

# Introduction

Hysteranthly, a trait that describes trees that seasonally flower before leafing out, is a common trait in temperate deciduous forests. It has been hypothesized that hysteranthly is an adaptation to allow for more efficient wind pollination. An alternative hypothesis posits that hysteranthly is part of an adaptation for early flowering and a product of stronger selection on leaf timing compared to flower timing by late season frost. To begin understand the prevalence and trait associations of hysteranthly, we use published trait data to model the traits that predict hysteranthly.

# Methods

Data source:

Michigan Trees, Michigan shrubs and vines

USFS Silvics manual

Tree source: Zanne et al 2014

Using R, modeled hysteranthly as a function of other traits, pollination syndrome, shade tolerance, maximum height, timing of flowering, timing of fruiting. We used a pglm model to correct for phylogenetic signal.

# Results

```
##
## Calculation of D statistic for the phylogenetic structure of a binary variable
##
## Data : mich.data
## Binary variable : pro
## Counts of states: 0 = 143
##                  1 = 49
## Phylogeny : mich.tree
## Number of permutations : 1000
##
## Estimated D : 0.2003316
## Probability of E(D) resulting from no (random) phylogenetic structure : 0
## Probability of E(D) resulting from Brownian phylogenetic structure : 0.123
##
## Calculation of D statistic for the phylogenetic structure of a binary variable
##
## Data : silv.data
## Binary variable : pro
## Counts of states: 0 = 55
##                  1 = 27
## Phylogeny : silv.tree
## Number of permutations : 1000
##
## Estimated D : 0.1282404
## Probability of E(D) resulting from no (random) phylogenetic structure : 0
## Probability of E(D) resulting from Brownian phylogenetic structure : 0.282
```

Figure 1: PhyloD for Michigan and Silvics Trees

```
##
## Call:
## phyloglm(formula = pro ~ pol + height_cent + flo_cent + fruit_cent +
##          shade_bin, data = mich.data, phy = mich.tree, method = "logistic_MPLE",
##          btol = 100, log.alpha.bound = 10, start.beta = NULL, start.alpha = NULL,
##          boot = 20, full.matrix = TRUE)
##           AIC      logLik Pen.logLik
##    122.95      -54.47      -50.42
##
## Method: logistic_MPLE
## Mean tip height: 188.2832
## Parameter estimate(s):
## alpha: 0.03704969
##      bootstrap mean: 0.0379379 (on log scale, then back transformed)
##      so possible upward bias.
##      bootstrap 95% CI: (0.003097604,0.7362004)
##
## Coefficients:
##              Estimate      StdErr    z.value lowerbootCI upperbootCI
## (Intercept) -2.562033    0.524067  -4.888754   -4.000646   -1.1502
## pol          1.294667    0.650830   1.989256   -0.215439    2.8407
## height_cent -0.763115    0.592595  -1.287752   -2.039963    0.2497
## flo_cent     -4.641285    0.928617  -4.998064   -5.611119   -2.8961
## fruit_cent   -0.779671    0.530785  -1.468903   -1.772326    0.1123
## shade_bin     0.091954    0.461651   0.199186   -0.530337    1.2134
##              p.value
## (Intercept) 1.015e-06 ***
## pol          0.04667 *
## height_cent  0.19783
## flo_cent     5.791e-07 ***
## fruit_cent   0.14186
## shade_bin    0.84212
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Note: Wald-type p-values for coefficients, conditional on alpha=0.03704969
##      Parametric bootstrap results based on 20 fitted replicates
```

Figure 2: model output for michigan data, centered

```
##
## Call:
## phyloglm(formula = pro ~ pol + flo_cent + height_cent + fruit_cent +
##          shade_bin, data = silv.data, phy = silv.tree, method = "logistic_MPLE",
##          btol = 60, log.alpha.bound = 4, start.beta = NULL, start.alpha = NULL,
##          boot = 20, full.matrix = TRUE)
##           AIC      logLik Pen.logLik
##      75.11    -30.55    -27.19
##
## Method: logistic_MPLE
## Mean tip height: 180.6283
## Parameter estimate(s):
## alpha: 0.01971612
##      bootstrap mean: 0.02336841 (on log scale, then back transformed)
##      so possible upward bias.
##      bootstrap 95% CI: (0.004811923,0.1599053)
##
## Coefficients:
##              Estimate      StdErr   z.value lowerbootCI upperbootCI  p.value
## (Intercept) -1.640142   0.689901  -2.377358   -2.445149    -0.2801  0.017437
## pol          0.931404   0.812539   1.146289   -0.964705     1.8714  0.251676
## flo_cent     -2.355447   0.858567  -2.743464   -4.591364    -0.6544  0.006079
## height_cent  0.050560   0.511821   0.098785   -1.105242     1.4079  0.921309
## fruit_cent   -0.908344   0.647718  -1.402377   -1.996558    -0.1556  0.160803
## shade_bin     0.266360   0.418324   0.636731   -0.240122     0.8140  0.524300
##
## (Intercept) *
## pol
## flo_cent      **
## height_cent
## fruit_cent
## shade_bin
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Note: Wald-type p-values for coefficients, conditional on alpha=0.01971612
##      Parametric bootstrap results based on 20 fitted replicates
```

