Let's check out some models

$$y_i = \alpha_{species[i]} + \beta_{urban_{species[i]}} U + \beta_{provenance_{species[i]}} P + \epsilon_i$$

$$\epsilon_i \sim N(0, \sigma_y)$$

$$\alpha_{species} \sim N(\mu_{\alpha}, \sigma_{\alpha})$$

$$\beta_{urban species} \sim N(\mu_{urban}, \sigma_{urban})$$

 $\beta_{provenancespecies} \sim N(\mu_{provenance}, \sigma_{provenance})$

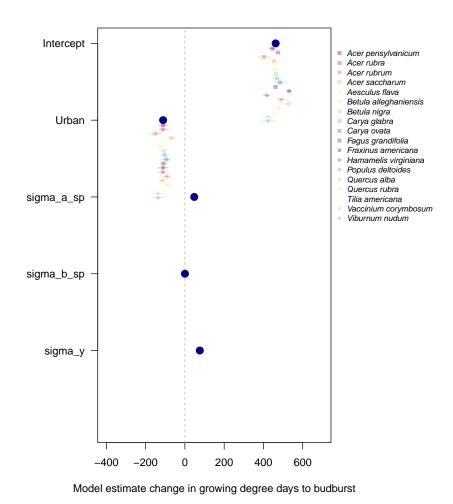


Figure 1: Effect of site on growing degree days until budburst using weather station data. More positive values indicate an increase in growing degree days whereas more negative values suggest fewer growing degree days. Dots and lines show means and 50% uncertainty intervals.

2

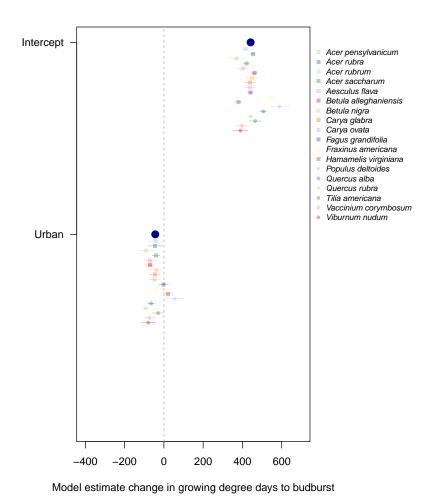


Figure 2: Effect of site on growing degree days until budburst using hobo logger data. More positive values indicate an increase in growing degree days whereas more negative values suggest fewer growing degree days. Dots and lines show means and 50% uncertainty intervals.

And then I build a model with phylogeny as a grouping factor and removed urban as an effect. Next move is to incorporate site somehow... but here's the tree.

Group-Level Effects:

~phylo (Number of levels: 17)

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat sd(Intercept) 44.38 24.98 2.15 92.68 1560 1.00

~spps (Number of levels: 17)

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat sd(Intercept) 46.33 24.81 2.46 94.53 1678 1.00

Population-Level Effects:

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat Intercept 386.61 18.77 347.68 423.40 8118 1.00

Family Specific Parameters:

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat sigma 85.85 3.38 79.56 92.78 20394 1.00

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample is a crude measure of effective sample size, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).

Fraxinus americana Viburnum nudum Vaccinium corymbosum Betula nigra Betula alleghaniensis Carya glabra Carya ovata Quercus alba Quercus rubra Fagus grandifolia Populus deltoides Acer rubrum Acer pensylvanicum Acer saccharum Aesculus flava Tilia americana Hamamelis virginiana -87.408 trait value 90.918 length=71.499

-

And then I added in site just now...

Group-Level Effects:

~phylo (Number of levels: 17)

Estimate Est.Error 1-95% CI u-95% CI Eff.Sample Rhat sd(Intercept) 42.73 21.51 4.09 87.24 3284 1.00 32.59 110.56 5683 1.00 sd(urban) 64.30 19.84 cor(Intercept,urban) -0.54 0.37 -0.98 0.44 2618 1.00

~spps (Number of levels: 17)

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat sd(Intercept) 31.90 18.46 1.59 69.83 2292 1.00

Population-Level Effects:

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
Intercept 463.87 19.96 423.18 502.90 9668 1.00
urban -122.45 22.83 -169.70 -78.93 9967 1.00

Family Specific Parameters:

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat sigma 72.48 2.91 67.02 78.52 17392 1.00

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample is a crude measure of effective sample size, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).

600 -500 -300 -200 -0.25 0.00 0.50 0.75 1.00 urban

Next steps:

- 1. Add in site to the phylogeny model and work through that more
- 2. Look at gridded climate data and compare!

- 3. Then do this all again for chilling!!
- 4. And then if we find that gridded climate data or weather station data is fairly good, maybe think about looking at all years of data and building phylogenetic models for all three cues.