

Theme song: Spring Again: Lou Rawls

Theme song: Sugar Magnolia: Grateful Dead

Introduction

Set the stage here.

Methods

Data

We obtained species level descriptions of floral-foliate sequences from two data sources: 1) Michigan Trees (?), and Michigan Shrubs and Vines (?), (hereafter: MTSV) and 2) The United States Forest Service's Silvics Manual (), hereafter: Silvics. We investigated several other floras and monographs for possible inclusion in this analysis, but we could find publications with adequate descriptions of floral-foliate sequences. The complete list of these publications can be found in the supplement.

From each data source, we coded hysteranthly as binary trait based on verbal descriptions. Entries described as "flowering before leaf development" or "flowering before or with leaves development" were coded as hysteranthous, while "flowering with leaf development", "flowering with or after leaf development" and "flowering after leaf development" were coded as non-hysteranthous. Using the same data sources, we obtained descriptions of several other traits that we determined to be biologically relevant to the various hypotheses relating to the prevalence of hysteranthly including pollination syndrome, maximum height, shade tolerance, time of flowering and time of fruit maturation. We coded pollination syndrome as binary trait (wind or animal pollinated). We also condensed verbal descriptions of shade tolerance to binary, collapsing descriptions "moderately, or medium shade tolerant", "tolerant" and "very tolerant" to tolerant, and "intolerant" as "intolerant". Flowering and fruit maturation time were described in both sources as a range of months. For both flowering and fruiting time, we calculated the average of the timespan, and coded it numerically in our dataset. probably will talk about this in the discussion but should note that silvics spanned greater geographic range In total 82 species were included in the Silvics dataset and 194 species in the MTSV

dataset.

Phylogeny

To investigate the phylogenetic signal of hysteranthly and control for phylogenetic structure in our datasets, we used a published angiosperm phylogenetic tree (?) pruned to match the species list from each dataset respectively. Species that were found in the trait data but not in the phylogenetic tree were added to the pruned phylogenetic trees at the genus level root. 12 species were added to the Silvics tree and 32 were added to the MTSV tree.

Statistical analysis

We performed all statistical analysis using R 2.14. To assess the phylogenetic structure in the trait of hysteranthly, we used Caper packaged () to calculate a phylogenetic D statistic (?) in both the Silvics and MTSV dataset. To test the hypotheses regarding the trait associations of hysteranthly, we used phylogenetic generalized linear model framework (?) to build a logistical regression model corrected for phylogenetic structure using the R package phyloglm (). The model was run with 50 bootstrapped resampling iterations for each dataset. Predictors were evaluated with average predictive and effect size comparisons. The effect of average flowering time was further evaluated with... *not sure how to talk about this* A fundamental challenge to interpreting the effect sizes of logistic regressions with both continuous and binary predictors is...*read the Gellman section on this again to figure out how to phrase your point.* To allow for a proper comparison of the relative effects of each predictor, we transformed the continuous predictors (height, average time of flowering and fruit maturation) to the logit scale by dividing the original values by the mean and two standard deviations (?) and used these transformed parameters and model inputs.

Results

Phylogenetic structure

27 out of the 82 species in the Silvics dataset were classified as hysteranthous. 49 of the 192 species in the MTSV datasets were classified as hysteranthous. For both datasets, they phylogenetic signal for hysteranthly

was relatively low. The D statistic for the Silvics data was 0.125. For the MTSV data, the D statistic was 0.18.

Trait associations

Average timing of flowering was the strongest predictor of hysteranthly, with the likelihood of hysteranthly increasing substantially with earlier flower. Average flowering time was the only predictor with 95% confidence intervals that did not overlap zero in both datasets (see figure). For the MTSV dataset, pollination syndrome also had a substantial effect, with the likelihood of hysteranthly increasing in wind pollinated taxa. For the Silvics dataset, we see a small effect of average time of fruit maturation, with earlier fruit maturation increasing the likelihood a species would be hysteranthous. The results of our modified Gotelli resampling (*different name for it? Cupid Shuffle*) show a substantial decrease in the magnitude of effect size of average flowering time after only 2 resamples, indicating that there is something unique about the flowering time of hysteranthous species when compared to other non-hysteranthous but early flowering species.

