

Getting started with the `glmmADMB` package

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1 Introduction/quick start

`glmmADMB` is a package, built on the open source AD Model Builder nonlinear fitting engine, for fitting generalized linear mixed models and extensions.

- response distributions: Poisson, binomial, negative binomial (NB1 and NB2 parameterizations), Gamma, Beta
- link functions: log, logit, probit
- zero-inflation (models with a constant zero-inflation value only)
- single, nested, or crossed random effects
- offsets
- post-fit MCMC chain for characterizing uncertainty

As of version 0.6-5, the package has been greatly revised to allow a wider range of response and link functions and to allow models with multiple random effects. For now, the resulting package is slower than the old (single-random-effect version), but we hope to increase its speed in the future.

2 Owls data

These data, taken from [2] and ultimately from [1], quantify the number of begging attempts by owlets (owl chicks) in different nests as a function of food treatment (deprived or satiated), the sex of the parent, and arrival time. The total number of calls from the nest is recorded, along with the total brood size, which is used as an offset to allow the use of a Poisson response.

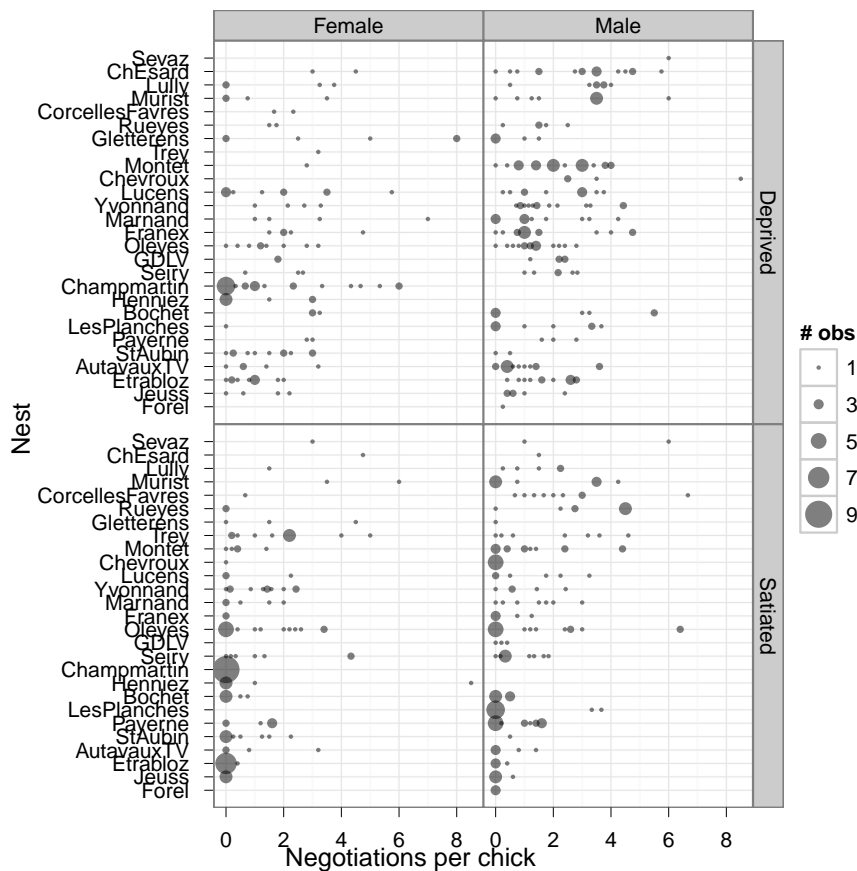
Since the same nests are measured repeatedly, the nest is used as a random effect. The model can be expressed as a zero-inflated generalized linear mixed model (ZIGLMM).

```

> library(glmADMB)
> Owls <- transform(Owls,
  Nest=reorder(Nest,NegPerChick),
  logBroodSize=log(BroodSize),
  NCalls=SiblingNegotiation,
  obs=seq(nrow(Owls)))

> G0 <- ggplot(Owls,aes(x=reorder(Nest,NegPerChick),
  y=NegPerChick))+
  xlab("Nest")+ylab("Negotiations per chick")+coord_flip()+
  facet_grid(FoodTreatment~SexParent)
> print(G0+stat_sum(aes(size=..n..),alpha=0.5)+zspace+
  scale_size_continuous(name="# obs",
    breaks=seq(1,9,by=2)))

```



The basic `glmADMB` fit — a zero-inflated Poisson model.

```

> gt1 <- system.time(gfit1 <- glmADMB(NCalls~(FoodTreatment+ArrivalTime)*

