

Flowering phenology in lodgepole pine

C. Susannah Tysor

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Lodgepole pine flowering biology

In spring

- ▶ Male strobili shed pollen
- ▶ Female strobili capture pollen

Wind pollinated

Flowering phenology matters

- ▶ Gene flow
 - ▶ assortative mating
 - ▶ (local) adaptation
 - ▶ clinal variation
- ▶ Seed orchard management
- ▶ Tree breeding
- ▶ Assisted migration

What controls the timing of flowering phenology in lodgepole pine?

- ▶ Chilling accumulation
- ▶ Forcing accumulation
- ▶ Genetics
- ▶ Assume met
- ▶ assume $> 5^{\circ}\text{C}$
- ▶ Is there clinal variation?

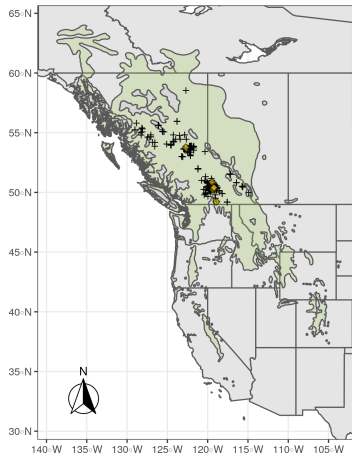
Data

- ▶ 748 clones of 259 genotypes
- ▶ grown in 7 seed orchards across BC
- ▶ flowering state recorded every few days over a one day to several week period
- ▶ 15 total years of data collection

Provenance

- ▶ seeds and scions from 143 natural stands
- ▶ grafted onto rootstock to create a clone bank
- ▶ clone bank scions selected based on superior growth, form

Map



How much forcing?

- ▶ Thermal time - transferable
- ▶ Test for provenance climate effect - MAT
- ▶ 4 models
 - ▶ Begin (male) pollen shed
 - ▶ End (male) pollen shed
 - ▶ Begin (female) receptivity
 - ▶ End (female) receptivity
- ▶ Account for variance due to site, year, genotype, and clone
- ▶ Account for unbalanced and censored data

Likelihood model

Likelihood of forcing observations would have a normal distribution

$$f_i \sim \text{Normal}(\phi_i, \sigma)$$

But all of my data is censored.

| Event | Sex | interval | left | right |
|-------|--------|----------|------|-------|
| begin | FEMALE | 0.63 | 0.37 | NA |
| begin | MALE | 0.35 | 0.65 | NA |
| end | FEMALE | 0.47 | NA | 0.53 |
| end | MALE | 0.48 | NA | 0.52 |

Likelihood model - for censored data

So we assume an underlying normal distribution that we're observing badly.

- ▶ Left censored start data (hazard function)

$$\Pr[f_i < U] = \int_{-\infty}^U \text{Normal}(y \mid \phi_i, \sigma) dy$$

- ▶ Right censored end data (survival function)

$$\Pr[f_i > L] = \int_L^{\infty} \text{Normal}(y \mid \phi_i, \sigma) dy$$

- ▶ Interval censored data

$$\Pr[L > f_i > U] = \int_L^U \text{Normal}(y \mid \phi_i, \sigma) dy$$

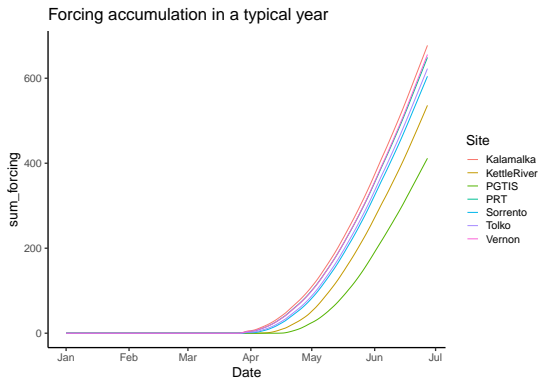
Modeling the mean

$$\phi_i = \alpha + \beta MAT + \delta_{Site,i} + \delta_{Year,i} + \delta_{Clone,i} + \delta_{Ramet,i}$$

- ▶ α : Overall mean forcing requirement
- ▶ β : Provenance climate effect using MAT as covariate
- ▶ δ : Offsets from the overall mean based on site, year, clone, and ramet

Priors

- ▶ limits based on possible forcing accumulation
- ▶ gamma distribution for intercept
- ▶ half normal for offset parameter standard deviations