Figure 3: model output for Silvic data, centered

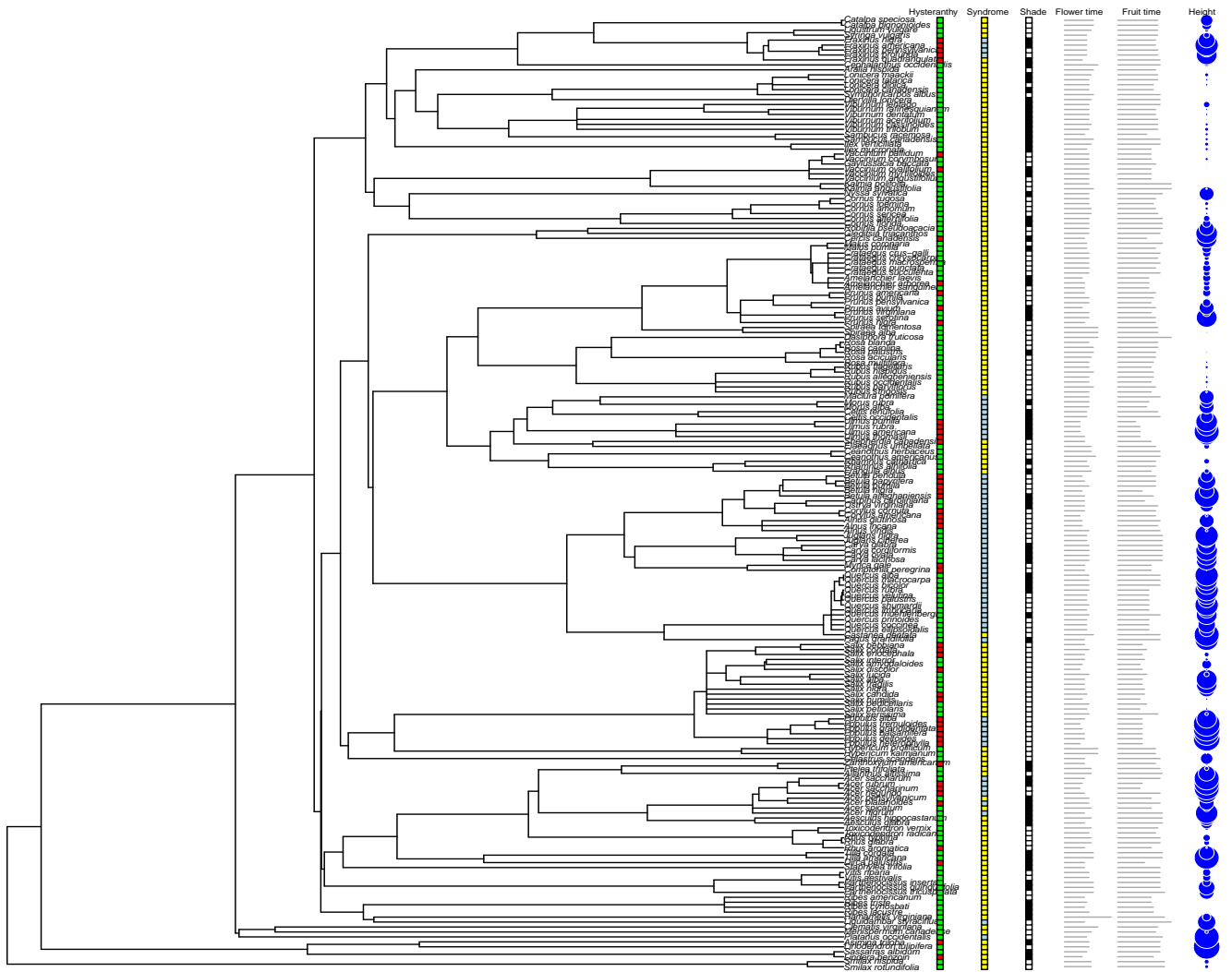


Figure 4: Phylogeny