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

April 6, 2023

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)
require(DHARMa, quietly = TRUE) ## may be missing ...
library(broom)
library(broom.mixed)
require(dotwhisker, quietly = TRUE)
library(ggplot2); theme_set(theme_bw())
library(texreg)
library(xtable)
if (huxtable_OK) library(huxtable)
## retrieve slow stuff
L <- gt_load("vignette_data/model_evaluation.rda")
```

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)
## 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

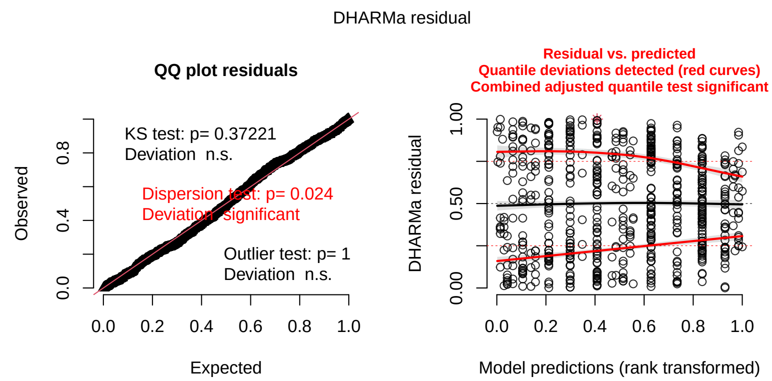
1.1 DHARMa

The DHARMa package provides diagnostics for hierarchical models. After running

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

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 χ^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)

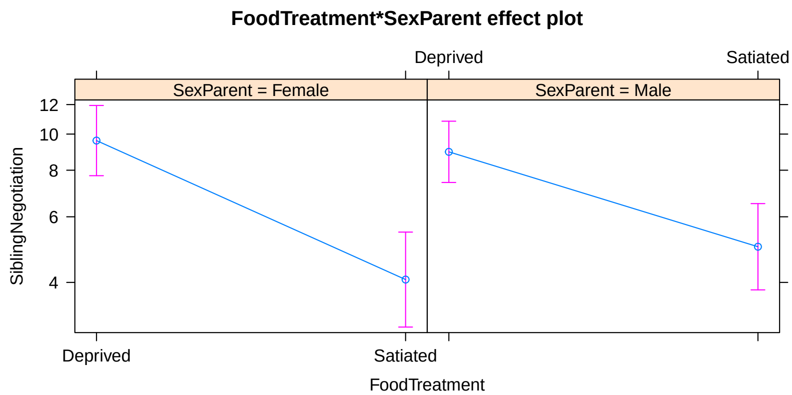
```r
if (requireNamespace("car") && getRversion() >= "3.6.0") {
    Anova(owls_nb1)  ## default type II
    Anova(owls_nb1,type="III")
}
```

Chisq	Df	Pr(>Chisq)
21.4	1	3.66e-06
46.1	1	1.1e-11
0.512	1	0.474
2.29	1	0.13

2.2 effects

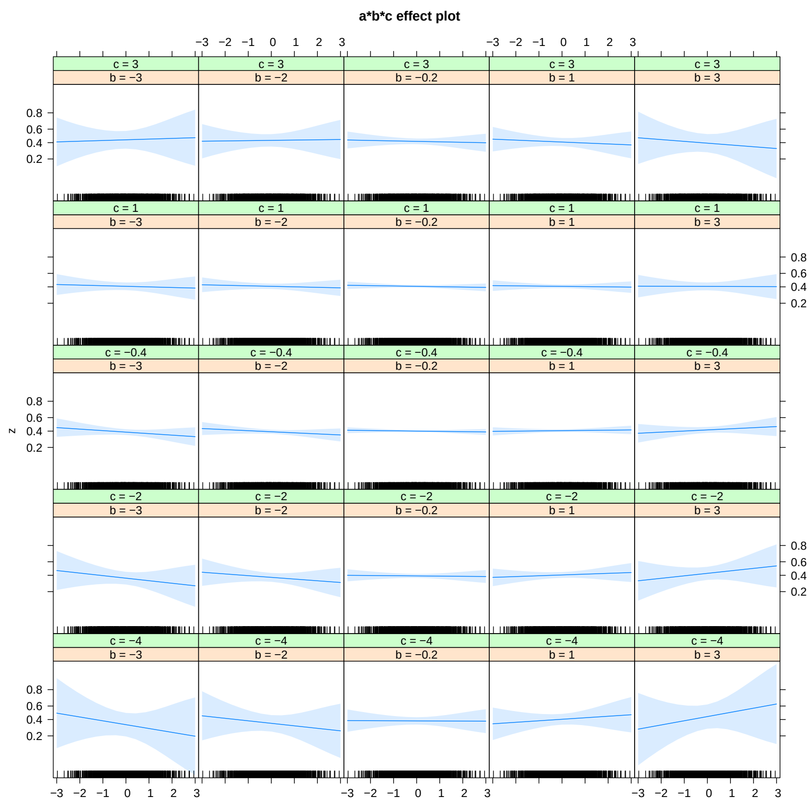
```r
effects_ok <- (requireNamespace("effects") && getRversion() >= "3.6.0")
if (effects_ok) {
    (ae <- allEffects(owls_nb1))
    plot(ae)
}