```

```

SexParent+
offset(logBroodSize)+(1|Nest),
data=Owls,
zeroInflation=TRUE,
family="poisson"))

> summary(gfit1)

Call:
glmmadmb(formula = NCalls ~ (FoodTreatment + ArrivalTime) * SexParent +
  offset(logBroodSize) + (1 | Nest), data = Owls, family = "poisson",
  zeroInflation = TRUE)

Coefficients:
                                Estimate Std. Error z value Pr(>|z|)
(Intercept)                   2.8562     0.3871   7.38 1.6e-13 ***
FoodTreatmentSatiated         -0.3314     0.0635  -5.22 1.8e-07 ***
ArrivalTime                   -0.0807     0.0156  -5.18 2.3e-07 ***
SexParentMale                  0.2882     0.3575   0.81  0.42
FoodTreatmentSatiated:SexParentMale  0.0740     0.0761   0.97  0.33
ArrivalTime:SexParentMale      -0.0150     0.0143  -1.05  0.29
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

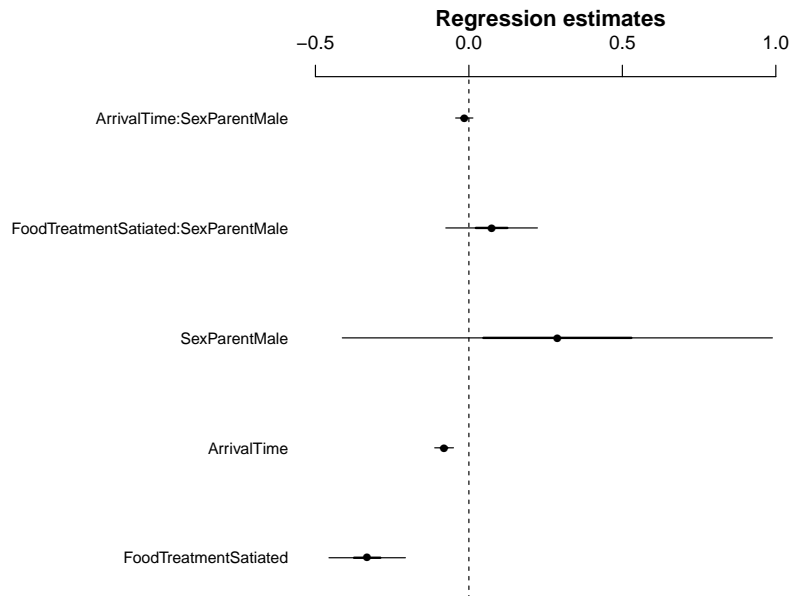
Number of observations: total=599, =27
Random effect variance(s):
$Nest
      (Intercept)
(Intercept)  0.14001

Zero-inflation: 0.25833 (std. err.: 0.018107 )

Log-likelihood: -1985.3

> library(coefplot2)
> coefplot2(gfit1)

```



We can also try a standard zero-inflated negative binomial model; the default is the “NB2” parameterization (variance = $\mu(1 + \mu/k)$).

```
> gt2 <- system.time(gfit2 <- glmmadmb(NCalls~(FoodTreatment+ArrivalTime)*SexParent+
  offset(logBroodSize)+(1|Nest),
  data=Owls,
  zeroInflation=TRUE,
  family="nbinom"))
```

This takes a little longer than the Poisson model (14.2 seconds).
Alternatively, use an “NB1” fit (variance = $\phi\mu$).

```
> gt3 <- system.time(gfit3 <- glmmadmb(NCalls~(FoodTreatment+ArrivalTime)*SexParent+
  offset(logBroodSize)+(1|Nest),
  data=Owls,
  zeroInflation=TRUE,
  family="nbinom1"))
```

Relax the assumption that total number of calls is strictly proportional to brood size (i.e. using $\log(\text{brood size})$ as an offset):

```
> gt4 <- system.time(gfit4 <- glmmadmb(NCalls~(FoodTreatment+ArrivalTime)*SexParent+
  BroodSize+(1|Nest),
  data=Owls,
  zeroInflation=TRUE,
  family="nbinom1"))
```

Every change we have made so far improves the fit — changing distributions improves it enormously, while changing the role of brood size makes only a modest (-1 AIC unit) difference:

```
> AIC(gfit1,gfit2,gfit3,gfit4)
```

```
      df      AIC
gfit1  8 3986.60
gfit2  9 3418.28
gfit3  9 3350.76
gfit4 10 3349.60
```

The standard set of accessors is available: extract coefficients (`coef`), fixed effects (`fixef` — a synonym for `coef`), random effects (`ranef`), residuals (`residuals`), fitted values (`fitted`), log-likelihood (`logLik`), summary (`summary`), standard errors (`stdEr`), variance-covariance matrix of coefficients (`vcov`), variance-covariance matrices of random effects (`VarCorr`), confidence intervals (`confint`) ...

```
> methods(class="glmmadmb")
```

```
[1] anova.glmmadmb*      coef.glmmadmb*        fitted.glmmadmb*
[4] fixef.glmmadmb*      logLik.glmmadmb*      print.glmmadmb*
[7] ranef.glmmadmb*      residuals.glmmadmb*   stdEr.glmmadmb*
[10] summary.glmmadmb*    VarCorr.glmmadmb*     vcov.glmmadmb*
```

Non-visible functions are asterisked

References

- [1] A. Roulin and L. Bersier. Nestling barn owls beg more intensely in the presence of their mother than in the presence of their father. *Animal Behaviour*, 74:1099–1106, 2007.
- [2] Alain F. Zuur, Elena N. Ieno, Neil J. Walker, Anatoly A. Saveliev, and Graham M. Smith. *Mixed Effects Models and Extensions in Ecology with R*. Springer, 1 edition, March 2009.