Fit in Stan via brms package

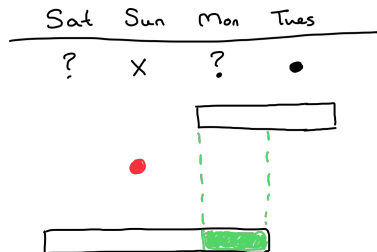
```
# model formula
bform <- brmsformula(sum_forcing | cens(censored, upper) ~
                    MAT + (1|Site) + (1|Clone) + (1|Year) + (1|Tree)

# model prior
bprior <- c(prior("gamma(3.65, 0.01)", class = "Intercept"),
            prior("normal(0,15)", class = "sigma"),
            prior("normal(0,9)", class = "sd"),
            prior("normal(0,5)", class = "b"))

# female/receptivity begin
fbfit <- brm(bform, data = fbdat,
            prior = bprior,
            init = initpars,
            iter = 4000,
            cores = 6,
            chains = 6)
```

Fit

Modelling events I didn't observe - so how can I check how my model is doing?



observations

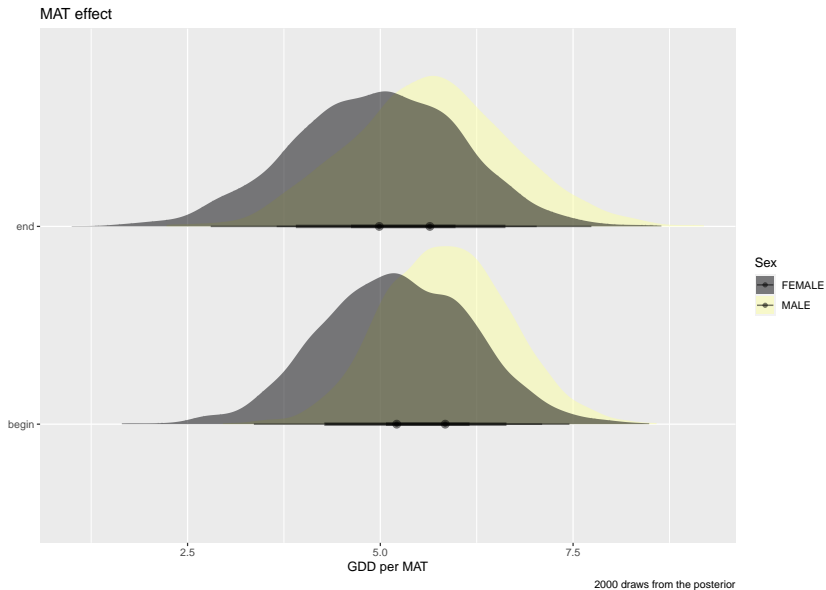
window of possibility

model prediction summarized
as point (mean)

model prediction as 1 sd
interval around mean

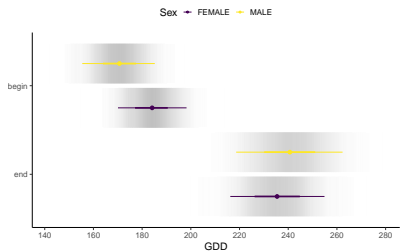
| Sex | Begin | Begin_sd | End | End_sd |
|--------|-------|----------|------|--------|
| FEMALE | 0.61 | 0.97 | 0.71 | 0.97 |
| MALE | 0.76 | 0.99 | 0.71 | 0.97 |