## 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

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

## $emmeans
## SexParent = Female:
##  FoodTreatment emmean     SE  df asymp.LCL asymp.UCL
##  Deprived        2.30 0.1104 Inf      2.09      2.52
##  Satiated        1.44 0.1493 Inf      1.15      1.74
##
## SexParent = Male:
##  FoodTreatment emmean     SE  df asymp.LCL asymp.UCL
##  Deprived        2.23 0.0964 Inf      2.04      2.42
##  Satiated        1.65 0.1357 Inf      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 z.ratio p.value
##  linear     -0.859 0.149 Inf  -5.776  <.0001
##
## SexParent = Male:
##  contrast estimate    SE  df z.ratio p.value
##  linear     -0.586 0.129 Inf  -4.531  <.0001
##
## Results are given on the log (not the response) scale.
```

Let us also consider a corresponding hurdle model:

```
owls_hnb1 <- update(owls_nb1, family = truncated_nbinom1, ziformula = ~.)
```

On the response scale, this model estimates the means of the component distribution as follows:

```r
emmeans(owls_hnb1, ~ FoodTreatment * SexParent, component = "cond", type = "respor

##  FoodTreatment SexParent response    SE  df asymp.LCL asymp.UCL
##  Deprived      Female       10.04 0.932 Inf      8.37     12.05
##  Satiated      Female        7.08 0.830 Inf      5.63      8.91
##  Deprived      Male          9.31 0.716 Inf      8.01     10.83
##  Satiated      Male          7.37 0.726 Inf      6.08      8.94
##
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale

# --- or ---
emmeans(owls_hnb1, ~ FoodTreatment * SexParent, component = "cmean")

##  FoodTreatment SexParent emmean    SE  df asymp.LCL asymp.UCL
##  Deprived      Female     10.19 0.888 Inf      8.45     11.93
##  Satiated      Female      7.46 0.738 Inf      6.02      8.91
##  Deprived      Male        9.50 0.677 Inf      8.17     10.83
##  Satiated      Male        7.72 0.653 Inf      6.44      9.00
##
## Confidence level used: 0.95
```

These estimates differ because the first ones are back-transformed from the linear predictor, which is based on the *un-truncated* component distribution, while the second ones are estimates of the means of the *truncated* distribution (with zero omitted). This discrepancy occurs only with hurdle models.

The response means combine both the conditional and the zero-inflation model:

```r
emmeans(owls_hnb1, ~ FoodTreatment * SexParent, component = "response")

