

¹ Budburst timing within a functional trait framework

²

³ Running title: Budburst responses associated with traits

⁴ **Summary**

- ⁵ 1. Phenology—the timing of recurring life history events—can vary substantially in different environments and for different species. While climate change has shifted phenology by altering its proximate drivers—such as temperature—changes in the ultimate drivers that select for species-level variation remain poorly explained. Theory suggests that species-level variation in phenology can result from shifting environmental pressures that favour different strategies across the **spring growing season**: from the early season, where higher abiotic risks and greater availability of nutrients and light favour cheaper leaves and acquisitive growth strategies, to later when a more benign environment and lower levels of light and nutrients favour conservative growth strategies. From this framework we can infer suites of traits that may co-vary with species phenologies, but the high variability in traits—and especially phenology—across environments, have made testing the role of phenology within a trait framework challenging.
- ¹⁶ 2. Using a modelling framework that accommodates this variability, we used phenological data from a **database of controlled environment experiments** and tree trait data from two trait databases to test the relationships between traits and three cues for tree budburst: spring temperatures (forcing), winter temperatures (chilling), and daylength (photoperiod).
- ²⁰ 3. We found mixed support for our predictions for how traits relate to budburst timing and cues. Species with low chilling and photoperiod cues—indicative of earlier budburst—had some traits related to acquisitive strategies (they were shorter with higher nitrogen leaves). Our one reproductive trait (seed mass), however showed no relationships to budburst cues, and other traits (e.g., specific leaf area) showed relationships in the opposite direction to our predictions.
- ²⁵ 4. Synthesis: Our findings show how spring leafout phenology partially fits within a functional trait framework of acquisitive to conservative growth strategies, and can lead to better predictions of how communities may shift in their growth strategies alongside changing phenology with future warming.

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²⁹ Key Words: Leafout, spring phenology, traits, trees, climate change, forest communities

³⁰ Introduction

³¹ The timing of life history events—phenology—can shape both ecosystem services and community
³² dynamics. Spring phenology, for example, defines the start and overall length of the growing season—
³³ shaping forest carbon storage and species interactions (Beard *et al.*, 2019; Cleland *et al.*, 2007; Gu
³⁴ *et al.*, 2022). Shifts in phenology with climate change across systems (Menzel *et al.*, 2006; Vitasse
³⁵ *et al.*, 2021) have thus led to growing concerns over their possible impacts.

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³⁷ Predicting these changes requires understanding the drivers of phenology both at a proximate scale—
³⁸ the environmental triggers that determine phenology each year, such as temperature and daylength—
³⁹ and, at an ultimate scale, where long-term environmental pressures may select for different phenologies
⁴⁰ across species, (e.g., certain species are early or late relative to other species each year Ovaskainen
⁴¹ *et al.*, 2013; Wolkovich & Donahue, 2021). At the proximate level, environmental conditions through-
⁴² out the winter and spring cause species to start growth at different times (as each species generally has
⁴³ a unique response to the environment). Groups of species may have more similar responses, however,
⁴⁴ because they are from similar functional groups, successional stages (Laube *et al.*, 2014b) or archi-
⁴⁵ tectures (Flynn & Wolkovich, 2018) that cause them to have similar growth strategies. But current
⁴⁶ work provides limited insights into the drivers of these differences across species and how they can be
⁴⁷ used to predict future changes in community dynamics (Chuine *et al.*, 2016; Flynn & Wolkovich, 2018;
⁴⁸ Laube *et al.*, 2014b).

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⁵⁰ At the ultimate level, plant phenologies may vary due to changing pressures across the growing sea-
⁵¹ son that select for different growth strategies. Species that start growth early often risk high tissue
⁵² loss—due to frost damage (Augspurger, 2009; Sakai & Larcher, 1987) or high herbivore apparentency
⁵³ (Wainwright *et al.*, 2012)—but benefit from higher resource availability (Hufkens *et al.*, 2012; Rathcke
⁵⁴ & Lacey, 1985). In contrast, later active species face greater biotic pressures, especially from high
⁵⁵ competition for resources (Lopez *et al.*, 2008; Wolkovich & Ettinger, 2014). Such differences could
⁵⁶ shape physical and phenological traits related to species growth strategies and fitness (Viole *et al.*,
⁵⁷ 2007). Species leaf and wood traits can reflect trade-offs between the construction costs and longevity
⁵⁸ of tissue (Reich *et al.*, 1997; Wright *et al.*, 2004), with cheaper-to-construct tissue being associated with
⁵⁹ faster growth rates (Westoby & Wright, 2006; Wright *et al.*, 2004). Previous studies have highlighted
⁶⁰ the associations between trade-offs in traits and phenology (Sporbert *et al.*, 2022; Wang *et al.*, 2021;
⁶¹ Wolkovich & Ettinger, 2014) (Fig 1), and indicate the potential for species traits to similarly range

