Supplementary Material: Budburst timing within a functional trait framework

Figures & Tables

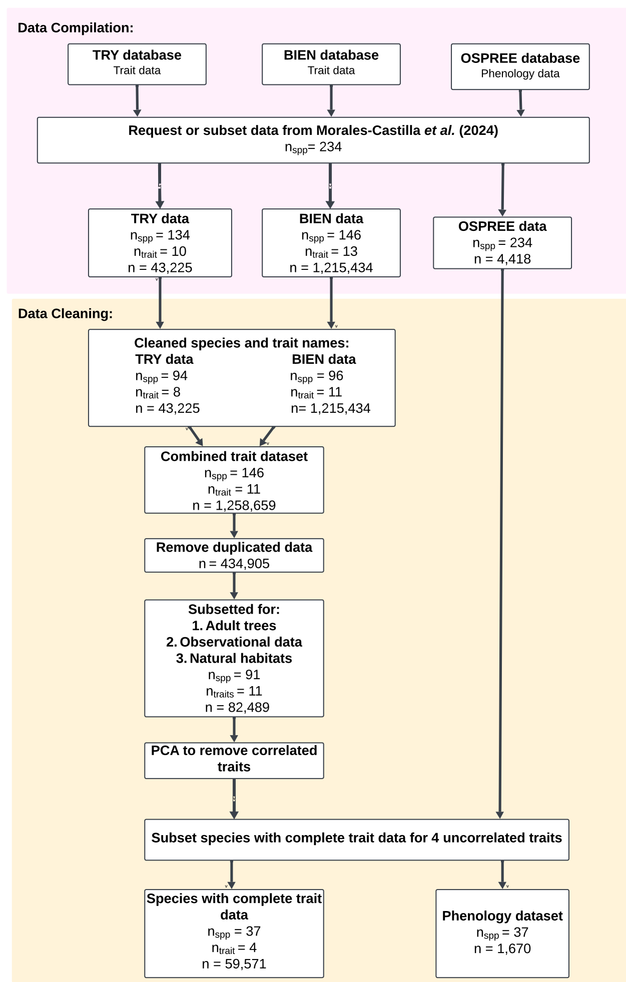

Figure S1: Our initial aim was to include all species from Morales-Castilla *et al.* (2024), however trait data was only available for a subset of these species. Data was cleaned extensively, with each step depicted by a box, and subset to only include traits for adult trees growing under natural conditions for which we had a complete suite of trait values.

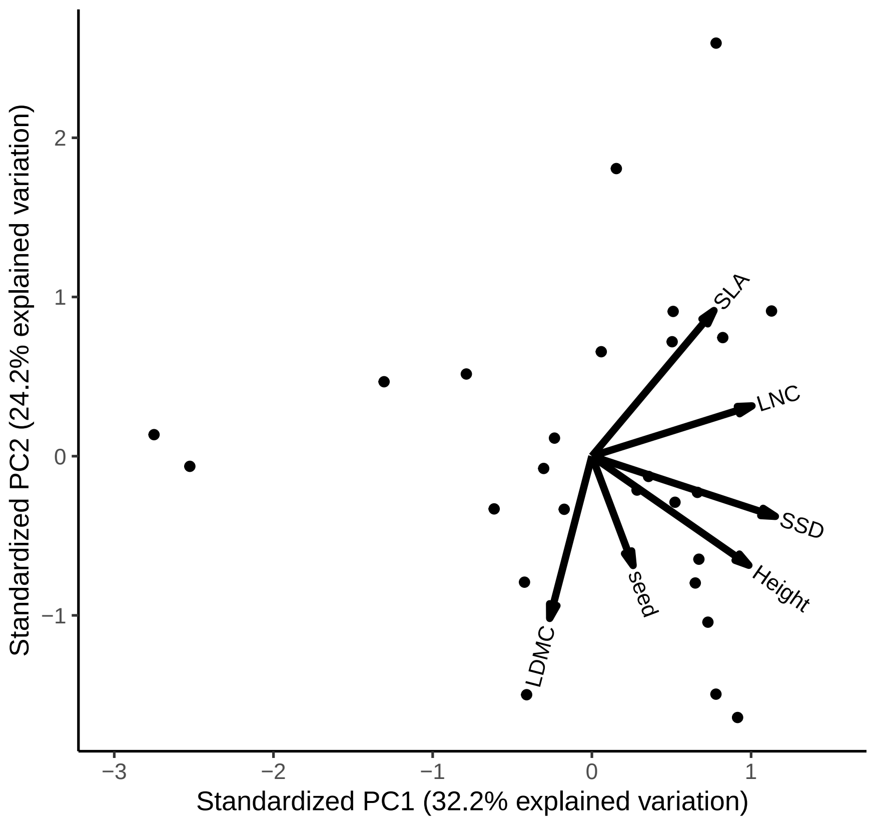

Figure S2: A projection of tree traits across the first and second principle component axis. Arrows represent the direction of vectors for the six functional traits with complete trait data. Points represent the 26 species for which complete trait data was available.

