed   cond        <NA> Food~    0.0681    0.0450      1.51 1.30e- 1
## 5 fixed   zi          <NA> (Int~   -2.06     0.292     -7.03 2.01e-12
## 6 ran_p~  cond        Nest  sd__~    0.350      NA         NA      NA
## # ... with 2 more variables: conf.low <dbl>, conf.high <dbl>

if (packageVersion("dotwhisker")>"0.4.1") {
  ## to get this version (which fixes various dotwhisker problems)
  ## use devtools::install_github("bbolker/broom.mixed") or
  ## wait for pull request acceptance/submission to CRAN/etc.
  dwplot(owls_nb1)+geom_vline(xintercept=0,lty=2)
} else {
  owls_nb1$coefficients <- TRUE ## hack!
  dwplot(owls_nb1,by_2sd=FALSE)+geom_vline(xintercept=0,lty=2)
}

```



### 3.1.1 issues

(these are more general `dwplot` issues)

- use black rather than `color(1)` when there's only a single model, i.e. only add `aes(colour=model)` conditionally? - draw points even if std err / confint are NA (draw `geom_point()` as well as `geom_pointrange()` ? need to apply all aesthetics, dodging, etc. to both ...)
- for glmmTMB models, allow labeling by component? or should this be done by manipulating the tidied frame first? (i.e.: `tidy(.) \%>\% tidy::unite(term,c(component,term))` )

## 3.2 coefficient tables with xtable

The `xtable` package can output data frames as L<sup>A</sup>T<sub>E</sub>X tables; this isn't quite as elegant as `stargazer` etc., but is not a bad start. I've sprinkled lots of hard line-breaks, spaces, and newlines in below: someone who was better at T<sub>E</sub>X could certainly do a better job. (`xtable` can also produce HTML output.)

```
ss <- summary(owls_nb1)
## print table; add space,
pxt <- function(x,title) {
  cat(sprintf("\n\n\\textbf{%s}\n\\ \\ \\ \\ \\vspace{2pt}\\ \\ \\ \\ \\n",title))
  print(xtable(x), floating=FALSE); cat("\n\n")
  cat("\\ \\ \\ \\ \\vspace{5pt}\\ \\ \\ \\ \\n")
}
```

```
pxt(lme4::formatVC(ss$varcor$cond),"random effects variances")
pxt(coef(ss)$cond,"conditional fixed effects")
pxt(coef(ss)$zi,"conditional zero-inflation effects")
```

#### random effects variances

	Groups	Name	Std.Dev.
1	Nest	(Intercept)	0.35019

### conditional fixed effects

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	0.43	0.09	4.63	0.00
FoodTreatment1	0.36	0.05	6.79	0.00
SexParent1	-0.03	0.05	-0.72	0.47
FoodTreatment1:SexParent1	0.07	0.05	1.51	0.13

### conditional zero-inflation effects

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-2.06	0.29	-7.03	0.00

## 3.3 coefficient tables with texreg

```
source(system.file("other_methods","extract.R",package="glmmTMB"))
texreg(owls_nb1,caption="Owls model", label="tab:owls")
```

See output in Table 1.

## 3.4 coefficient tables with huxtable

The `huxtable` package allows output in either  $\text{\LaTeX}$  or HTML: this example is tuned for  $\text{\LaTeX}$ .

```
cc <- c("intercept (mean)"="(Intercept)",
        "food treatment (starvation)"="FoodTreatment1",
        "parental sex (M)"="SexParent1",
        "food  $\times$  sex"="FoodTreatment1:SexParent1")
```

	Model 1
(Intercept)	0.43*** (0.09)
FoodTreatment1	0.36*** (0.05)
SexParent1	-0.03 (0.05)
FoodTreatment1:SexParent1	0.07 (0.05)
zi_(Intercept)	-2.06*** (0.29)

\*\*\* $p < 0.001$ , \*\* $p < 0.01$ , \* $p < 0.05$

Table 1: Owls model

```
h0 <- huxreg(" "=owls_nb1, # give model blank name so we don't get '(1)'
            tidy_args=list(effects="fixed"),
            coefs=cc,
            error_pos="right",
            statistics="nobs" # don't include logLik and AIC
            )
names(h0)[2:3] <- c("estimate","std. err.")
## allow use of math notation in name
h1 <- set_cell_properties(h0,row=5,col=1,escape_contents=FALSE)
cat(to_latex(h1,tabular_only=TRUE))
```

intercept (mean)	0.427 ***	(0.092)
food treatment (starvation)	0.361 ***	(0.053)
parental sex (M)	-0.033	(0.047)
food × sex	0.068	(0.045)
nobs	599	

\*\*\*  $p < 0.001$ ; \*\*  $p < 0.01$ ; \*  $p < 0.05$ .

### 3.4.1 issues



- `huxtable` needs quite a few additional  $\text{\LaTeX}$  packages: use `report_latex_dependencies()` to see what they are.

## 4 to do

- more plotting methods ( `sjplot` )
- output with `memisc`
- AUC etc. with `ModelMetrics`