and trait map for Michigan data

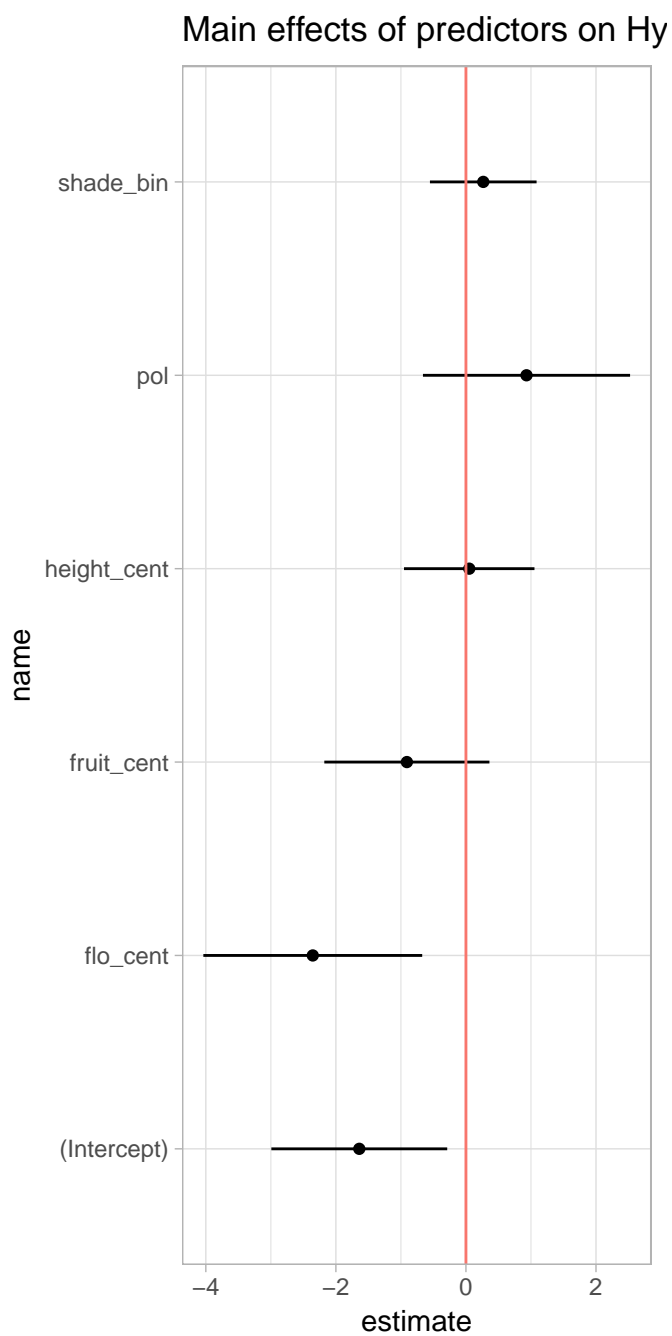
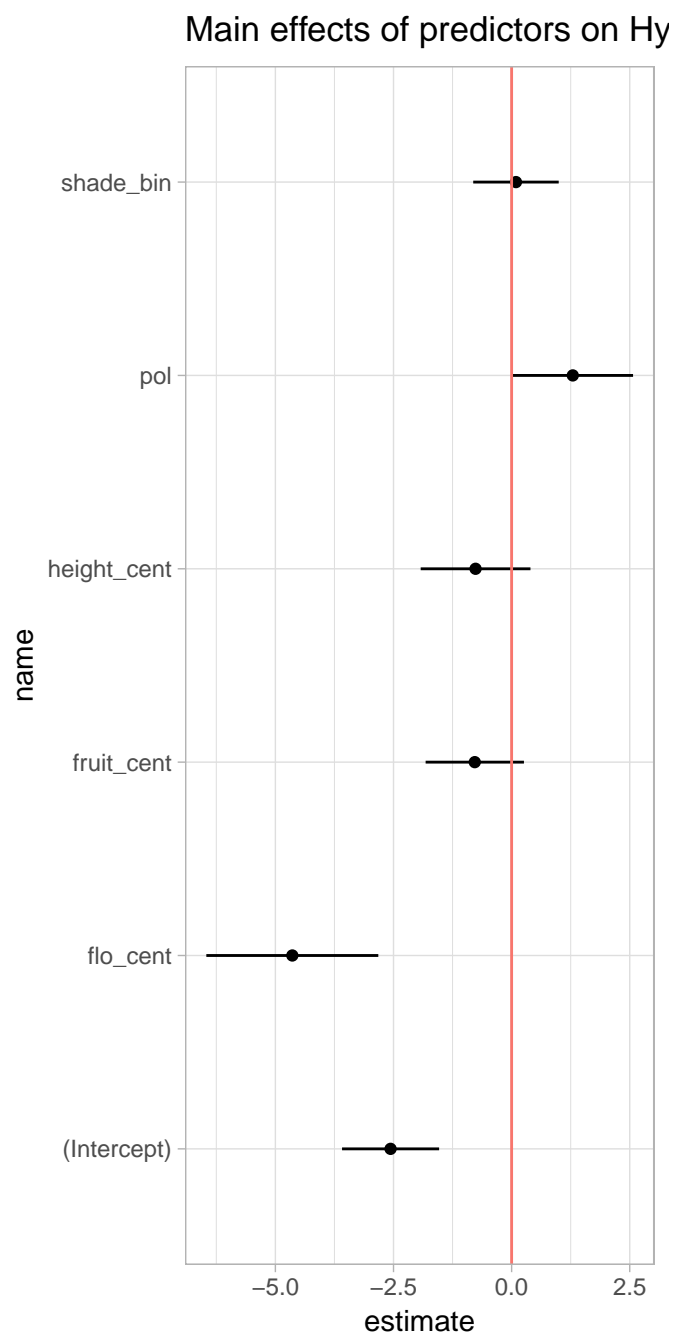


