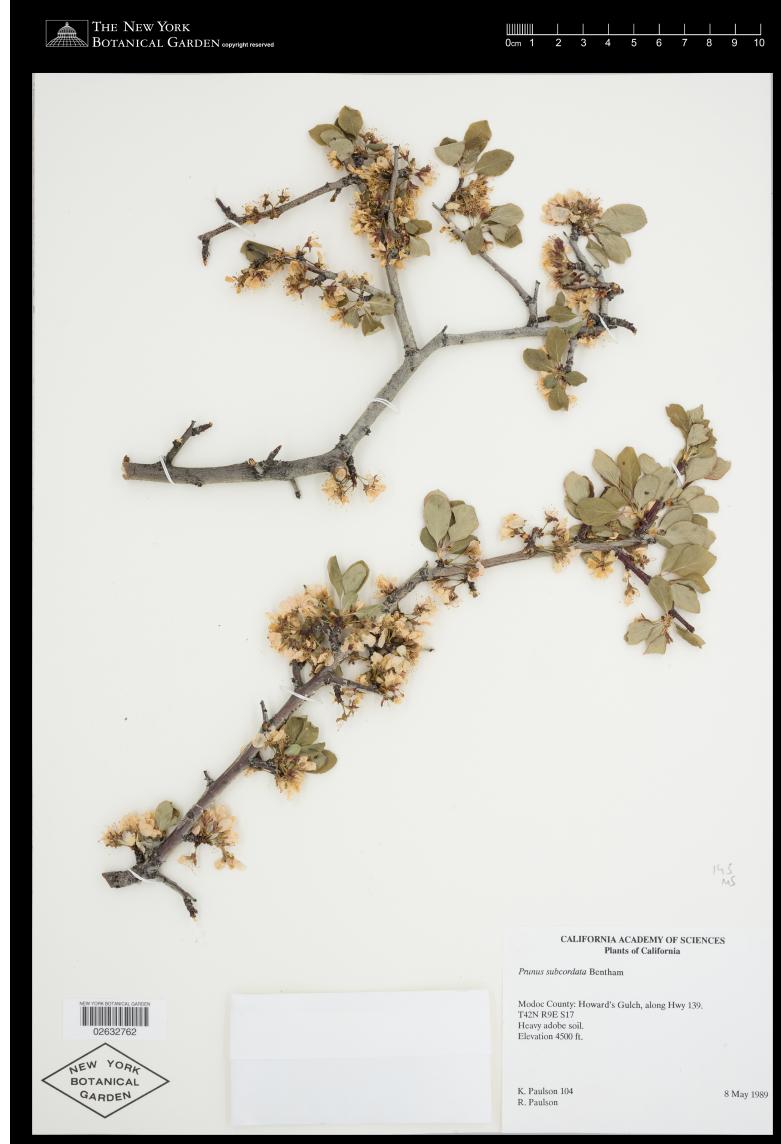


Ecological drivers of Flower leaf sequence variation in the American plum



Part 1: Account for uncertainty in classification

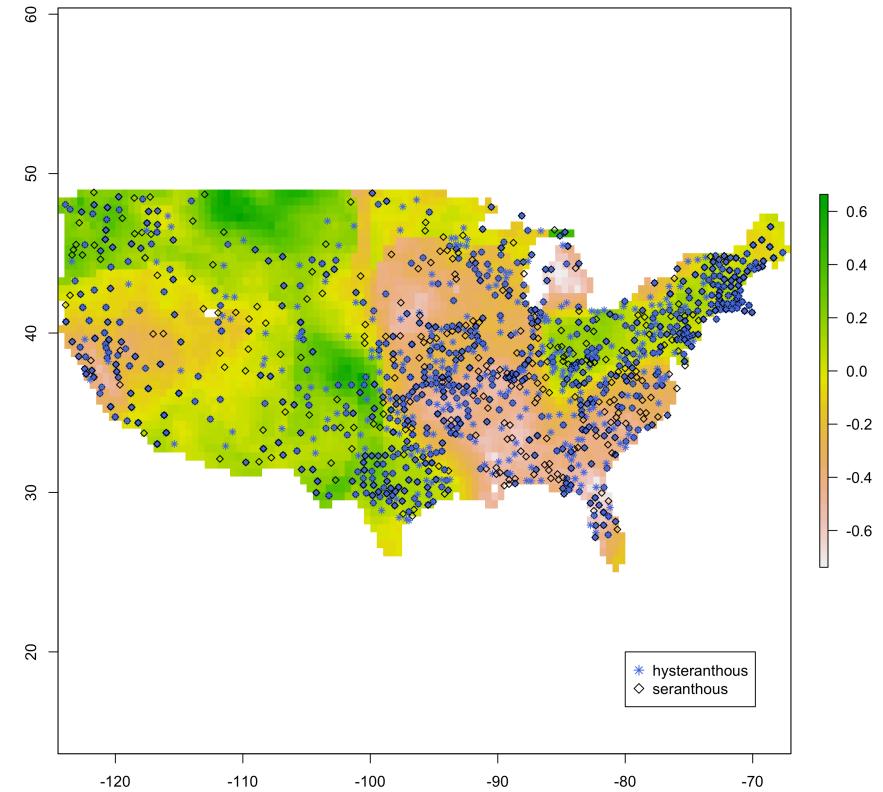
	species	Wight_1915	FNA	Agree
1	<i>angustifolia</i>	B	B/W	N
2	<i>gracilis</i>	B	B/W	N
3	<i>umbellata</i>	B	B/W	N
4	<i>nigra</i>	B	B/W	N
5	<i>alleghaniensis</i>	B	B	
6	<i>geniculata</i>	B	B	Y
7	<i>maritima</i>	B	B	Y
8	<i>texana</i>	B	B/W	N
9	<i>rivularis</i>	B/W	B/W	Y
10	<i>mexicana</i>	B/W	B	N
11	<i>munsonia</i>	B/W	B/W	
12	<i>americana</i>	W	B/W	N
13	<i>hortulana</i>	W	B/W	N
14	<i>subcordata</i>	W	W	Y

Part 2: Determine the ecological and functional traits that influence FLS variation