##  FoodTreatment SexParent emmean    SE  df asymp.LCL asymp.UCL
##  Deprived      Female      8.86 0.874 Inf      7.14     10.57
##  Satiated      Female      3.99 0.692 Inf      2.63      5.35
##  Deprived      Male        8.72 0.668 Inf      7.41     10.03
##  Satiated      Male        4.74 0.662 Inf      3.44      6.03
##
## Confidence level used: 0.95
```

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
##   2.374   0.006   2.388
```

```
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.

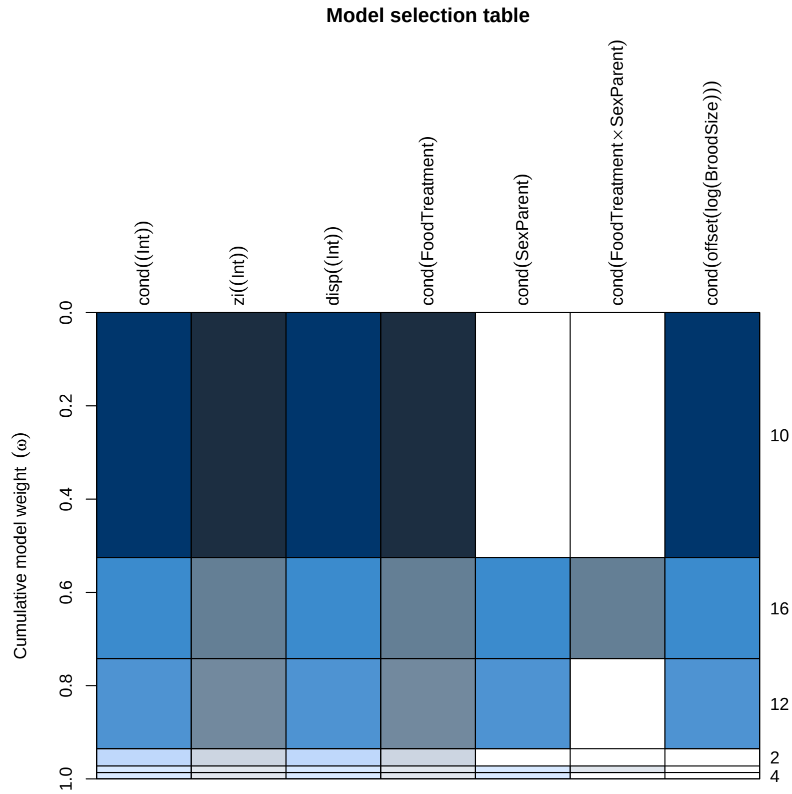
2.5 Model selection and averaging with MuMIn

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:

```
print(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"), 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)
```

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




```r
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

```
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  0.98368
## 4 - 2 == 0  -0.5880     0.4703  -1.250  0.58569
## 4 - 3 == 0  -0.4516     0.4843  -0.933  0.78117
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

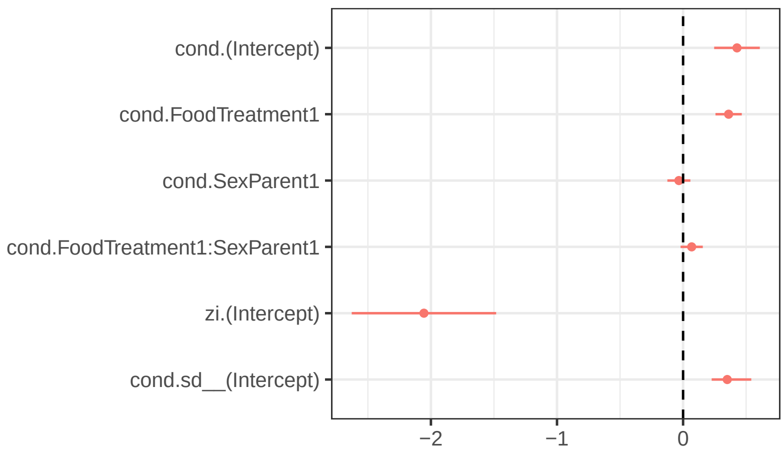
3 Extracting coefficients, coefficient plots and tables

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.

```
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(co`

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 TeX 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`

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
(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

```
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.

```
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",
```

```
                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 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.