Discussion

Figures

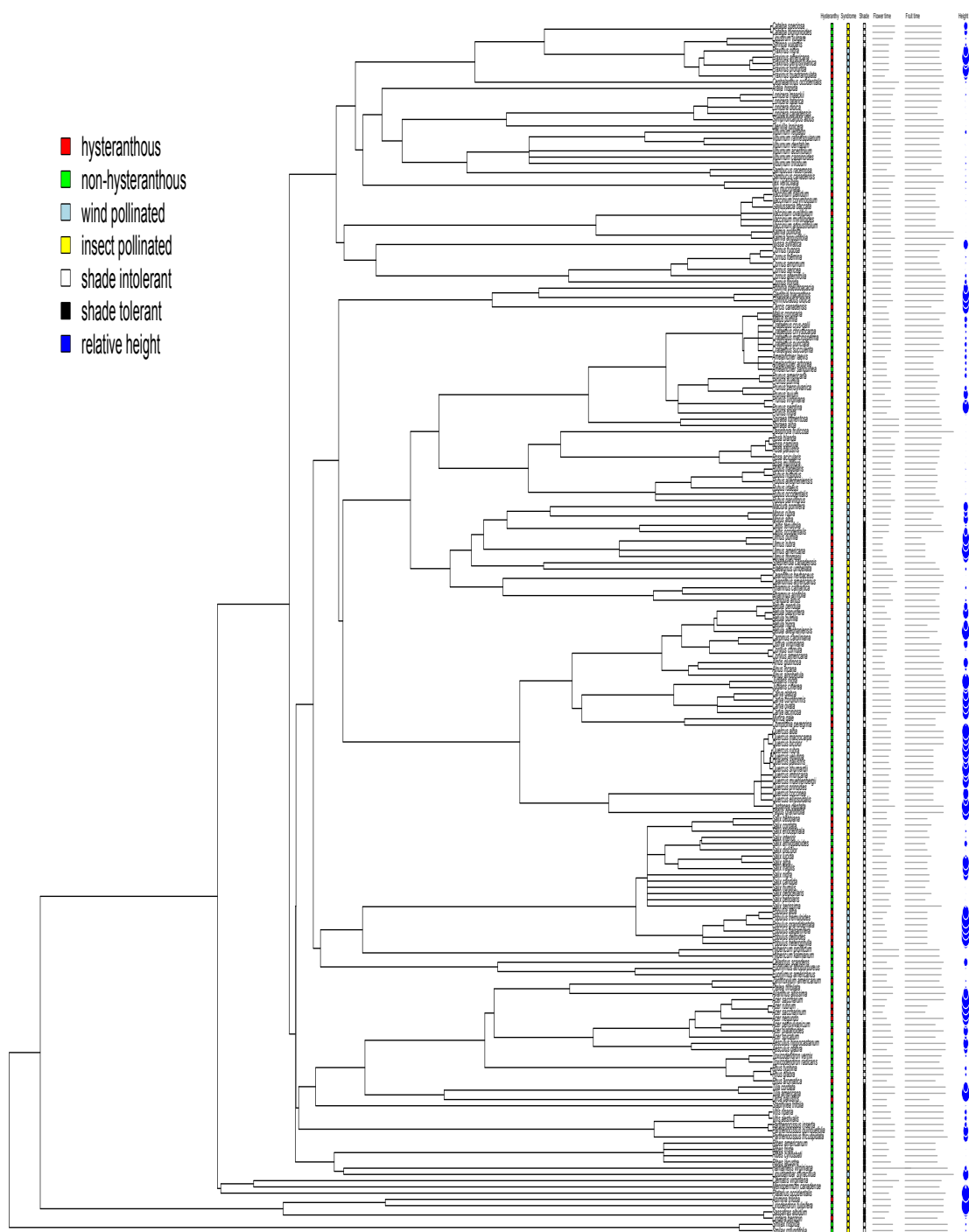


Figure 1: I can't figure out how to make this figure more better to look at. Ideas: Just hysteranthous, and/or no tip labels