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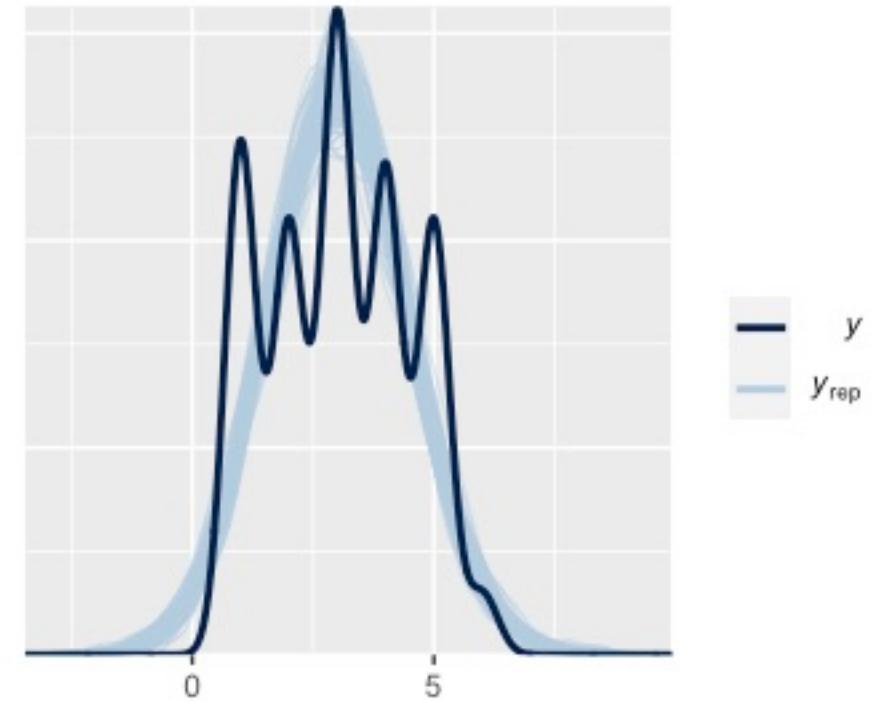
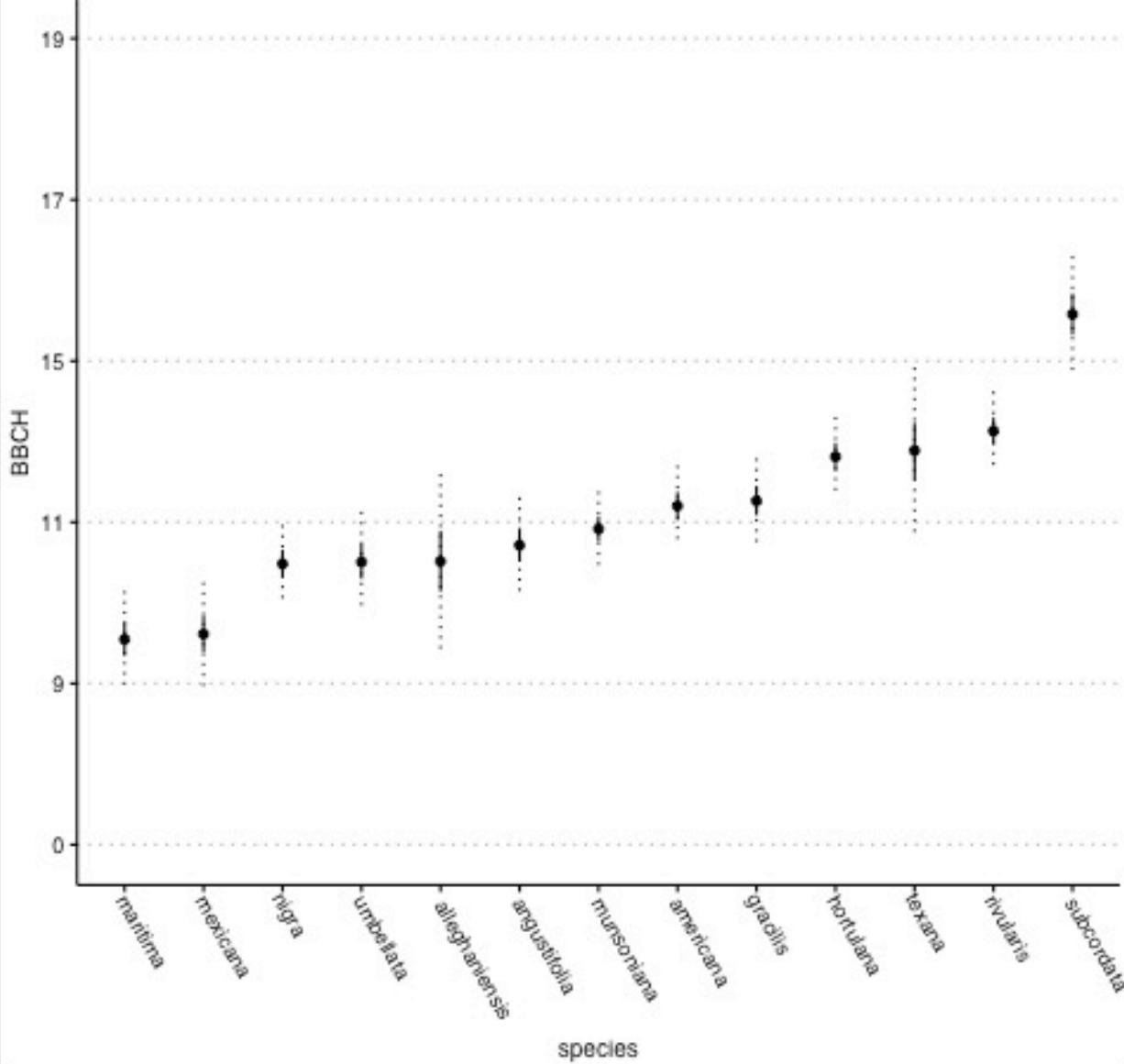
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Why I (think) need join modeling

