Ecological drivers of hysteranthous flowering vary across taxonomic scale in the North American cherries (Prunus spp.) or Aridity and pollinator attraction drive hysteranthous flowering in the North American cherries (Prunus spp.)

October 15, 2021

To do:

- 1. Full genus analyses with ordinal model (Got alot of the way there in FNA.R)
- 2. check prunocerasus analyses
- 3. Figure out phylogeny issues
- 4. Quantify hysteranthy in biologically pollinated taxa or summarize families it is present in. Off the top of my head for N.A. taxa the Rosaceae, Magnoliaceae, Fabacieae, Cornaceae, Annonaceae, Ericaceae.

Introduction

Generally speaking, hysteranthy is unique and common in temperate forest. Seems functionial. The most common, and well tested, explaination is that is hysteranthy evolved for wind-pollination. However that doesn't explain its prevalence in biotically pollinated taxa. Quote some statistic based new phyt paper. Tests of the function on hysteranthy in biotically pollinated taxa are exceedingly rare in the literature,, but may be critial for predicting species responses to global change.

While direct tests are limited, investigation of hysteranthy beneifit from a rich theoretical literature and several hypotheses have emerge.

Review them briefly and make predictions

- 1. Drought adaptation: (could be plastic or selected) aridity in range
- 2. insect visability: floral morphology
- 3. Null functionality early flowering. Fruit size or phenology
- 4. Phylogeny may also matter

While each hypothesis generates testible predictions there are several methodological challenges.

- 1. Unmeasured species difference compensate for measure traits
- 2. data quality based on expert opinion

These issues could be over come with:

- 1. character deconstruction
- 2. detailed quantitative measurements of flower leaf sequence phenology

We do this:

- 1. Coarse analyses of the flower-leaf sequences of North American *Prunus* species and their hypothesis relevant traits based on published data
- 2. Higher resolution inquiry of the fLower-leaf sequences and associated character traits based on our own measurements from a century worth of herbaria samples on a section of the Prunus subgenus Prunocerasus the American plums

Methods

0.1 Descriptions of the genus, and section

Say why they are ideal for this analyses

0.2 Genus level analyses

Data source Methods for analysis

0.3 Section level analyse

Methods for herbaria measurements Methods for analysis

Results

Discussion

There will probably be things about taxonomic scale. In attraction showing up at the genus but not section level. Major discussion of why.

Pollinator attraction and drought tolerance are a suite of traits and we only measured one axis of them and even with character deconstruction this could matter

Mechanistic experiments would still be useful, ie does water limitation influence FLS plasticity

Figures

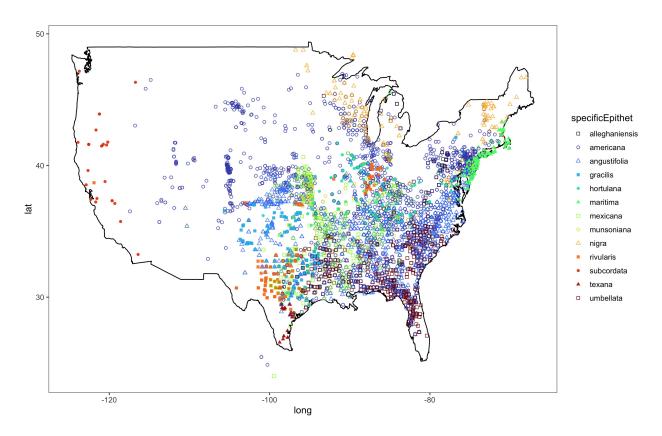


Figure 1: Map to show where data come from and to point out the two never hysteranthy species are highly endemic

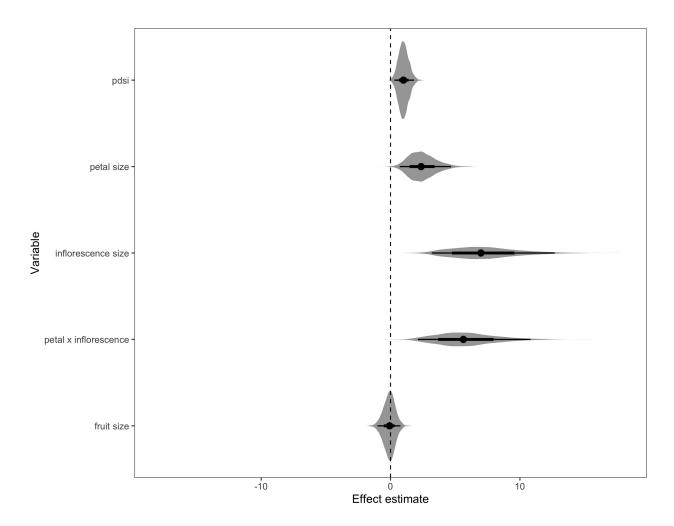


Figure 2: From the full genus analysis: Positive is less hysteranthus so aridity increases ihysteranthy, flower size decreases (ie smaller flowers- more hysteranthous) and no relationship with fruit size