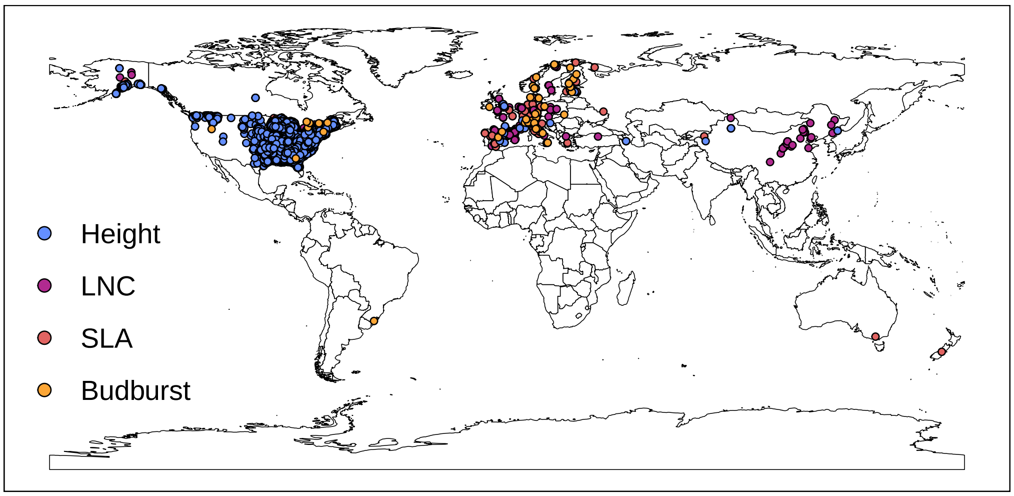

Figure S3: We obtained data from the TRY and BIEN plant trait databases and the OSPREE database of plant phenology experiments for temperate tree species. Following our cleaning of the data and selection of uncorrelated traits, our final dataset included 37 species from 24 unique datasources for the trait data and 34 unique studies for the budburst data. Our data is focused on temperate ecosystems globally with most data originating from North America and Europe.