Results - Provenance effect similar for end and begin

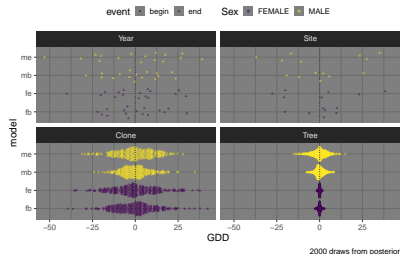


Results - Mean and variation

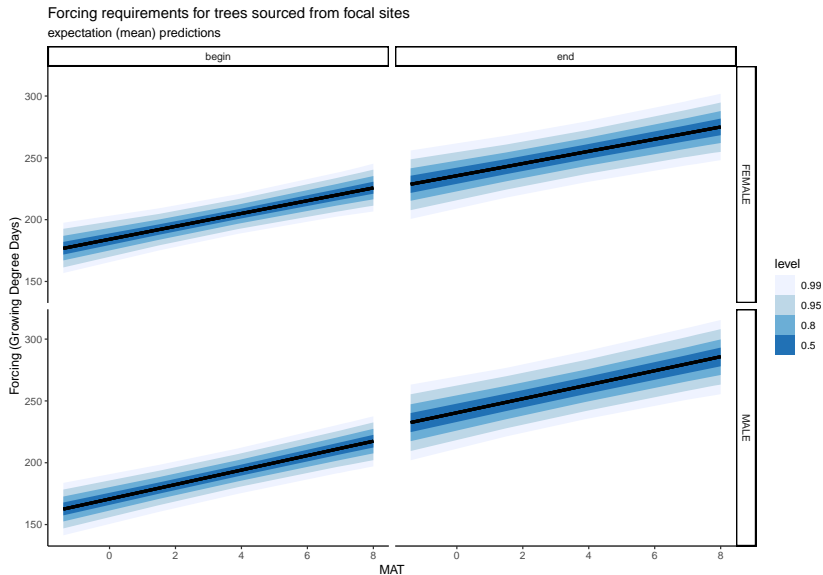
Intercepts



Offset medians



Results - Forcing predictions expectation



Day of year predictions intro

Temperature timeseries -> forcing accumulation timeseries

Then match to forcing predictions

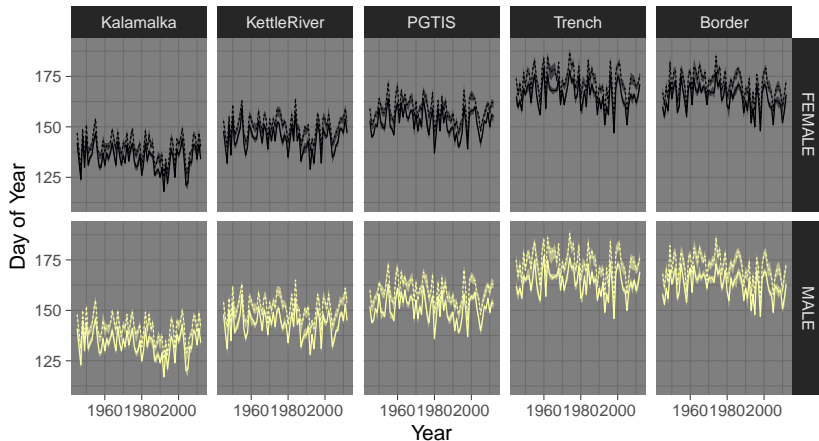
Focus on 5 sites (as provenances as sites)

| Site | MAT | Elevation |
|-------------|------|-----------|
| Border | -1.4 | 671 |
| Trench | 1.5 | 659 |
| PGTIS | 3.9 | 598 |
| KettleRiver | 6.9 | 632 |
| Kalamalka | 8.0 | 486 |