62 from the acquisitive (fast) to more conservative (slow) growth strategies associated with existing trait
63 frameworks (Chave *et al.*, 2009; Wright *et al.*, 2004).

64

65 Globally, gradients from acquisitive to conservative strategies appear common, and form the foundation
66 of the leaf and wood economic spectra (Chave *et al.*, 2009; Díaz *et al.*, 2016; Westoby, 1998; Westoby &
67 Wright, 2006; Wright *et al.*, 2004), but they make limited predictions of trait variability (Viole *et al.*,
68 2012). As a result, highly variable traits like phenology are often excluded from trait studies, leaving
69 the relationships between broader trait syndromes and phenology largely unknown. Understanding
70 these relationships, however, is critical to forecasting community dynamics and responses to climate
71 change. Most studies have examined the relationship between traits and phenology for a single or
72 limited number of sites, (as reviewed by Wolkovich & Cleland (2014); Wolkovich & Donahue (2021)
73 but see Rauschkolb *et al.* (2024); Sporbert *et al.* (2022)). At these spatial scales the problem of proximate
74 drivers causing phenological variation can be more easily ignored. Adding phenology to broader
75 trait frameworks becomes more complex when high levels of variation occurs across large spatial and
76 temporal ranges.

77

78 Recent climate change has highlighted how variable plant phenology is when observed over time and
79 space across different species (Rudolf, 2019; Vitasse, 2013; Yu *et al.*, 2010), with many studies documenting
80 how quickly phenology can shift with warming (Fitter & Fitter, 2002; Menzel *et al.*, 2006).
81 But experiments conducted under controlled environments have shown that it is possible to consistently
82 define early to late phenology from the known underlying cues (Chuine & Cour, 1999; Flynn &
83 Wolkovich, 2018; Harrington & Gould, 2015). This work has found early species to generally require
84 only small amounts of forcing (accumulated warm—usually spring—temperatures), chilling (accumulated
85 cool—usually fall and winter—temperatures), and shorter photoperiod to leaf out, and thus have
86 relatively small responses to each of these cues in experiments. In contrast, later species have larger
87 responses to chilling and/or longer photoperiods, and larger forcing responses (Flynn & Wolkovich,
88 2018; Laube *et al.*, 2014b). The consistency of these relationships allows us to better understand the
89 drivers of phenological variation across plant communities and diverse species assemblages.

90

91 Studies of spring phenology in temperate forests may provide the best opportunity to integrate phenology
92 into functional trait research. In addition to how well we understand the environmental cues
93 that trigger early versus late leafout, spring in many forests includes strong gradients in frost risk
94 or nutrient availability (Fig 1). We might predict some variability in how traits relate to different
95 growth strategies (driven by different selective pressures), which then lead to differences across groups
96 of species (Horbach *et al.*, 2023; Sporbert *et al.*, 2022; Wang *et al.*, 2021)—such as the differences in

traits that facilitate frost tolerance versus avoidance (Bucher & Rosbakh, 2021; Lenz *et al.*, 2013; Sakai & Larcher, 1987) or to herbivory (Coley *et al.*, 1985). Broadly we predict acquisitive species to be shorter, with leaf traits favorable to the low light conditions of the understory later in the growing season—that is, they should produce leaves with high specific leaf area (SLA) that are nitrogen rich (Díaz *et al.*, 2016; Reich *et al.*, 1997; Wright *et al.*, 2004) (Fig 1). We would predict such species to exhibit early phenology, budbursting under low chilling and cool spring conditions (low forcing) when photoperiods are short. Canopy species that budburst later via larger cue responses and when competition for soil resources is greater, would then have traits associated with conservative growth—taller with denser wood (Chave *et al.*, 2009; Laughlin *et al.*, 2010) and leaf traits suited for the higher light conditions of the canopy (low SLA and low LNC, Fig 1). Seed size may similarly be predicted from this acquisitive to conservative continuum, as acquisitive species produce smaller seeds and the taller and more conservative species produce larger—better provisioned—seeds (Díaz *et al.*, 2016) Fig 1).