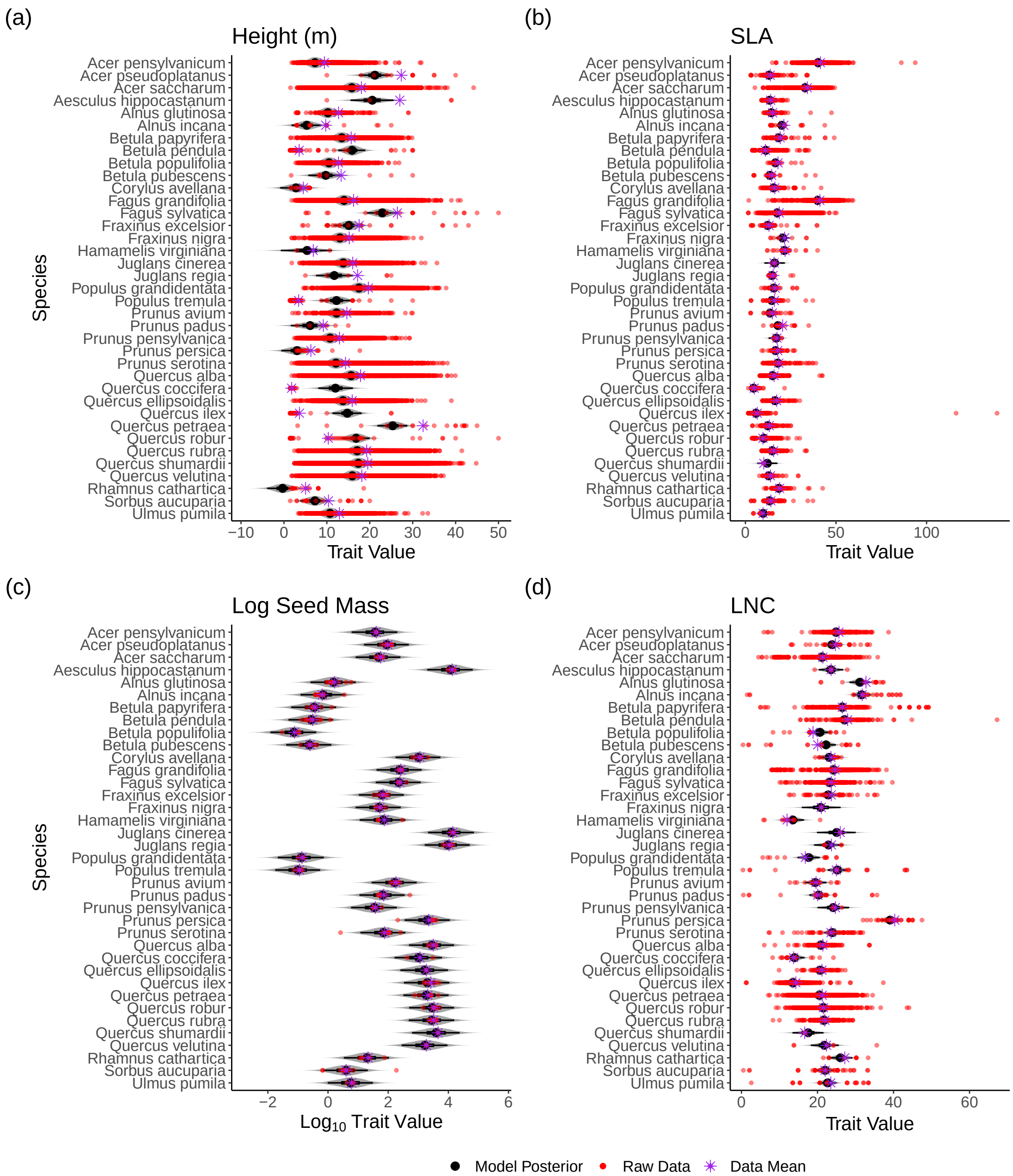

Figure S4: For most traits, we found the species-level model posterior distributions from our joint model of trait effects on budburst cues were well-aligned with the raw data for our 37 woody deciduous plant species. Four functional traits—(a) height, (b) SLA, (c) seed mass, and (d) LNC— were modeled individually, with the calculated trait value being used to jointly model species' responses to standardized chilling, forcing, and photoperiod cues. Model posteriors are shown in black, with the thicker line depicting the 50% uncertainty interval and the thinner black line the 95% uncertainty interval. The raw data is shown in red and the species-level means from the raw data are denoted as a purple stars.

Table S1: Bibliographic information for trait data sources from both BIEN and TRY trait databases. Datasets without references or incomplete references are denoted below as 'unreferenced'.

