glms for proportion abscised

E.E. Jackson

02 May, 2020

```r
rm(list = ls())
require(tidyverse)
require(lme4)
library(knitr)
library(report)
opts_chunk$set(tidy.opts=list(width.cutoff=50),tidy=TRUE)
```

Read dataset

```r
fruitDat <- read.csv("../output/tables/cleanData.csv")
dm <- read.csv("../output/tables/dispersalMode.csv")
```

generalized linear models

```r
# make sure that predator presence is a factor and
# add dispersal mode
fruitDat <- fruitDat %>% mutate(seedpred_pres = factor(ifelse(seedpred_pres ==
    0, "No", "Yes"))) %>% left_join(select(dm, dispersal_mode = bio,
    sp), by = "sp")
```

```
## Warning: Column `sp` joining factors with different levels, coercing to
## character vector
```

```r
## maximal model ##

fullmod <- glm(cbind(abscised_seeds, viable_seeds) ~
    seedpred_pres + log10(seed_dry) * height_avg +
        cvseed + log10(cofruit) + bcireproductive +
        endocarp_investment + dispersal_mode, data = na.omit(fruitDat),
    family = quasibinomial(link = logit))

summary(fullmod)
```

```
##
## Call:
## glm(formula = cbind(abscised_seeds, viable_seeds) ~ seedpred_pres +
##     log10(seed_dry) * height_avg + cvseed + log10(cofruit) +
##     bcireproductive + endocarp_investment + dispersal_mode, family = quasibinomial(link = logit),
##     data = na.omit(fruitDat))
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
```

```
## -157.491     -29.260    -14.413       2.352     154.992
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)              10.8988963  4.3172100   2.525  0.01266 *
## seedpred_presYes         -0.4958303  0.2635752  -1.881  0.06195 .
## log10(seed_dry)           1.5971701  0.3311972   4.822 3.55e-06 ***
## height_avg               -0.0221898  0.0226628  -0.979  0.32915
## cvseed                    0.2713713  0.2311544   1.174  0.24233
## log10(cofruit)           -3.7709992  1.7764612  -2.123  0.03547 *
## bcireproductive           0.0001493  0.0004791   0.312  0.75572
## endocarp_investment       3.1138708  0.3021776  10.305  < 2e-16 ***
## dispersal_modebiotic     -0.5457911  0.2486120  -2.195  0.02973 *
## log10(seed_dry):height_avg -0.0314552  0.0116534  -2.699  0.00778 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 2707.83)
##
##     Null deviance: 2335424  on 154  degrees of freedom
## Residual deviance:  327287  on 145  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

```
anova(fullmod, test = "F")
```

```
## Analysis of Deviance Table
##
## Model: quasibinomial, link: logit
##
## Response: cbind(abscised_seeds, viable_seeds)
##
## Terms added sequentially (first to last)
##
##
##                            Df Deviance Resid. Df Resid. Dev        F    Pr(>F)
## NULL                                        154    2335424
## seedpred_pres               1  1064490       153    1270934 393.1156 < 2.2e-16
## log10(seed_dry)             1   240590       152    1030344  88.8497 < 2.2e-16
## height_avg                  1    28248       151    1002096  10.4320  0.001532
## cvseed                      1    88768       150     913329  32.7818 5.725e-08
## log10(cofruit)              1   229539       149     683789  84.7687 3.449e-16
## bcireproductive             1    35133       148     648657  12.9745  0.000433
## endocarp_investment         1   272138       147     376519 100.5004 < 2.2e-16
## dispersal_mode              1    28871       146     347648  10.6620  0.001365
## log10(seed_dry):height_avg  1    20361       145     327287   7.5192  0.006874
##
## NULL
## seedpred_pres              ***
## log10(seed_dry)            ***
## height_avg                 **
## cvseed                     ***
## log10(cofruit)             ***
## bcireproductive            ***
```

```
## endocarp_investment        ***
## dispersal_mode             **
## log10(seed_dry):height_avg **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```