

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)
## temporarily disabled: causes problems with <<caranova1>> chunk?
## library(huhtable)
## 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

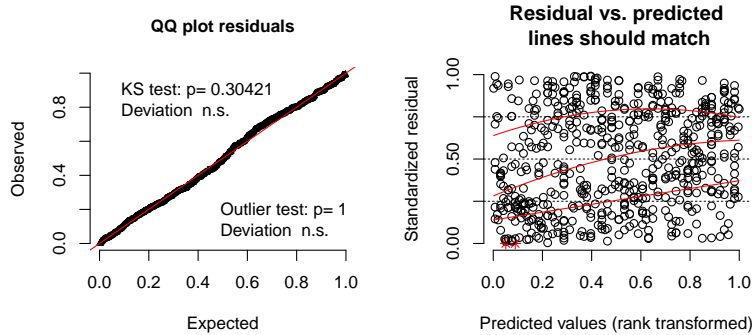
The DHARMA package provides diagnostics for hierarchical models. After running

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

you can plot the results:

```
plot(owls_nb1_simres)
```

DHARMa scaled residual plots



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)

```

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

```

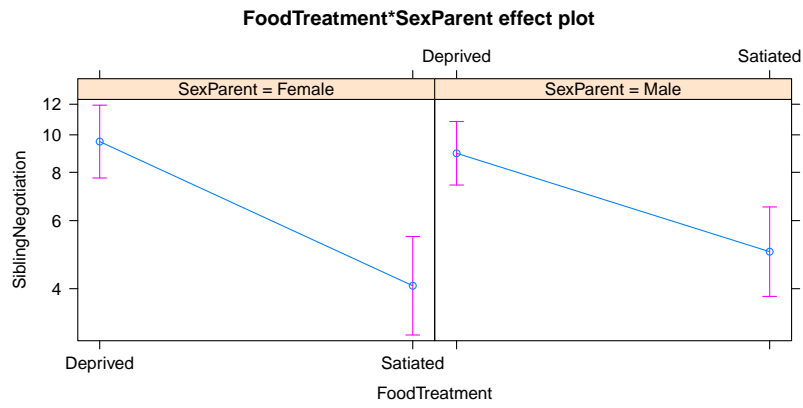
2.2 effects

```

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

