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

July 13, 2021

The purpose of this vignette is to describe (and test) the functions in various downstream packages that are available for summarizing and otherwise interpreting \texttt{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)
require(DHARMa, quietly = TRUE) ## may be missing ...
library(broom)
library(broom.mixed)
library(dotwhisker)
library(ggplot2); theme_set(theme_bw())
library(texreg)
library(xtable)
if (huxtable_OK) 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)
```

```r
data("cbpp",package="lme4")
cbpp_b1 <- glmmTMB(incidence/size~period+(1|herd),
weights=size,family=binomial,
data=cbpp)
```

```r
## 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)
```

## model checking and diagnostics

### DHARMa

The DHARMa package provides diagnostics for hierarchical models. After running

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

you can plot the results:

```r
plot(owls_nb1_simres)
```
DHARMa provides lots of other methods based on the simulated residuals: see vignette("DHARMa", package="DHARMa")

1.1.1 issues

- 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
(the error can probably be ignored)

```r
if (effects_ok) {
  plot(allEffects(simex_b1))
}
```
2.3 `emmeans`

```r
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
### 6.208 0.000 6.208

print(owls_nb1_d1)

## Single term deletions
##
## ## Model:
## ## SiblingNegotiation ~ FoodTreatment * SexParent + (1 | Nest) +
## ##   offset(log(BroodSize))
## ## <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:
print(owls_nb1_dredge)

## Global model call: glmmTMB(formula = SiblingNegotiation ~ FoodTreatment * SexParent + (1 | Nest) + offset(log(BroodSize)), data = Owls, family = nbinom1, ziformula = ~1, contrasts = list(FoodTreatment = "contr.sum", SexParent = "contr.sum"), na.action = na.fail, 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:
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

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  0.00638 **
## 3 - 1 == 0  -1.1287    0.3266  -3.455  0.00283 **
## 4 - 1 == 0  -1.5803    0.4274  -3.697  0.00111 **
## 3 - 2 == 0  -0.1363    0.3807  -0.358  0.72364
## 4 - 2 == 0  -0.5880    0.4703  -1.250  0.21222
## 4 - 3 == 0  -0.4516    0.4843  -0.933  0.35165
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)
  t1 <- transform(t1,
      term=sprintf("%s.%s", component, term))

  if (packageVersion("dotwhisker")>"0.4.1") {
    dw <- dwplot(t1)
  } else {
    owls_nb1$coefficients <- TRUE  ## hack!
    dw <- dwplot(owls_nb1, by_2sd=FALSE)
  }

  print(dw+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(.) \%>\% tidyr::unite(term,c(component))`)

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) {
  cat(sprintf("\\n\\n``textbf{\%s}\n\\n \\\n``vspace{2pt}\" \",title))
```
```r
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

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

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

For now, to avoid needing to import the texreg package, we are providing the required extract.glmmTMB in a separate R file that you can import with source(), as follows:
### Model 1

<table>
<thead>
<tr>
<th>Term</th>
<th>Coefficient</th>
<th>Std. Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>0.43***</td>
<td>(0.09)</td>
</tr>
<tr>
<td>FoodTreatment1</td>
<td>0.36***</td>
<td>(0.05)</td>
</tr>
<tr>
<td>SexParent1</td>
<td>-0.03</td>
<td>(0.05)</td>
</tr>
<tr>
<td>FoodTreatment1:SexParent1</td>
<td>0.07</td>
<td>(0.05)</td>
</tr>
<tr>
<td>zi_(Intercept)</td>
<td>-2.06***</td>
<td>(0.29)</td>
</tr>
</tbody>
</table>

***p < 0.001; **p < 0.01; *p < 0.05

Table 1: Owls model

```r
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 \LaTeX{} or HTML: this example is tuned for \LaTeX{}.

```r
if (!huxtable_OK) {
cat("Sorry, huxtable+LaTeX is unreliable on this platform; skipping\n")
} else {
cc <- c("intercept (mean)"="(Intercept)",
"food treatment (starvation)"="FoodTreatment1",
"parental sex (M)"="SexParent1",
"food \times sex"="FoodTreatment1:SexParent1")
h0 <- huxreg(" " = owls_nb1, # give model blank name so we don't get '(1)'
tidy_args = list(effects="fixed"),
coefs = cc,
error_pos = "right",
```

14
```r
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))
```

<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 × sex</td>
<td>0.068</td>
<td>(0.045)</td>
</tr>
</tbody>
</table>

nobs 599

*** 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 `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 car package) in the future.

```r
source(system.file("other_methods","influence_mixed.R", package="glmmTMB"))
```

```r
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 16 seconds (on an old Macbook Pro). The `car::infIndexPlot()` function is one way of displaying the results:

```r
car::infIndexPlot(owls_nb1_influence)
```

Or, you can transform the results and plot them however you like:
inf <- as.data.frame(owls_nb1_influence["fixed.effects[-Nest]"])
inf <- transform(inf,
    nest=rownames(inf),
    cooks=cooks.distance(owls_nb1_influence))
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")
        ## n.b. may need expand_scale() in older ggplot versions ?
        + scale_x_reverse(expand=expansion(mult=0.15))
        + scale_y_continuous(expand=expansion(mult=0.15))
        + geom_text(data=subset(inf_long,ord>24),
            aes(label=nest),vjust=-1.05)
    )
    print(gg_infl)
}

## Loading required package: reshape2

```r
# Loading required package: reshape2
```
5  to do

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