

Flowering phenology in lodgepole pine

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Lodgepole pine flowering biology

In spring

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

Wind pollinated

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
- ▶ Warmth accumulation
- ▶ Genetics
- ▶ Assume met
- ▶ assume “forcing”
temperatures $> 5\text{ }^{\circ}\text{C}$
- ▶ Is there clinal variation?

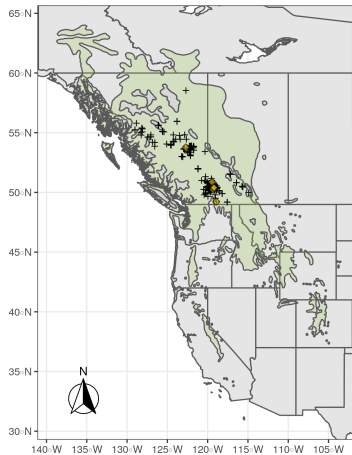
Data

- ▶ 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

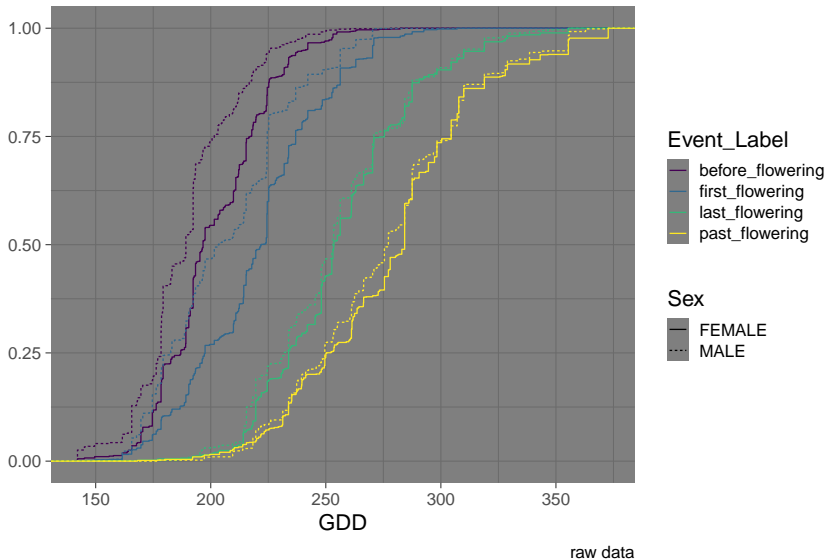
- ▶ seeds and scions from 143 natural stands
- ▶ grafted onto rootstock to create a clone bank
- ▶ clone bank scions selected based on superior growth, form

Map



Data

Cumulative distribution of accumulated forcing at observation



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

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

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

Priors

Limit parameter estimates to forcing accumulations possible at our sites during late spring, when lodgepole pine are known to flower in British Columbia and approximately known length of the flowering period from prior work

Forcing accumulation is always positive and the overall distribution across reasonable ranges is strongly right skewed, so we used a gamma distribution with shape (α) and rate (β) parameters derived from the mean and standard deviation of the May-June historical forcing accumulation.

site and year have relatively few levels with which to estimate σ_{factor} , half normal priors with their relatively thin tails were used to help constrain offset parameter standard deviations

Fitting

- Stan via brms package

```
initpars <- lapply(1:6, function(id) list(sigma = 30, Inter  
  
# model formula  
bform <- brmsformula(sum_forcing | cens(censored, upper) ~  
  
# 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,  
            save_model = "female_begin.stan",  
            file = "female_begin",  
            prior = bprior,  
            init = initpars,
```

Fit

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

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

Slide with R Output

```
summary(cars)
```

##	speed	dist
##	Min. : 4.0	Min. : 2.00
##	1st Qu.:12.0	1st Qu.: 26.00
##	Median :15.0	Median : 36.00
##	Mean :15.4	Mean : 42.98
##	3rd Qu.:19.0	3rd Qu.: 56.00
##	Max. :25.0	Max. :120.00

Slide with Plot