```

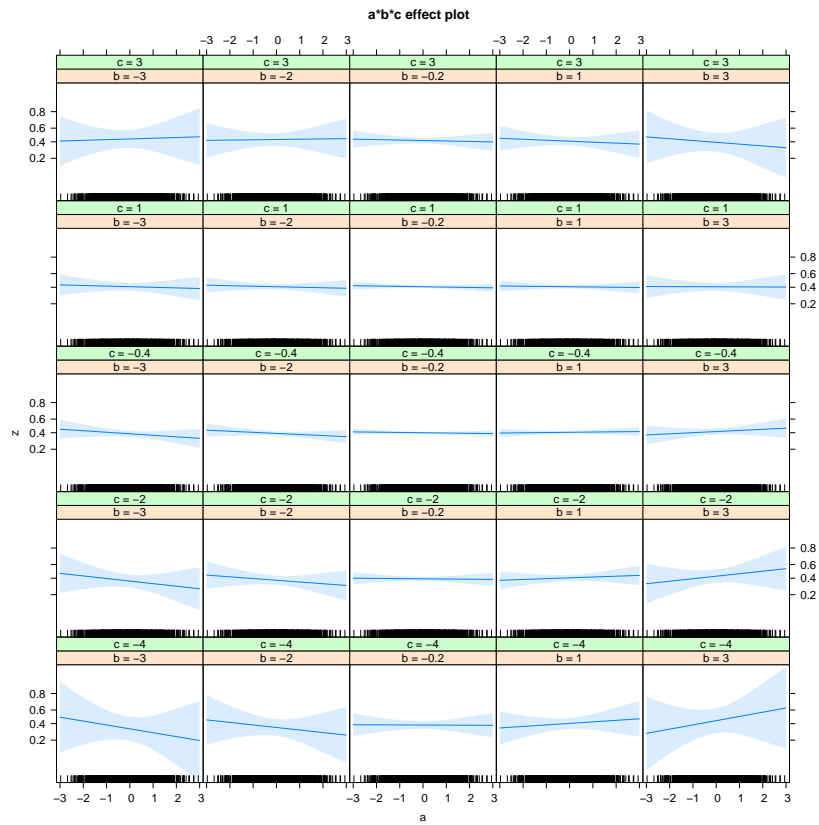


(the error can probably be ignored)

```

if (effects_ok) {
  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  
##    1.974    0.019    2.089
```

```
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

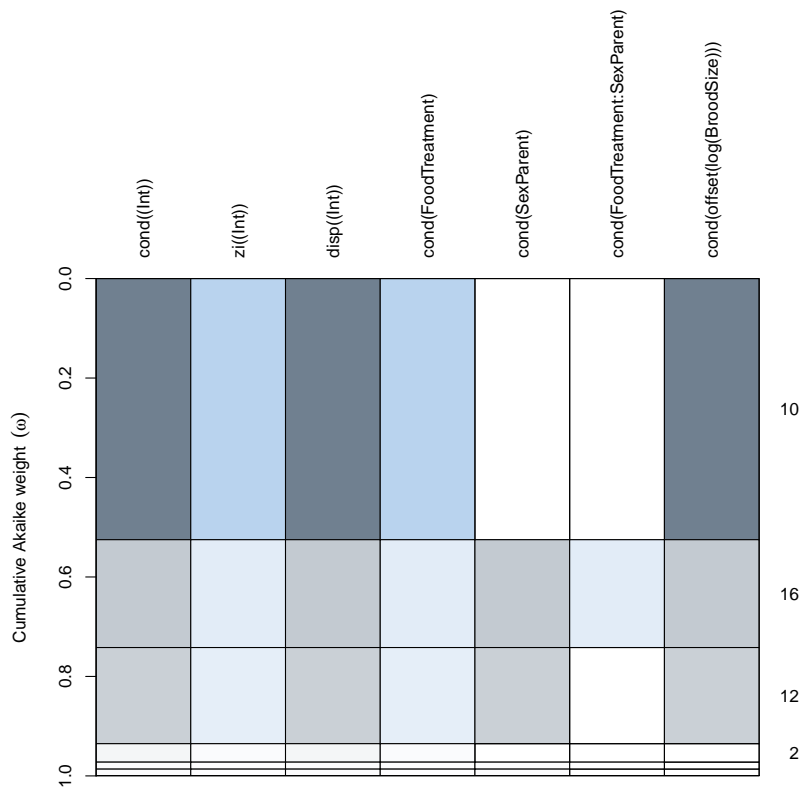
## Global model call: glmmTMB(formula = SiblingNegotiation ~ FoodTreatment * SexPa
##      (1 | Nest) + offset(log(BroodSize)), data = Owls, family = nbinom1,
##      ziformula = ~1, contrasts = list(FoodTreatment = "contr.sum",
##      SexParent = "contr.sum"), dispformula = ~1)
## ---
## Model selection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

```
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
```

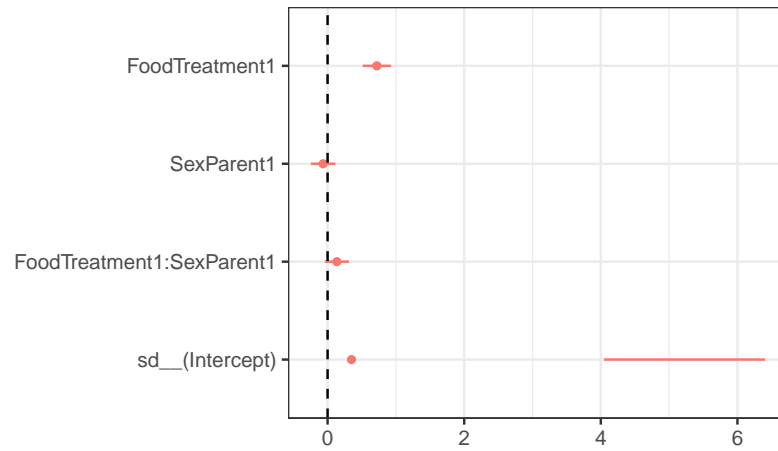
```
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
## (Adjusted p values reported -- single-step method)
```

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))  
  if (packageVersion("dotwhisker")>"0.4.1") {  
    dw <- dwplot(owls_nb1)  
  } 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, 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 \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) {
```


	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(), as follows:

```
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 . *The current version (5.0.0) is giving us a little bit of trouble, so we've temporarily disabled evaluation of this code chunk ...*