Results - MAT Day of Year

Predicted flowering periods

posterior expectation, ribbons = uncertainty, lines = medians



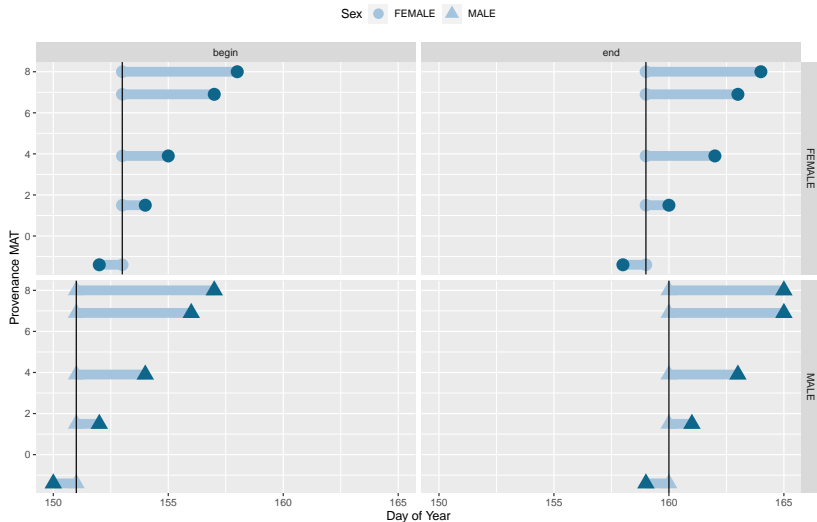
event — begin - - - end

Sex ■ FEMALE ■ MALE

Results - DoY expectations in common garden

Change in flowering day of year expectation with MAT effect

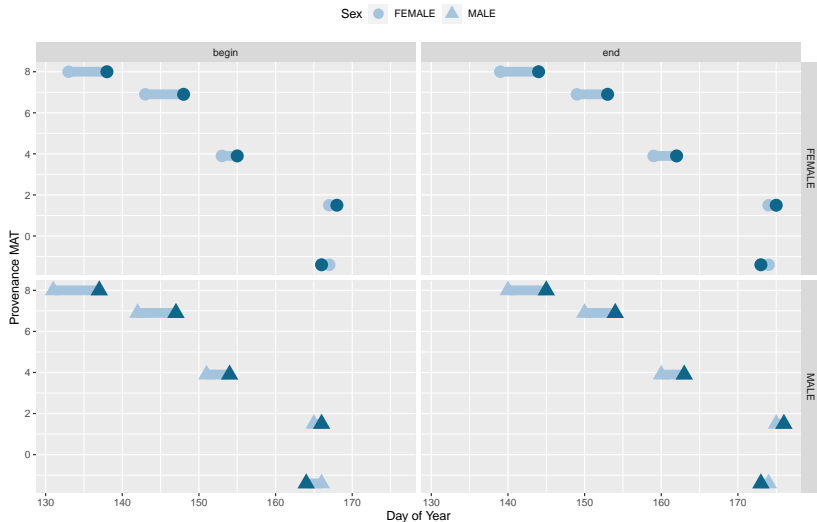
typical year, trees grown at PGTIS



Results - DoY expectations on the landscape

Change in flowering day of year expectation with MAT effect

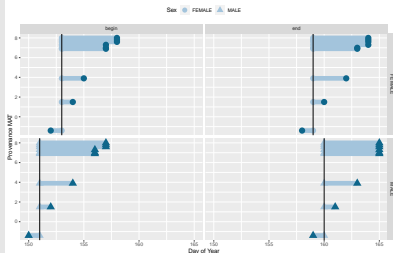
typical year, trees grown at home



Results - MAT Day of Year

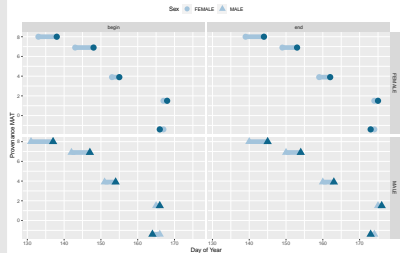
Common garden

Change in flowering day of year expectation with MAT effect
typical year, trees grown at PGIS



Home

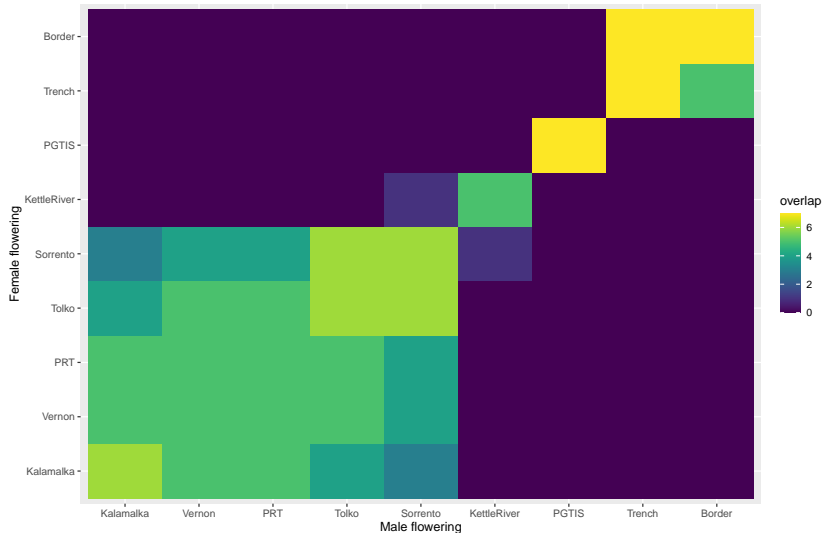
Change in flowering day of year expectation with MAT effect
typical year, trees grown at home



Overlap

Days of overlap in a typical year

provenance MAT label on diagonal



Summary

- ▶ Males have longer period and start slightly before, end after females
- ▶ ~5 more GDD per 1 degree MAT required for flowering
- ▶ Countergradient variation should increase flowering period overlap
- ▶ Overlap depends on geographic location and provenance climate
- ▶ Anybody can predict flowering time in lodgepole with just daily temperature data and MAT - with no modelling required.

Questions

- ▶ But why is there countergradient variation?

More

- ▶ Climate change (1 month shift, no big overlap changes)
- ▶ Does it all wash away in the light of individual variation?

Extra