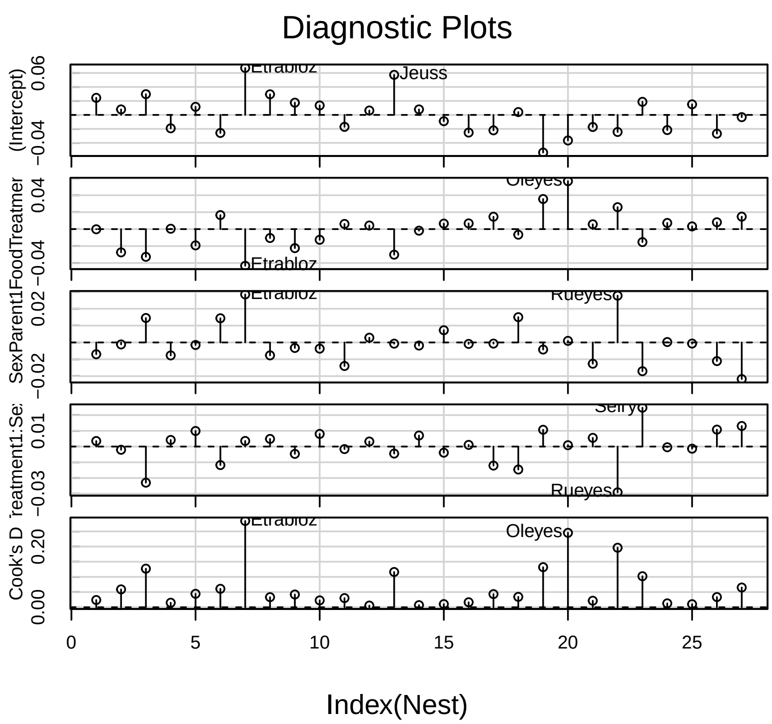
We've adapted the `car::influence.merMod` function to handle `glmmTMB` models; because it uses brute force, it can be slow, especially if evaluating the influence of individual observations. For now, it is included as a separate source file rather than exported as a method (see below), although it may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

```
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")
)
```

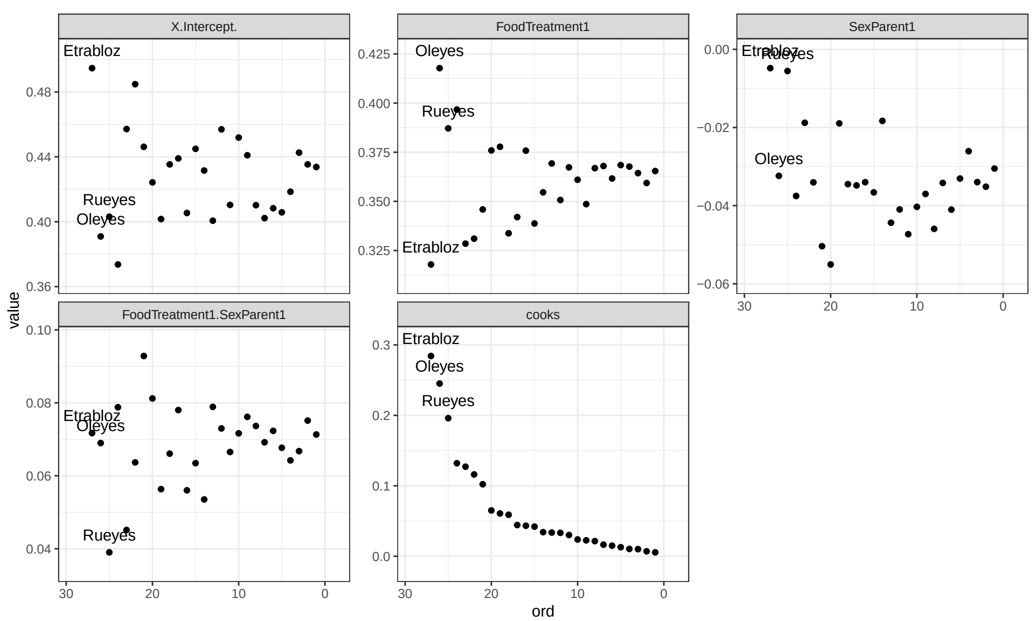
Re-fitting the model with each of the 27 nests excluded takes 16 seconds (on an old Macbook Pro). The `car::infIndexPlot()` function is one way of displaying the results:

```
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)
}
```



5 to do

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