```
library("huxtable")
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))

```

3.4.1 issues

- `huxtable` needs quite a few additional L^AT_EX 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.

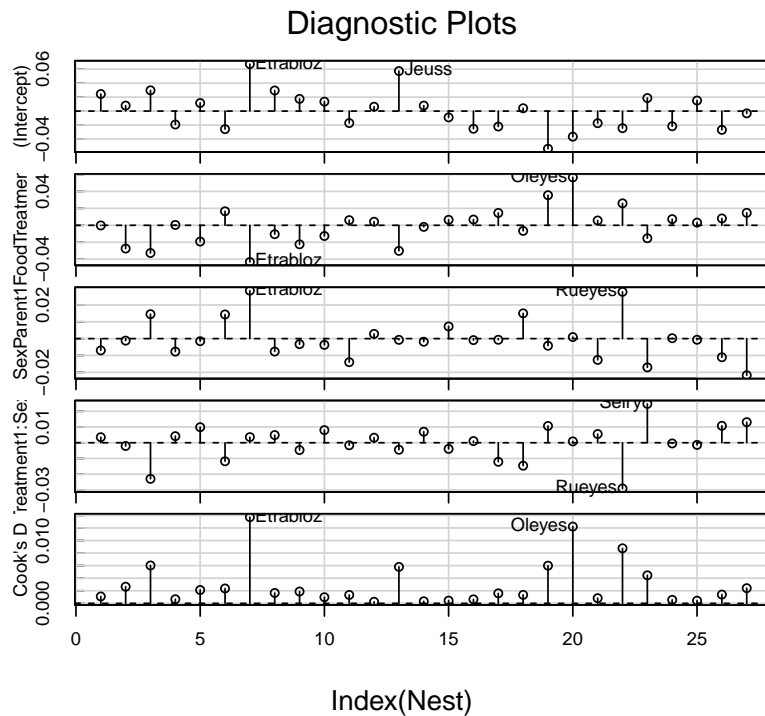
We’ve adapted the `car::influence.merMod` function to handle `glmmTMB` models; because it uses brute force, it can be slow, especially if evaluating the influence of individual observations. For now, it is included as a separate source file rather than exported as a method (see below), although it may 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 50 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:

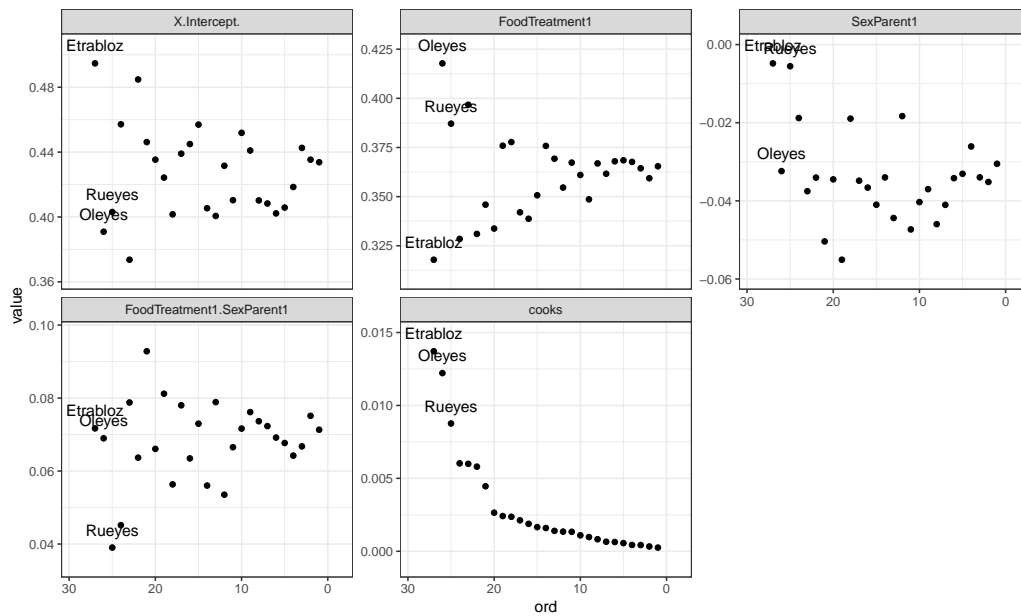
```
inf <- as.data.frame(owls_nb1_influence[["fixed.effects[-Nest]"]])
inf <- transform(inf,
                 nest=rownames(inf),
                 cooks=cooks.distance(owls_nb1_influence))
inf$ord <- rank(inf$cooks)
if (require(reshape2)) {
  inf_long <- melt(inf, id.vars=c("ord","nest"))
  gg_infl <- (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