Database	Reference	Trait name	Unit	No. observations	No. Species
BIEN	Mchugh *et al.* (2015)	Height	m	26	8
BIEN	Marx *et al.* (2016)	Height	m	2	2
BIEN	Price *et al.* (2014)	Height	m	27	19
BIEN	Unreferenced	Height	m	18	16
BIEN	Kleyer *et al.* (2008)	Height	m	90	19
BIEN	Unreferenced	Height	m	10	10
BIEN	Moles, Angela; unreferenced	Height	m	21	14
BIEN	Reams, Greg; unreferenced	Height	m	47036	19
BIEN	Grime, Hodgson, & Hunt; unreferenced	Height	m	5	5
BIEN	Unreferenced	Height	m	8	5
BIEN	Pérez-de Lis *et al.* (2017)	Height	m	18	1
BIEN	Robinson *et al.* (2015)	Height	m	120	1
BIEN	Anderson-teixeira *et al.* (2015)	Height	m	20	1
TRY	Bond-Lamberty *et al.* (2002)	Height	m	2	1
TRY	Unpublished	Height	m	275	3
TRY	Wright *et al.* (2004)	Height	m	28	19
TRY	Prentice *et al.* (2011)	Height	m	2	2
TRY	Schweingruber & Landolt (2010)	Height	m	21	21
TRY	Unpublished	Height	m	35	2
TRY	Moles *et al.* (2004)	Height	m	5	5
TRY	Cavender-Bares *et al.* (2006)	Height	m	1	1
TRY	Diaz *et al.* (2004)	Height	m	11	10
TRY	Craine *et al.* (2009)	LNC	mg/g	287	12
TRY	Wilson *et al.* (2000)	LNC	mg/g	44	2
TRY	Wenxuan *et al.* (2012)	LNC	mg/g	7	4
TRY	Yahan *et al.* (2013)	LNC	mg/g	7	3
TRY	Wright *et al.* (2004)	LNC	mg/g	65	32
TRY	Prentice *et al.* (2011)	LNC	mg/g	3	2
TRY	Vergutz *et al.* (2012)	LNC	mg/g	120	20
TRY	Atkin *et al.* (2015)	LNC	mg/g	24	8
TRY	Marie *et al.* (2015)	LNC	mg/g	72	22
TRY	Cornelissen *et al.* (2003)	LNC	mg/g	2	1
TRY	Unpublished	LNC	mg/g	3216	37
TRY	Wang *et al.* (2017)	LNC	mg/g	6	2
BIEN	Marx *et al.* (2016)	Seed mass	mg	3	3
BIEN	Unreferenced	Seed mass	mg	4	2
BIEN	Liu *et al.* (2018)	Seed mass	mg	250	37
BIEN	Ameztegui *et al.* (2017)	Seed mass	mg	12	12
BIEN	Paine *et al.* (2015)	Seed mass	mg	12	7
TRY	Wilson *et al.* (2000)	SLA	mm2 mg-1	44	2
TRY	Unpublished	SLA	mm2 mg-1	204	3
TRY	Wright *et al.* (2004)	SLA	mm2 mg-1	93	33
TRY	Prentice *et al.* (2011)	SLA	mm2 mg-1	2	2
TRY	Kleyer *et al.* (2008)	SLA	mm2 mg-1	102	18
TRY	Unpublished	SLA	mm2 mg-1	83	2
TRY	Atkin *et al.* (2015)	SLA	mm2 mg-1	40	11
TRY	Marie *et al.* (2015)	SLA	mm2 mg-1	86	23
TRY	Cornelissen *et al.* (2003)	SLA	mm2 mg-1	615	14
TRY	Unpublished	SLA	mm2 mg-1	6307	37
TRY	Wang *et al.* (2017)	SLA	mm2 mg-1	6	2
TRY	Shipley & Vu (2002)	SLA	mm2 mg-1	20	2
TRY	Cavender-Bares *et al.* (2006)	SLA	mm2 mg-1	42	2
TRY	Unpublished	SLA	mm2 mg-1	1	1
TRY	Diaz *et al.* (2004)	SLA	mm2 mg-1	11	10

Table S2: Summary of estimates from our model of height ($n = 42781$) using data from 37 focal species. Values represent the mean estimate for model parameters as well as the lower and upper limits (25%–75%) of the 50% uncertainty interval and the lower and upper limits (5%–95%) of the 90% uncertainty interval (UI). The strength of the relationship can be assessed by comparing across UI, with parameters with intervals that cross zero depicting weak relationships.

	mean	5%	25%	75%	95%
$\mu_{grand.trait}$	13.3	10.0	11.9	14.6	16.5
$\mu_{k,g}$	32.1	27.7	30.3	33.9	36.6
μ_{force}	-10.7	-15.2	-12.5	-8.8	-6.2
μ_{chill}	-4.0	-11.1	-6.5	-1.1	2.8
μ_{photo}	1.0	-2.7	-0.5	2.5	4.7
$\beta_{trait.force}$	0.2	-0.1	0.0	0.3	0.5
$\beta_{trait.chill}$	-0.5	-1.0	-0.7	-0.3	-0.1
$\beta_{trait.photo}$	-0.2	-0.5	-0.4	-0.1	0.0
$\sigma_{species}$	6.0	4.9	5.5	6.5	7.3
σ_{study}	7.5	5.7	6.6	8.3	9.8
σ_{trait}	5.4	5.4	5.4	5.4	5.4
σ_{pheno}	15.1	11.8	13.6	16.4	18.6
σ_{force}	5.0	3.3	4.2	5.7	7.0
σ_{chill}	8.8	5.8	7.2	10.0	12.7
σ_{photo}	3.5	2.2	2.9	4.1	5.3
σ_{d}	14.2	13.8	14.	14.3	14.6

Table S3: Summary of estimates from our model of seed mass ($n = 281$) using data from 37 focal species. Values represent the mean estimate for model parameters as well as the lower and upper limits (25%–75%) of the 50% uncertainty interval and the lower and upper limits (5%–95%) of the 90% uncertainty interval (UI). The strength of the relationship can be assessed by comparing across UI, with parameters with intervals that cross zero depicting weak relationships.

