Introduction

Hysteranthy, a trait that describes trees that seasonally flower before leafing out, is a common trait in temperate decidious forests. It has been hypothesized that hysteranthy is an adaptation to allow for more effecient wind pollination. An alternative hypothesis posits that hysteranthy 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 prevelance and trait associations of hysteranthy, we use published trait data to model the traits the predict hysteranthy.

Methods

Data source:
Michigan Trees,Michigan shrubs and vines
USFS Silvics mannual
Tree source: Zanne et al 2014
Using R, Modeled hysteranty as a function of other traits, pollination syndrome, shade tolerance, maximum height, timing of flowering, timing of fruiting. We used a pgls 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 = 145
##                      1 = 49
##   Phylogeny :  mich.tree
##   Number of permutations :  1000
##
## Estimated D :  0.1787884
## Probability of E(D) resulting from no (random) phylogenetic structure :  0
## Probability of E(D) resulting from Brownian phylogenetic structure    :  0.14
##
## Calculation of D statistic for the phylogenetic structure of a binary variable
##
##   Data :  mich.data
##   Binary variable :  pro2
##   Counts of states:  0 = 93
##                      1 = 101
##   Phylogeny :  mich.tree
##   Number of permutations :  1000
##
## Estimated D :  0.06808238
## Probability of E(D) resulting from no (random) phylogenetic structure :  0
## Probability of E(D) resulting from Brownian phylogenetic structure    :  0.326
##
## 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 :  0.1185273
## Probability of E(D) resulting from no (random) phylogenetic structure :  0
## Probability of E(D) resulting from Brownian phylogenetic structure    :  0.315
##
## Calculation of D statistic for the phylogenetic structure of a binary variable
##
##   Data :  silv.data
##   Binary variable :  pro2
##   Counts of states:  0 = 20
##                      1 = 62
##   Phylogeny :  silv.tree
##   Number of permutations :  1000
##
## Estimated D :  0.6436797
## Probability of E(D) resulting from no (random) phylogenetic structure :  0.02
## Probability of E(D) resulting from Brownian phylogenetic structure    :  0.009
```

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
##     122.53    -54.26     -50.25
## 
## Method: logistic_MPLE
## Mean tip height: 188.2832
## Parameter estimate(s):
## alpha: 0.0340704
##        bootstrap mean: 0.02458562 (on log scale, then back transformed)
##        so possible downward bias.
##        bootstrap 95% CI: (0.001433308,0.1479936)
## 
## Coefficients:
##              Estimate    StdErr  z.value lowerbootCI upperbootCI   p.value
## (Intercept) -2.64643   0.53707 -4.92754    -2.98964     -1.5348 8.327e-07
## pol          1.31973   0.65732  2.00774    -0.57088      2.1288   0.04467
## height_cent -0.75234   0.58822 -1.27901    -2.04533      0.3403   0.20089
## flo_cent    -4.62838   0.92810 -4.98692    -6.15766     -3.0215 6.135e-07
## fruit_cent  -0.79559   0.53463 -1.48813    -1.89233     -0.0940   0.13672
## shade_bin    0.11850   0.46232  0.25633    -0.63560      0.6796   0.79770
## 
## (Intercept) ***
## pol         *
## height_cent
## flo_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=0.0340704
##       Parametric bootstrap results based on 20 fitted replicates
```

Figure 2: model output for michigan data, centered

```
## 
## Call:
## phyloglm(formula = pro2 ~ 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 = 50, full.matrix = TRUE)
##        AIC    logLik Pen.logLik
##     139.51    -62.76     -58.94
## 
## Method: logistic_MPLE
## Mean tip height: 188.2832
## Parameter estimate(s):
## alpha: 0.01340074
##       bootstrap mean: 0.01358865 (on log scale, then back transformed)
##       so possible upward bias.
##       bootstrap 95% CI: (0.002549091,0.1066822)
## 
## Coefficients:
##              Estimate    StdErr   z.value lowerbootCI upperbootCI
## (Intercept) -0.404435  0.450617 -0.897514   -1.256594      0.1652
## pol          1.788847  0.719117  2.487560    0.442072      3.4166
## height_cent  1.201576  0.584053  2.057305    0.164773      1.9927
## flo_cent    -2.334775  0.645637 -3.616232   -3.631143     -1.2905
## fruit_cent  -1.806378  0.653893 -2.762500   -2.861381     -0.8077
## shade_bin    0.583238  0.410533  1.420687   -0.041609      1.4582
##               p.value
## (Intercept) 0.3694447
## pol         0.0128623 *
## height_cent 0.0396569 *
## flo_cent    0.0002989 ***
## fruit_cent  0.0057361 **
## shade_bin   0.1554079
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Note: Wald-type p-values for coefficients, conditional on alpha=0.01340074
##       Parametric bootstrap results based on 50 fitted replicates
```

Figure 3: model output for FUNCTIONAL hysteranthy 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: 0.01522847 (on log scale, then back transformed)