109

To test these predictions between budburst responses to environmental cues and common functional traits (height, SLA, seed mass, and LNC), we merged available data from global databases of plant traits—BIEN (Maitner *et al.*, 2018) and TRY (Kattge *et al.*, 2020)—with global budburst data from the OSPREE database of controlled environment studies (Ettinger *et al.*, 2020). We developed a hierarchical Bayesian joint model that predicts phenological responses to forcing, chilling and photoperiod treatments based on species-level trait values, while allowing additional variation due to species. This approach takes a step towards predicting variation via species traits instead of species identity (when traits explain a significant portion of the variation, species identity will explain only a small amount), which could help forecast species phenological responses based on trait values alone.

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120 Methods

We merged three major databases for our analysis. We gathered phenological data from the OSPREE database (Ettinger *et al.*, 2020), which contains data from experiments of dormant plant tissue from woody plants growing either in the field or in controlled environments. From OSPREE, we used the available budburst data for temperate tree species from studies that each manipulated forcing, chilling and photoperiod. We originally constructed the OSPREE database by performing a systematic review of the literature, and searched both ISI Web of Science and Google Scholar using the following two search terms:

128

- 129 1. TOPIC = (budburst OR leafout) AND (photoperiod or daylength) AND temperature*

130 2. TOPIC = (budburst OR leafout) AND dorman*

131

132 We then scraped the data from all articles reporting experiments that manipulated both photoperiod
133 and/or temperature cues of woody species budburst, leafout, or flowering phenology, and for which
134 there was a quantifiable response to each cue. We updated this database in July 2019 reviewing all
135 new articles found using the previous search terms. Additional details on the methods used to as-
136 semble, clean, and update this database are discussed by Ettinger *et al.* (2020) and Morales-Castilla
137 *et al.* (2024). For the purpose of this study, we obtained a subset of the budburst data from OSPREE
138 database and initially aimed to use data for the subset of 234 species used in Morales-Castilla *et al.*
139 (2024).

140

141 We gathered trait data from the TRY and BIEN (v. 4.0) databases (Kattge *et al.*, 2020; Maitner
142 *et al.*, 2018), both of which are large trait databases that include plant trait observations across many
143 individuals, species, and studies (Table S1) and are available through slightly different mechanisms.
144 BIEN is accessible via the BIEN R package (here we used v. 1.2.5, Maitner *et al.*, 2018), and TRY
145 is requested. We obtained data from both databases on 5 December 2018, and requested an updated
146 version of the TRY data on 10 April 2019. We initially searched for trait data on the subset of 234
147 OSPREE species used in Morales-Castilla *et al.* (2024). From BIEN, this resulted in 94 of the 234
148 species available in the database, for which there were 13 unique traits. From the TRY database
149 we received data for 10 unique traits for 96 of the 234 requested species (Kattge *et al.*, 2020). For our
150 purposes, we were interested in the trait-phenology relationships of adult trees, and therefore subset
151 the available data to only include traits measured from adult individuals. We assumed that by subset-
152 ting tree heights to be 1.38 m or greater the individuals in our analysis would be old enough to meet
153 the standard measurement height used in North America when measuring DBH (Powell, 2016). We fur-
154 ther removed all data from manipulative experiments or from plants growing in non-natural habitats.
155 We also grouped trait values where appropriate, for example pooling trait values for specific leaf area
156 (SLA) with those denoted as ‘SLA with petioles’, and ‘SLA without petioles’ in our analysis (see Table
157 S1). We also removed data that was duplicated in both the TRY and BIEN datasets ($n = 434,905$).
158 For a full depiction of our data cleaning process and decisions see Fig. S3.