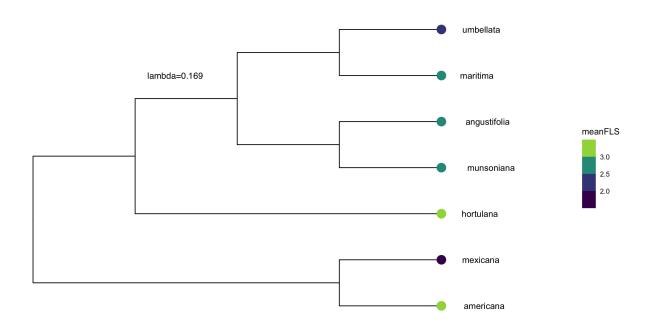


Figure 3: place holder for the phylgenies

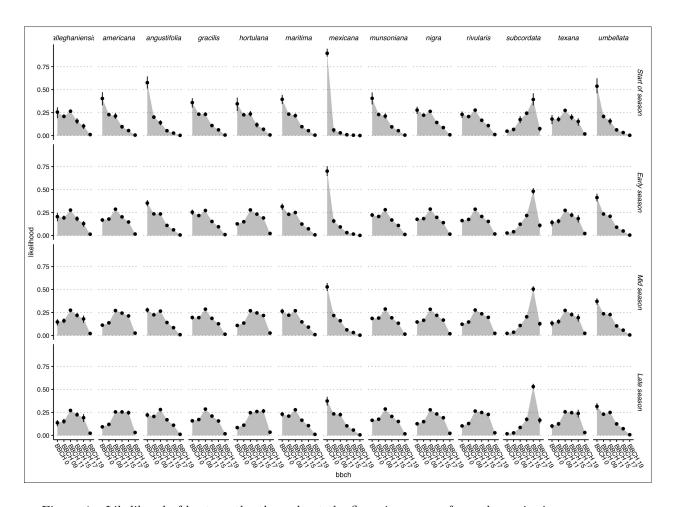


Figure 4: Likelihood of hysteranthy throughout the flowering season for each species in prunocerasus

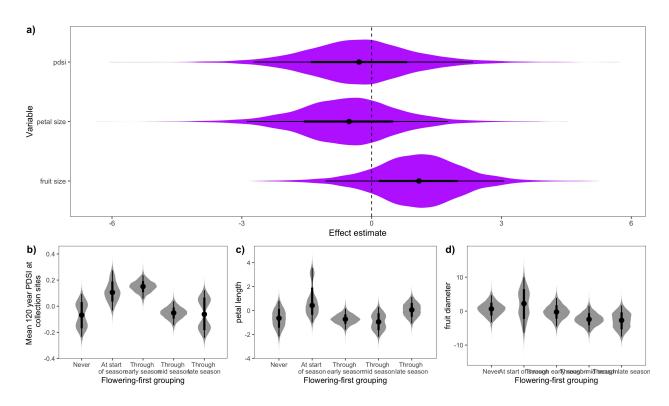


Figure 5: Effect estimates. Why are they so different in prunucerasus? 1. measurement error model increases uncertainty. 2. outlyers have stronger influence. 3. Maybe too closely related (all flower to somedegree while leave are developing)

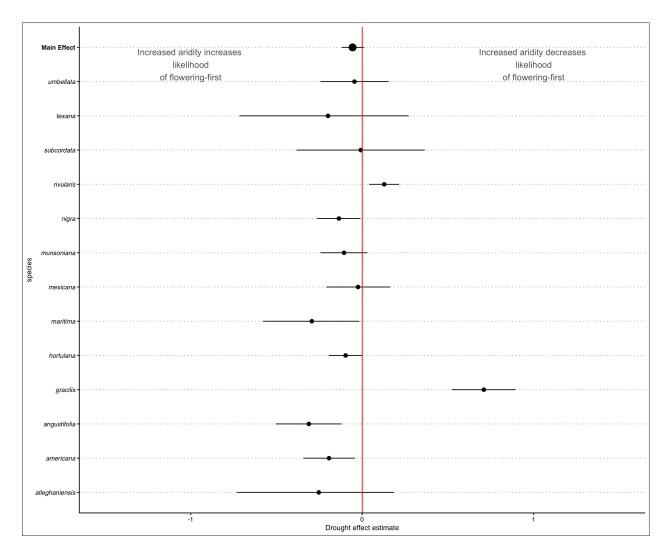


Figure 6: Hysteranthy more likely in drought years (negative values). Need to remake this figure in bayesplot