Figure 5: Trait effect sizes

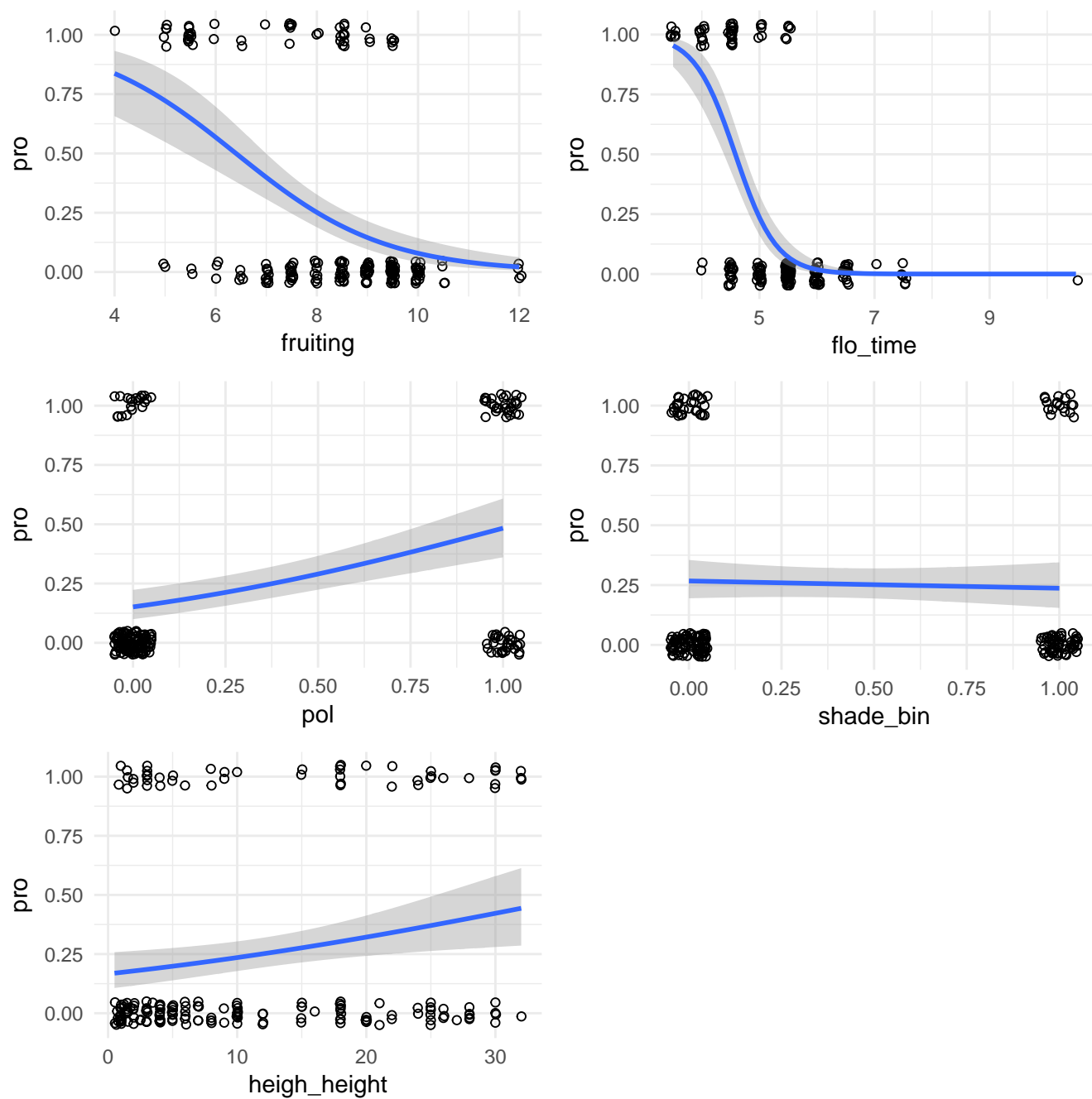


Figure 6: Michigan