	mean	5%	25%	75%	95%
$\mu_{grand.trait}$	1.9	1.0	1.5	2.2	2.7
$\mu_{k,g}$	31.4	27.1	29.6	33.1	35.8
μ_{force}	-8.2	-10.8	-9.2	-7.1	-5.6
μ_{chill}	-9.4	-14.0	-11.2	-7.5	-4.8
μ_{photo}	-1.3	-3.4	-2.1	-0.4	0.8
$\beta_{trait.force}$	-0.3	-1.4	-0.8	0.1	0.9
$\beta_{trait.chill}$	-1.1	-2.9	-1.8	-0.4	0.7
$\beta_{trait.photo}$	-0.6	-1.5	-0.9	-0.2	0.4
$\sigma_{species}$	1.6	1.3	1.5	1.7	2.0
σ_{study}	1.0	0.8	0.9	1.0	1.1
σ_{trait}	0.2	0.2	0.2	0.3	0.3
σ_{pheno}	14.8	11.2	13.3	16.3	18.6
σ_{force}	4.9	3.4	4.2	5.5	6.7
σ_{chill}	10.7	7.1	8.8	12.1	15.4
σ_{photo}	3.6	2.3	3.0	4.1	5.1
σ_{d}	14.1	13.7	14.0	14.3	14.5

Table S4: Summary of estimates from our model of specific leaf area (SLA, $n = 7656$) using data from 37 focal species. Values represent the mean estimate for model parameters as well as the lower and upper limits (25%–75%) of the 50% uncertainty interval and the lower and upper limits (5%–95%) of the 90% uncertainty interval (UI). The strength of the relationship can be assessed by comparing across UI, with parameters with intervals that cross zero depicting weak relationships.

	mean	5%	25%	75%	95%
$\mu_{grand.trait}$	16.8	14.5	15.8	17.8	19.3
$\mu_{k,g}$	31.3	27.2	29.6	33.0	35.6
μ_{force}	-11.4	-16.2	-13.1	-9.6	-7.2
μ_{chill}	-16.7	-24.6	-19.8	-13.3	-9.1
μ_{photo}	1.9	-2.4	0.2	3.6	5.8
$\beta_{trait.force}$	0.2	-0.1	0.1	0.3	0.4
$\beta_{trait.chill}$	0.3	-0.1	0.2	0.5	0.7
$\beta_{trait.photo}$	-0.2	-0.5	-0.3	-0.1	0.0
$\sigma_{species}$	7.8	6.4	7.1	8.4	9.4
σ_{study}	3.3	2.0	2.6	3.8	5.1
σ_{trait}	6.2	6.1	6.1	6.2	6.3
σ_{pheno}	13.9	10.7	12.4	15.3	17.6
σ_{force}	5.0	3.3	4.2	5.6	7.0
σ_{chill}	10.6	7.2	8.9	12.0	14.8
σ_{photo}	3.5	2.3	2.9	3.9	5.0
σ_{d}	14.2	13.8	14.0	14.3	14.6

Table S5: Summary of estimates from our model of leaf nitrogen content (LNC, $n = 3853$) using data from 37 focal species. Values represent the mean estimate for model parameters as well as the lower and upper limits (25%–75%) of the 50% uncertainty interval and the lower and upper limits (5%–95%) of the 90% uncertainty interval (UI). The strength of the relationship can be assessed by comparing across UI, with parameters with intervals that cross zero depicting weak relationships.

	mean	5%	25%	75%	95%
$\mu_{grand.trait}$	22.6	20.4	21.7	23.5	24.9
$\mu_{k,g}$	31.1	27.1	29.4	32.8	35.3
μ_{force}	-19.3	-27.9	-22.9	-15.8	-10.5
μ_{chill}	-27.1	-38.5	-31.7	-22.4	-15.4
μ_{photo}	-9.4	-17.0	-12.5	-6.2	-1.9
$\beta_{trait.force}$	0.5	0.1	0.3	0.6	0.8
$\beta_{trait.chill}$	0.7	0.2	0.5	0.9	1.2
$\beta_{trait.photo}$	0.3	0.0	0.2	0.4	0.6
$\sigma_{species}$	5.1	4.2	4.7	5.5	6.2
σ_{study}	3.6	2.2	2.9	4.1	5.3
σ_{trait}	5.1	5.0	5.1	5.2	5.2
σ_{pheno}	14.0	10.9	12.7	15.3	17.4
σ_{force}	4.6	3.0	3.8	5.2	6.6
σ_{chill}	8.9	6.1	7.5	10.1	12.5
σ_{photo}	3.6	2.4	3.0	4.1	5.0
σ_{d}	14.2	13.8	14.0	14.3	14.6

