Post-model-fitting procedures with \texttt{glmmTMB} models: diagnostics, inference, and model output

March 15, 2020

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.

```r
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:

```r
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

```r
owls_nb1_simres <- simulateResiduals(owls_nb1)

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)
if (requireNamespace("car") && getRversion() >= "3.6.0") {
  Anova(owls_nb1)  ## default type II
  Anova(owls_nb1,type="III")
}

<table>
<thead>
<tr>
<th>Chisq</th>
<th>Df</th>
<th>Pr(&gt;Chisq)</th>
</tr>
</thead>
<tbody>
<tr>
<td>21.4</td>
<td>1</td>
<td>3.66e-06</td>
</tr>
<tr>
<td>46.1</td>
<td>1</td>
<td>1.1e-11</td>
</tr>
<tr>
<td>0.512</td>
<td>1</td>
<td>0.474</td>
</tr>
<tr>
<td>2.29</td>
<td>1</td>
<td>0.13</td>
</tr>
</tbody>
</table>

### 2.2 effects

effects_ok <- (requireNamespace("effects") && getRversion() >= "3.6.0")
if (effects_ok) {
  (ae <- allEffects(owls_nb1))
  plot(ae)
}

## Warning in Effect.glmmTMB(predictors, mod, vcov. = vcov., ...):
## overriding variance function for effects: computed variances may
## be incorrect

![FoodTreatment*SexParent effect plot](image_url)
if (effects_ok) {
    plot(allEffects(simex_b1))
}

2.3 emmeans

emmeans(owls_nb1, poly ~ FoodTreatment | SexParent)

## 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):

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

```
## user system elapsed
## 1.894  0.020  1.930
```

```r
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:

```r
owls_nb1_dredge
```

```r
op <- par(mar=c(2,5,14,3))
plot(owls_nb1_dredge)
```
<table>
<thead>
<tr>
<th>cond((Int))</th>
<th>zi((Int))</th>
<th>disp((Int))</th>
<th>cond(FoodTreatment)</th>
<th>cond(SexParent)</th>
<th>cond(FoodTreatment:SexParent)</th>
<th>cond(offset(log(BroodSize)))</th>
<th>AICc</th>
<th>Cumulative Akaike weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.428</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>2.09</td>
<td>1.0</td>
</tr>
<tr>
<td>0.427</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>2.06</td>
<td>0.8</td>
</tr>
<tr>
<td>0.426</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>2.1</td>
<td>0.6</td>
</tr>
<tr>
<td>1.83</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>1.99</td>
<td>0.4</td>
</tr>
<tr>
<td>1.83</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>1.96</td>
<td>0.2</td>
</tr>
<tr>
<td>1.83</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>2</td>
<td>0.1</td>
</tr>
<tr>
<td>1.83</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>2</td>
<td>0.1</td>
</tr>
<tr>
<td>0.63</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>1.37</td>
<td>0.0</td>
</tr>
<tr>
<td>2.1</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>1.23</td>
<td>0.0</td>
</tr>
<tr>
<td>2.09</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>1.24</td>
<td>0.0</td>
</tr>
</tbody>
</table>
par(op) ## restore graphics parameters

Model averaging:

```r
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

```r
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.

```r
if (requireNamespace("broom.mixed") && requireNamespace("dotwhisker")) {
  (t1 <- broom.mixed::tidy(owls_nb1, conf.int = TRUE))
  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 `dwpot` 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(.) \%>\% tidyr::unite(term,c(component,term))`)

3.2 coefficient tables with `xtable`

The `xtable` package can output data frames as `\LaTeX` 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 `\LaTeX` could certainly do a better job. (`xtable` can also produce HTML output.)

