

# Cross Validation

Ok, to get a more absolute idea of how good my models are, I want to calculate som R2s.

```
# Load some libraries.
library('tidyverse')
library('lme4')
library('AICcmodavg')

# Read in the points.
points <- read.csv('../h_data/interim/points.csv', stringsAsFactors=FALSE)

# Get the final data set.
n.points <- points %>%
  filter(n_hab >= 0) %>%
  filter(cover %in% c('TC', 'TM', 'TB')) %>%
  select(-v.comp) %>%
  drop_na()

# Build the models.
b.canopy <- glmer(case ~ n_hab + canopy.closure + (1|site), data=n.points, family=binomial(link='logit'))
fb.canopy <- glmer(case ~ f_hab + canopy.closure + (1|site), data=n.points, family=binomial(link='logit'))
s.canopy <- glmer(case ~ canopy.closure + (1|site), data=n.points, family=binomial(link='logit'))
n.hab <- glmer(case ~ n_hab + (1|site), data=n.points, family=binomial(link='logit'))
f.hab <- glmer(case ~ f_hab + (1|site), data=n.points, family=binomial(link='logit'))
can.age <- glmer(case ~ age + canopy.closure + (1|site), data=n.points, family=binomial(link='logit'))
s.age <- glmer(case ~ age + (1|site), data=n.points, family=binomial(link='logit'))
site <- glmer(case ~ 1 + (1|site), data=n.points, family=binomial(link='logit'))
models <- c(b.canopy, fb.canopy, s.canopy, n.hab, f.hab, can.age, s.age, site)
modnames <- c('canopy + nest hab', 'canopy + f hab', 'canopy alone', 'nest hab alone', 'f hab alone', 'canopy alone', 'nest hab alone', 'f hab alone', 'canopy alone', 'nest hab alone', 'f hab alone')
aictab(models, modnames=modnames)

##
## Model selection based on AICc:
##
##           K   AICc Delta_AICc AICcWt Cum.Wt      LL
## canopy + nest hab 4 561.34      0.00  0.47  0.47 -276.64
## canopy + f hab    4 562.33      0.99  0.28  0.75 -277.13
## canopy alone      3 564.32      2.98  0.11  0.86 -279.14
## nest hab alone    3 565.46      4.12  0.06  0.92 -279.71
```

```
## canopy + age      4 565.84      4.51  0.05  0.96 -278.89
## f hab alone       3 566.71      5.37  0.03  1.00 -280.34
## site              2 571.91     10.58  0.00  1.00 -283.95
## age alone         3 573.58     12.25  0.00  1.00 -283.77
```

And then calculate the  $R^2$ .  $R2m$  being the marginal  $R^2$ , the amount of variance explained by the fixed factors alone, and  $R2c$  being the conditional  $R^2$ , the amount of variance explained by both fixed and random factors.

```
library('MuMIn')
```

```
r.squaredGLMM(b.canopy)
```

```
##              R2m      R2c
## theoretical 0.05762594 0.12844303
## delta      0.02379519 0.05303733
```

```
r.squaredGLMM(n.hab)
```

```
##              R2m      R2c
## theoretical 0.02964582 0.08335153
## delta      0.01188064 0.03340335
```