Stan model code

```
data {
  int<lower = 1> n_spec;
  int<lower = 1> N;
  int<lower = 1, upper = n_spec> trait_species[N];
  int<lower = 1> n_study;
  int<lower = 1, upper = n_study> study[N];
  vector[N] yTraiti;

  int<lower = 1> Nph;
  int<lower = 1, upper = n_spec> phenology_species[Nph];
  vector[Nph] yPhenoi;
  vector[Nph] forcei;
  vector[Nph] chilli;
  vector[Nph] photoi;
}

parameters{

  real mu_grand;
  vector[n_spec] muSp;
  vector[n_study] muStudy;
  real<lower = 0> sigma_traity;
  real<lower = 0> sigma_sp;
  real<lower = 0> sigma_study;

  real alphaForceSp[n_spec];
  real muForceSp;
  real<lower = 0> sigmaForceSp;
  real alphaChillSp[n_spec];
  real muChillSp;
  real<lower = 0> sigmaChillSp;
  real alphaPhotoSp[n_spec];
  real muPhotoSp;
  real<lower = 0> sigmaPhotoSp;
  real alphaPhenoSp[n_spec];
  real muPhenoSp;
  real<lower = 0> sigmaPhenoSp;
  real betaTraitxForce;
  real betaTraitxChill;
  real betaTraitxPhoto;
  real<lower = 0> sigmapheno_y;
}

transformed parameters{

  vector[N] y_hat;
  vector[n_spec] mu_grand_sp;

  real betaForceSp[n_spec];
```

```
  real betaPhotoSp[n_spec];
  real betaChillSp[n_spec];

  for(i in 1:n_spec){
    mu_grand_sp[i] = mu_grand + muSp[i];
  }
  for (i in 1:N){
    y_hat[i] = mu_grand + muSp[trait_species[i]] + muStudy[study[i]];
  }

  for (isp in 1:n_spec){
    betaForceSp[isp] = alphaForceSp[isp] + betaTraitxForce * (mu_grand_sp[isp]);
  }
  for (isp in 1:n_spec){
    betaPhotoSp[isp] = alphaPhotoSp[isp] + betaTraitxPhoto * (mu_grand_sp[isp]);
  }
  for (isp in 1:n_spec){
    betaChillSp[isp] = alphaChillSp[isp] + betaTraitxChill * (mu_grand_sp[isp]);
  }
}

model{
  yTraiti ~ normal(y_hat, sigma_traity);
  muSp ~ normal(0, sigma_sp);
  muStudy ~ normal(0, sigma_study);
  mu_grand ~ normal(20,10);
  sigma_sp ~ normal(4,5);
  sigma_study ~ normal(2,5);
  sigma_traity ~ normal(3,5);

  for (i in 1:Nph){
    yPhenoi[i] ~ normal(alphaPhenoSp[phenology_species[i]] +
    betaForceSp[phenology_species[i]] * forcei[i] +
    betaPhotoSp[phenology_species[i]] * photoi[i] +
    betaChillSp[phenology_species[i]] * chilli[i],
    sigmapheno_y);
  }

  alphaPhenoSp ~ normal(muPhenoSp, sigmaPhenoSp);
  alphaForceSp ~ normal(muForceSp, sigmaForceSp);
  alphaChillSp ~ normal(muChillSp, sigmaChillSp);
  alphaPhotoSp ~ normal(muPhotoSp, sigmaPhotoSp);

  muPhenoSp ~ normal(40,10);
  sigmaPhenoSp ~ normal(5,5);

  sigmapheno_y ~ normal(10,5);

  muForceSp ~ normal(-15,10);
  sigmaForceSp ~ normal(5,5);

  muChillSp ~ normal(-15,10);
```

```
  sigmaChillSp ~ normal(5,5);

  muPhotoSp ~ normal(-15,10);
  sigmaPhotoSp ~ normal(5,5);

  betaTraitxForce ~ normal(0,1);
  betaTraitxPhoto ~ normal(0,1);
  betaTraitxChill ~ normal(0,1);

}
```

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