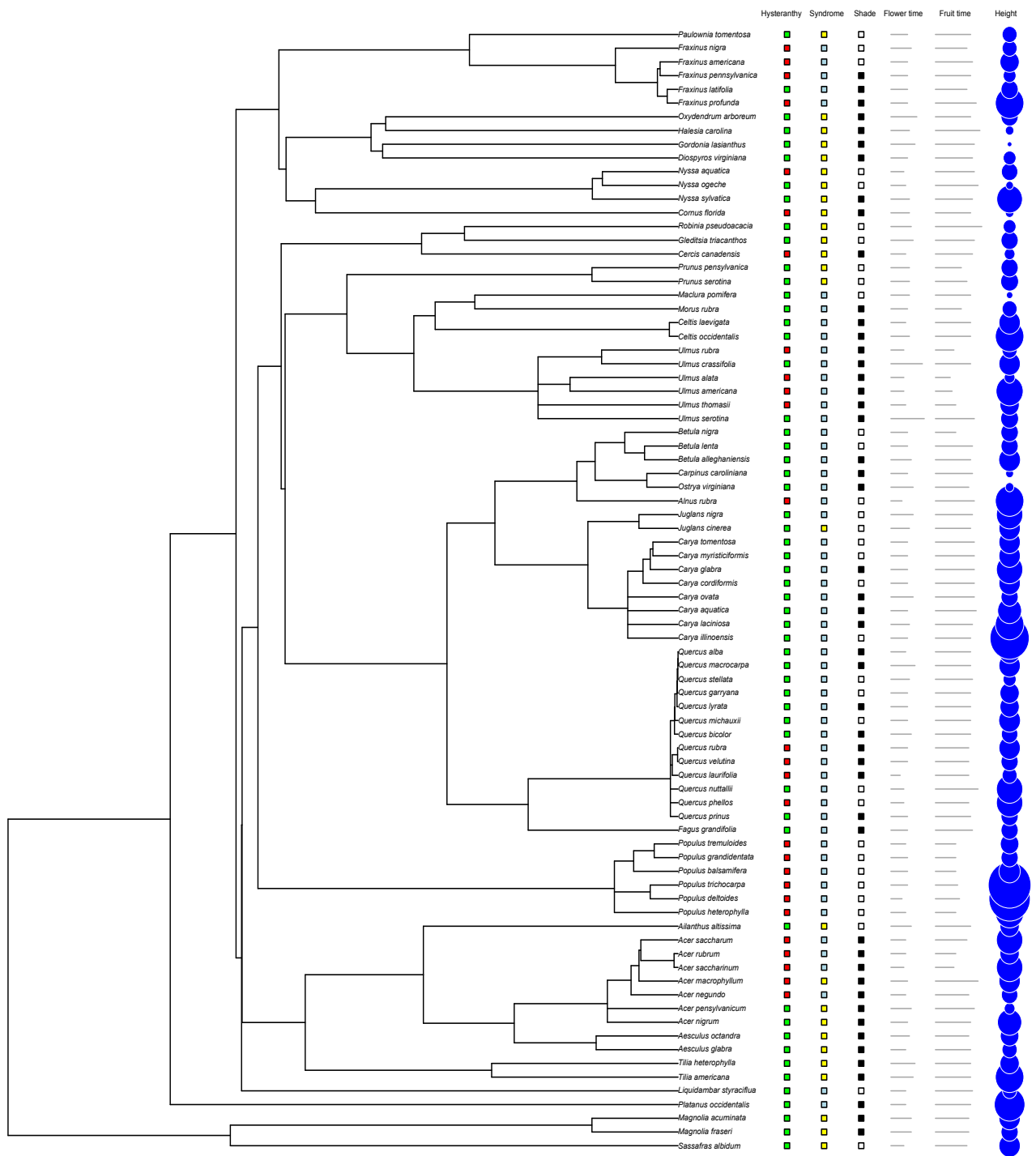


Figure 2: Eventaully these two figures will be side by side

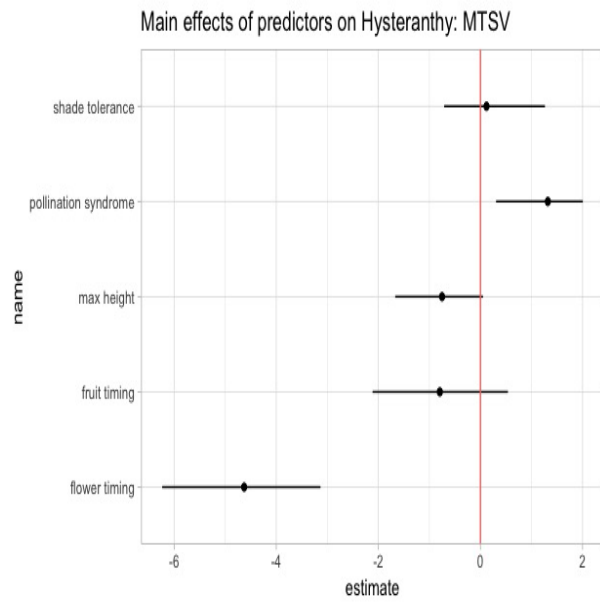


Figure 3: Eventually these two figures will be side by side

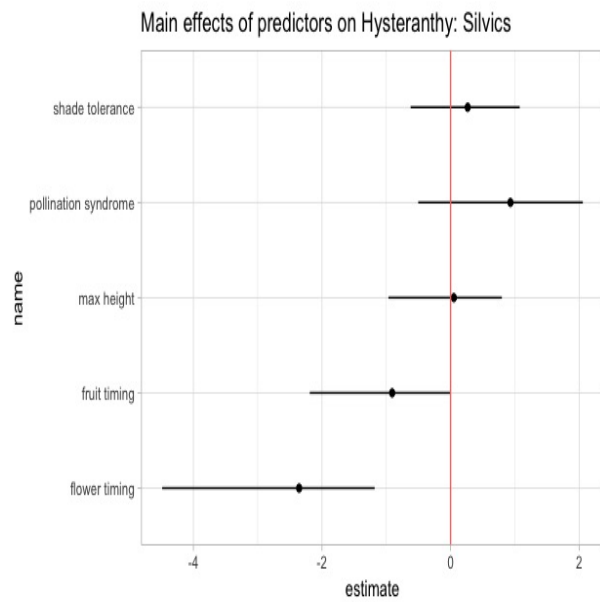


Figure 4: Eventually these two figures will be side by side