##        so possible downward bias.
##        bootstrap 95% CI: (0.002376346,0.07236766)
## 
## Coefficients:
##                Estimate     StdErr    z.value lowerbootCI upperbootCI  p.value
## (Intercept) -1.640142   0.689901  -2.377358   -2.656956     -0.8335 0.017437
## pol          0.931404   0.812539   1.146289   -0.155230      2.0164 0.251676
## flo_cent    -2.355447   0.858567  -2.743464   -4.145462     -1.0928 0.006079
## height_cent  0.050560   0.511821   0.098785   -0.388123      0.9282 0.921309
## fruit_cent  -0.908344   0.647718  -1.402377   -1.812641      0.2735 0.160803
## shade_bin    0.266360   0.418324   0.636731   -0.326497      1.0165 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 4: model output for Silvic data, centered

```
##
## Call:
## phyloglm(formula = pro2 ~ 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 = 50, full.matrix = TRUE)
##       AIC    logLik Pen.logLik
##      65.49    -25.74     -22.87
##
## Method: logistic_MPLE
## Mean tip height: 180.6283
## Parameter estimate(s):
## alpha: 0.02100817
##      bootstrap mean: 0.01923607 (on log scale, then back transformed)
##      so possible downward bias.
##      bootstrap 95% CI: (0.002245216,0.1012712)
##
## Coefficients:
##             Estimate    StdErr  z.value lowerbootCI upperbootCI   p.value
## (Intercept)  0.82817   0.63820  1.29766    -0.19758      1.5536 0.1944049
## pol          0.52522   0.74148  0.70833    -0.40756      1.3253 0.4787385
## flo_cent    -2.70179   0.81499 -3.31511    -4.21142     -1.3924 0.0009161
## height_cent -0.11894   0.58724 -0.20254    -1.07653      1.0706 0.8394939
## fruit_cent  -1.17423   0.87946 -1.33518    -2.46219      0.4855 0.1818175
## shade_bin   -0.24491   0.49262 -0.49715    -1.02625      0.5442 0.6190828
##
## (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=0.02100817
##       Parametric bootstrap results based on 50 fitted replicates
```

Figure 5: model output for FUNCTIONAL Silvic data, centered
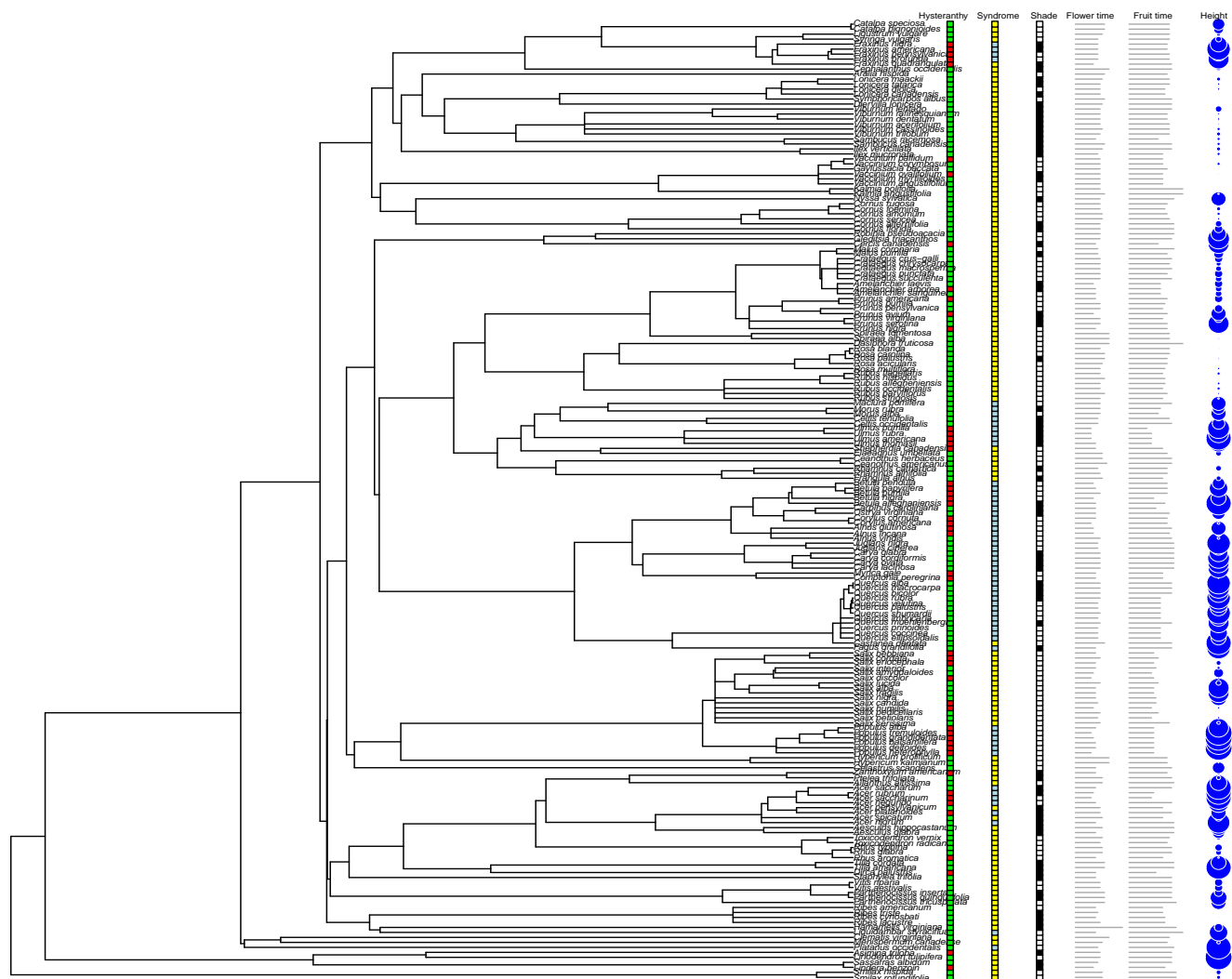
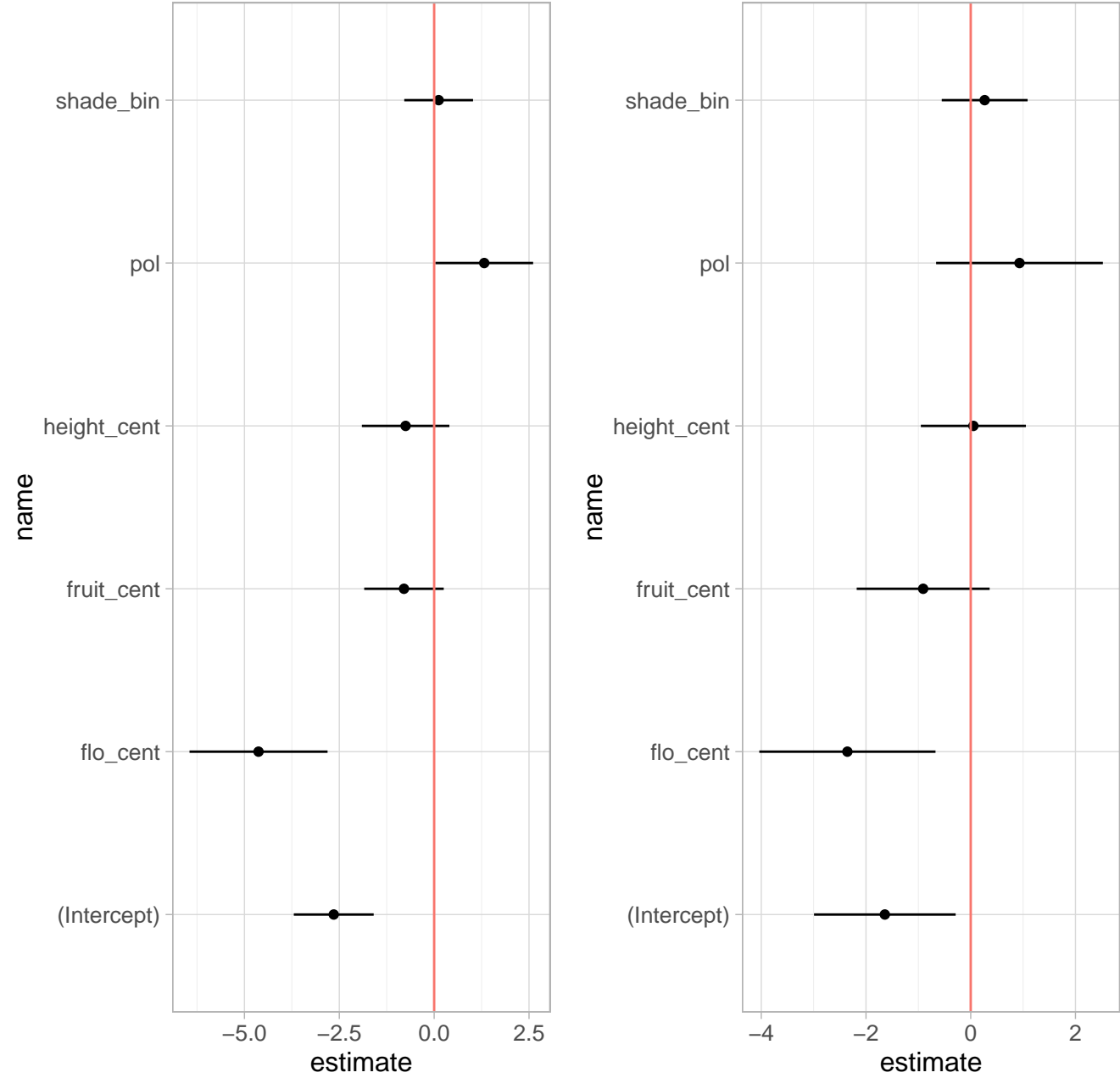Figure 6: Phylogeny and trait map for Michigan data
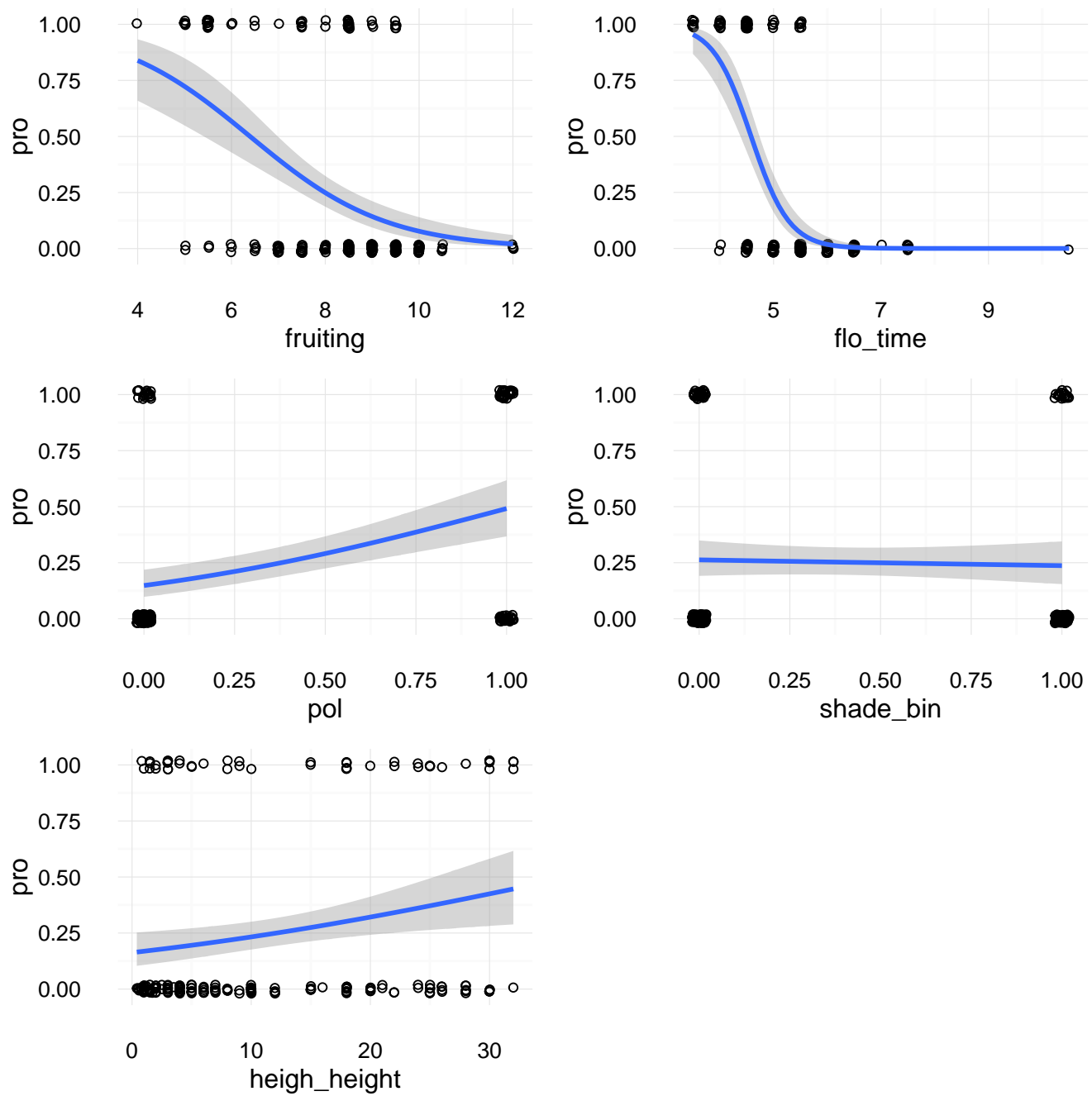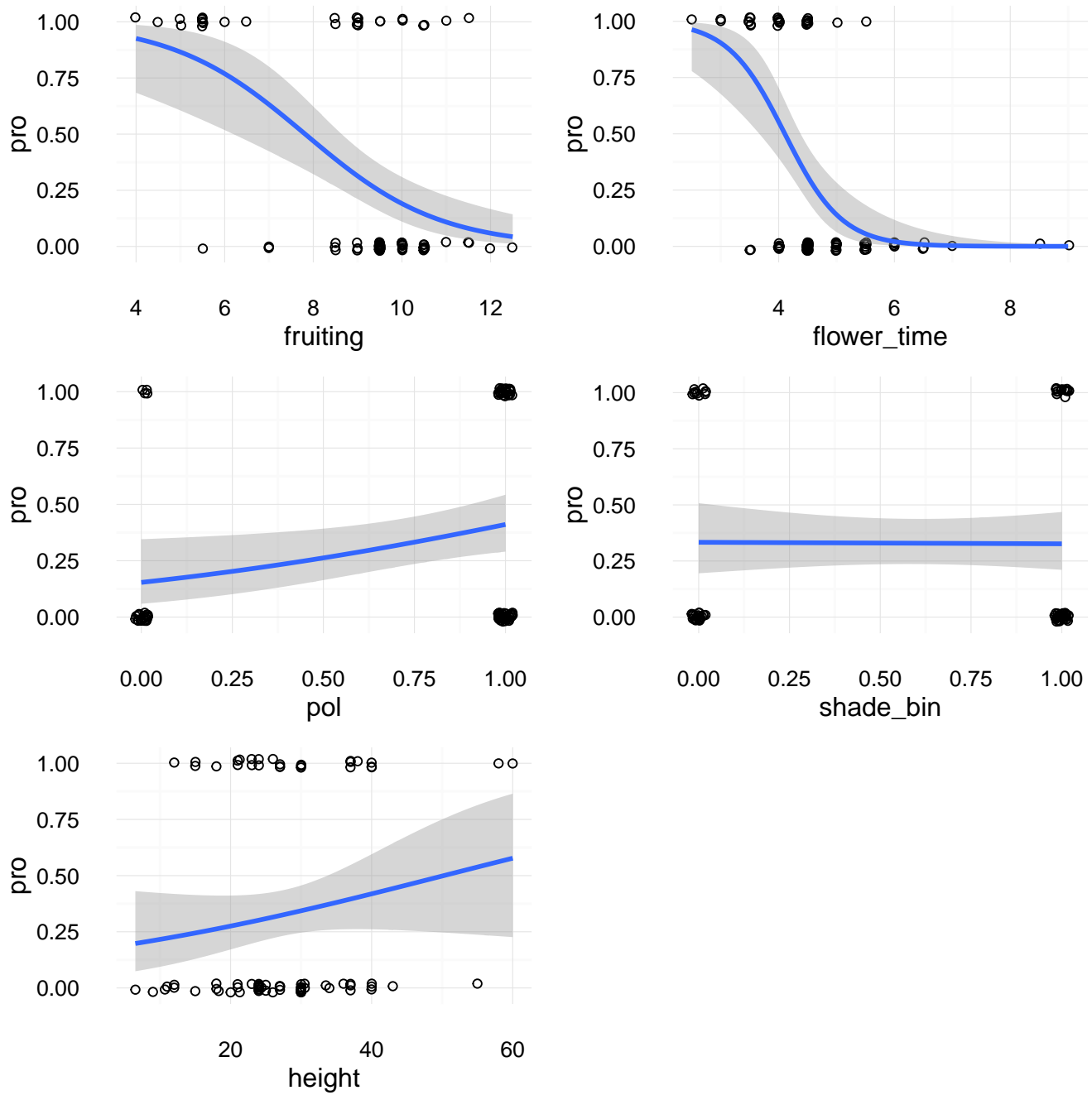
Figure 7: Trait effect sizes

Figure 8: Michigan binomial plots

Figure 9: Silvics binomial plots