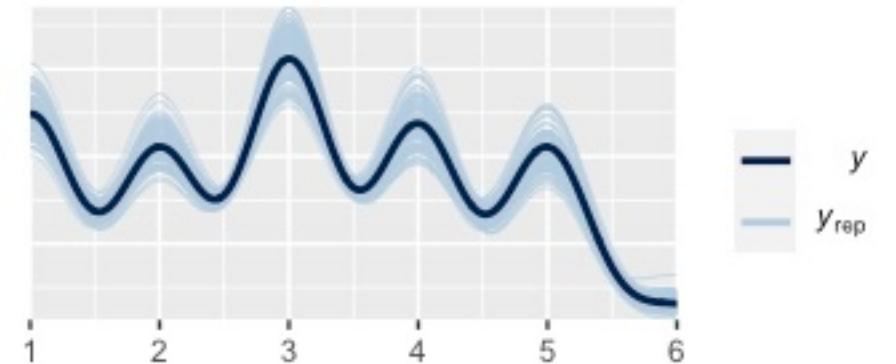
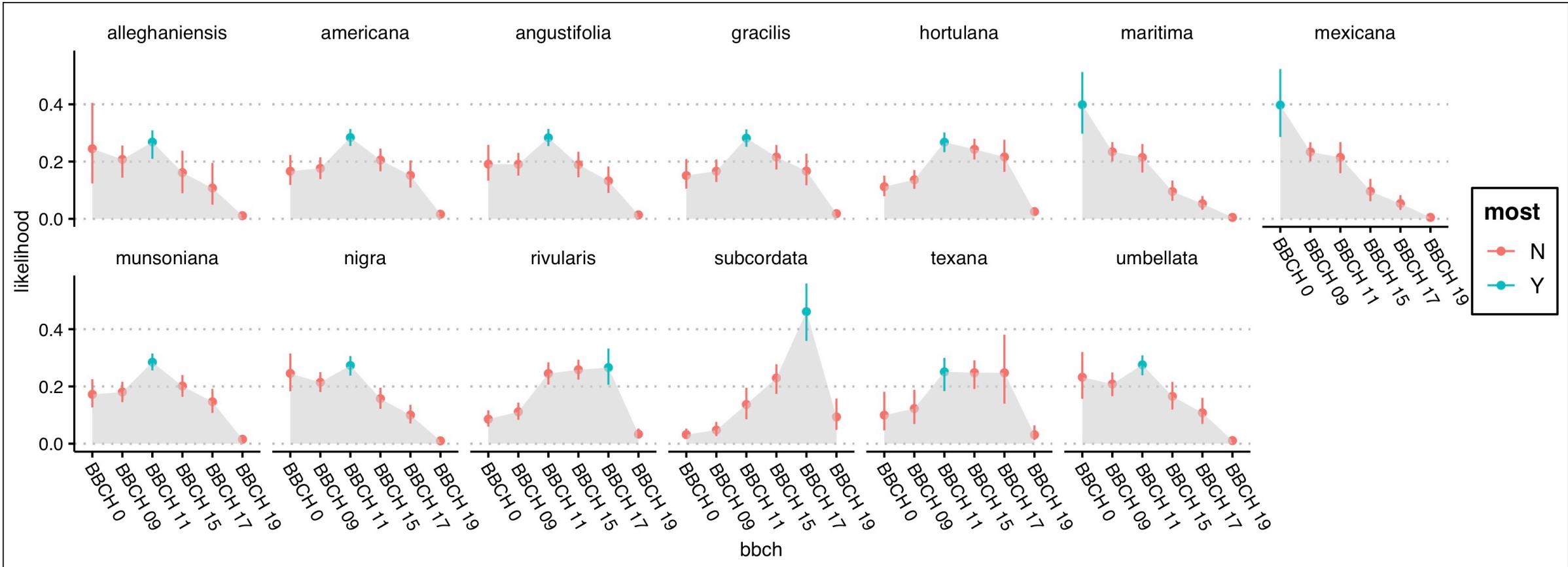
- Predictors are all at different scales, and I am using them to try and characterize species levels differences. Eg.
- FLS: 1009 specimens (17-119 specimens/species)
- PDSI: 2000 specimens (30-200 specimens/species)
- Petal length: 321 specimens (5-10 length measurements/specimen), 5-30 specimens/species
- Fruit diameter: 464 specimens (1-5 diameter measurements/ specimen), 5-30 specimens/species

Predicted vegetative stage during flowering



$BBCH \sim DOY + (1 | species)$

In this model, I “control for DOY”



TO do/ help

- Learn how to interpret ordinal regression output to fit fake data.
- Figure out how to add predictor(s) to ordinal model's fake data generation.
- Code said predictor into stan model
- Build the predictor submodel in stan
- Joint them up