binomial plots

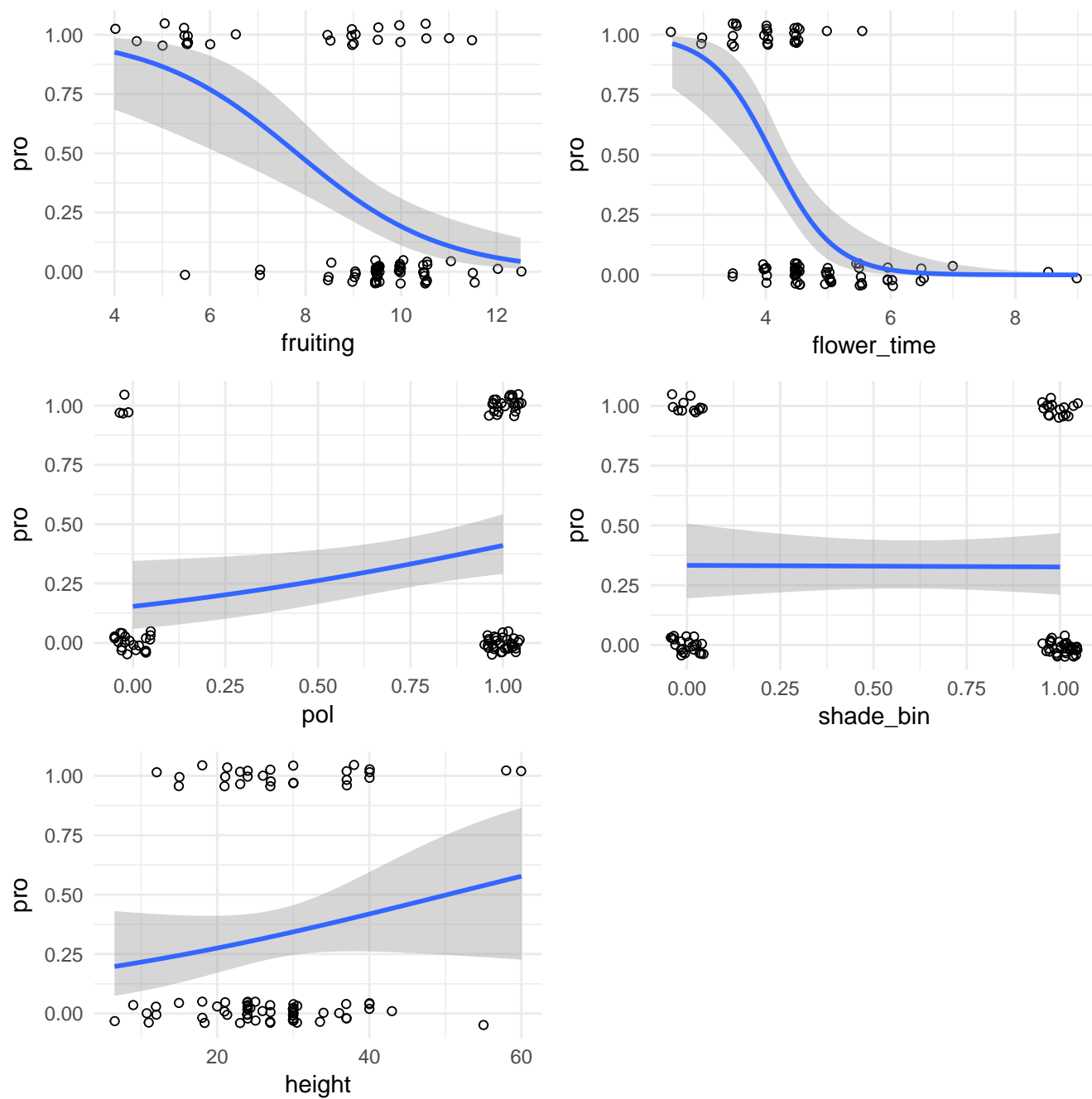


Figure 7: Silvics binomial plots