```r
ss <- summary(owls_nb1)
## print table; add space,
pxt <- function(x,title) {
```
random effects variances

<table>
<thead>
<tr>
<th>Groups</th>
<th>Name</th>
<th>Std.Dev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Nest (Intercept)</td>
<td>0.35019</td>
</tr>
</tbody>
</table>

contingual 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    |

contingual 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
### Table 1: Owls model

<table>
<thead>
<tr>
<th></th>
<th>Model 1</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>0.43***</td>
</tr>
<tr>
<td></td>
<td>(0.09)</td>
</tr>
<tr>
<td>FoodTreatment1</td>
<td>0.36***</td>
</tr>
<tr>
<td></td>
<td>(0.05)</td>
</tr>
<tr>
<td>SexParent1</td>
<td>-0.03</td>
</tr>
<tr>
<td></td>
<td>(0.05)</td>
</tr>
<tr>
<td>FoodTreatment1:SexParent1</td>
<td>0.07</td>
</tr>
<tr>
<td></td>
<td>(0.05)</td>
</tr>
<tr>
<td>zi_(Intercept)</td>
<td>-2.06***</td>
</tr>
<tr>
<td></td>
<td>(0.29)</td>
</tr>
</tbody>
</table>

***p < 0.001, **p < 0.01, *p < 0.05

3.4 **Coefficient tables with huxtable**

The **huxtable** package allows output in either \( \LaTeX \) or HTML: this example is tuned for \( \LaTeX \).

```r
cc <- c("intercept (mean)"="(Intercept)",
        "food treatment (starvation)"="FoodTreatment1",
        "parental sex (M)"="SexParent1",
        "food \times sex"="FoodTreatment1:SexParent1")
h0 <- huxreg(""=owls_nb1, tidys=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.")
```

See output in Table 1.
## allow use of math notation in name

```r
h1 <- set_cell_properties(h0,row=5,col=1,escape_contents=FALSE)
cat(to_latex(h1,tabular_only=TRUE))
```

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>intercept (mean)</td>
<td>0.427</td>
<td>***</td>
</tr>
<tr>
<td>food treatment (starvation)</td>
<td>0.361</td>
<td>***</td>
</tr>
<tr>
<td>parental sex (M)</td>
<td>-0.033</td>
<td></td>
</tr>
<tr>
<td>food $\times$ sex</td>
<td>0.068</td>
<td></td>
</tr>
<tr>
<td>nobs</td>
<td>599</td>
<td></td>
</tr>
</tbody>
</table>

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

### 3.4.1 issues

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

### 4 influence measures

Influence measures quantify the effects of particular observations, or groups of observations, on the results of a statistical model; leverage and Cook’s distance are the two most common formats for influence measures. If a projection matrix (or “hat matrix”) is available, influence measures can be computed efficiently; otherwise, the same quantities can be estimated by brute-force methods, refitting the model with each group or observation successively left out.

We’ve adapted the `car::influence.merMod` function to handle \texttt{glmmTMB} models; because it uses brute force, it can be slow, especially if evaluating the influence of individual observations. For now, it is included as a separate source file rather than exported as a method (see below), although it may be included in the package (or incorporated in the \texttt{car} package) in the future.

```r
source(system.file("other_methods","influence_mixed.R", package="glmmTMB"))
```
owls_nb1_influence_time <- system.time(
  owls_nb1_influence <- influence_mixed(owls_nb1, groups="Nest")
)

Re-fitting the model with each of the 27 nests excluded takes 50 seconds (on an old Macbook Pro). The \texttt{car::infIndexPlot()} function is one way of displaying the results:

\texttt{car::infIndexPlot(owls_nb1_influence)}

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{diagram.png}
\caption{Diagnostic Plots}
\end{figure}

Or, you can transform the results and plot them however you like:

\begin{verbatim}
inf <- as.data.frame(owls_nb1_influence["fixed.effects[-Nest]"]) inf <- transform(inf, nest=rownames(inf), cooks=cooks.distance(owls_nb1_influence))
\end{verbatim}
inf$ord <- rank(inf$cooks)
if (require(reshape2)) {
  inf_long <- melt(inf, id.vars=c("ord","nest"))
  gg_infl <- (ggplot(inf_long,aes(ord,value))
    + geom_point()
    + facet_wrap(~variable, scale="free_y")
    + scale_x_reverse(expand=expand_scale(mult=0.15))
    + scale_y_continuous(expand=expand_scale(mult=0.15))
    + geom_text(data=subset(inf_long,ord>24),
      aes(label=nest),vjust=-1.05)
  )
  print(gg_infl)
}

## Warning: ‘expand_scale()’ is deprecated; use ‘expansion()’ instead.
## Warning: ‘expand_scale()’ is deprecated; use ‘expansion()’ instead.

5 to do

- more plotting methods (sjplot)
• output with \texttt{memisc}

• AUC etc. with \texttt{ModelMetrics}