159

160 For our analysis, we only included species for which we had a complete trait profile (i.e., all traits
161 measured for all species). We initially considered six commonly measured traits—SLA, leaf dry matter
162 content (LDMC), height, seed mass, stem specific density (SSD), and LNC—for which 26 species
163 had at least one trait measurement for each of the traits. We then used a principle component
164 analysis (PCA) to identify which (if any) of our six traits were strongly correlated. The first principal

component explained 32% of variation while the second explained 24.2% of the variation (Fig. S2), with high correlations between SLA and LDMC, and between height and SSD (Fig. S2). By excluding the trait from each of these highly correlated trait pairs with the least amount of data (specifically LDMC and SSD) we were able to increase the number of species in our dataset from the 26 species with complete data for six traits, to 37 species with complete data for four traits. The data for these 37 species were from 24 unique studies (samples sizes: height $n = 47781$, seed mass $n = 281$, LNC $n = 3853$, SLA $n = 7656$). We subsampled the height measurements of the 13 most frequently measured tree to reduce their influence on our height model. Since each of these 13 species were measured 19 times more frequently than most other species, we randomly sampled 3000 height measurements for each individual species, while including all height data for the remaining, less frequently measured, 24 species.

Joint model of trait and phenology

To understand connections between phenology and species traits, we developed a Bayesian joint model for each trait: height, SLA, LNC, and seed mass to relate to species budburst responses. We consider this a ‘joint’ model because it involves two sub-models—one that models trait observations and a second that uses shared latent processes to model how a given trait relates to the cues that shape the phenological observations. In particular, we assume that trait values are the result of multiple sources of variation, including species (α_{species}) and study-level variation (α_{study}), that combine into one observed trait value (trait sub-model). This trait value (α_{trait}) has a separate interaction with the three cues (β_{chilling} , β_{forcing} , $\beta_{\text{photoperiod}}$) that determines phenology—specifically the day of year of budburst (phenology sub-model). Below we describe the two sub-models, noting which parameters are shared across sub-models and which are independent.

Trait sub-model

Our trait sub-model describes the processes that shape a given trait observations for 1 to n species across each of the 1 to m studies in our trait dataset. We use hierarchical modeling to partition trait values by measurement error (σ_m^2), species identity ($\alpha_{\text{species}_i}$), and study (α_{study_j}). In particular, we assume that a trait observation for species i from study j , $Y_{\text{trait}_{i,j}}$, has the following normal distribution:

$$Y_{\text{trait}_{i,j}} \sim \mathcal{N}(\mu_{i,j}, \sigma_m^2) \quad (1)$$

193 with

$$\mu_{i,j} = \alpha_{\text{grand trait}} + \alpha_{\text{species}_i} + \alpha_{\text{study}_j} \quad (2)$$

194 where $\alpha_{\text{species}_i}$ and α_{study_j} are elements of the normal random vectors:

$$\begin{aligned} \boldsymbol{\alpha}_{\text{trait}} &= \alpha_{\text{grand trait}} + \alpha_{\text{species}_i} \\ \boldsymbol{\alpha}_{\text{species}} &= \{\alpha_{\text{species}_1}, \dots, \alpha_{\text{species}_n}\}^T \text{ such that } \boldsymbol{\alpha}_{\text{species}} \sim \mathcal{N}(0, \sigma_{\text{species}}^2) \end{aligned} \quad (3)$$

$$\begin{aligned} \boldsymbol{\alpha}_{\text{study}} &= \{\alpha_{\text{study}_1}, \dots, \alpha_{\text{study}_m}\}^T \text{ such that } \boldsymbol{\alpha}_{\text{study}} \sim \mathcal{N}(0, \sigma_{\text{study}}^2) \\ \end{aligned} \quad (4)$$

195 The latent parameter or overall mean trait value ($\alpha_{\text{grand trait}}$) represents a trait value that is indepen-
196 dent of the species ($\alpha_{\text{species},i}$) and study-level ($\alpha_{\text{study},j}$) offsets from that trait value. The σ_m^2 parameter
197 is the measurement error, and $\sigma_{\text{species}}^2$ and σ_{study}^2 represent species and study-level variances in trait
198 values. Of these parameters, the $\boldsymbol{\alpha}_{\text{trait}}$ are shared by the phenology sub-model.

199 Phenology sub-model

200 Our phenology sub-model describes the processes that determine the relationships between traits and
201 environmental cues and their effects on phenological observations for 1 to n species, specifically the
202 timing (day of year) of budburst from the updated OSPREE dataset. [The observations of budburst](#)
203 for species k under g treatment levels of each cue (c_g, f_g, p_g , for chilling, forcing and photoperiod
204 treatments, respectively, which we z -scored to allow direct comparison between cues) is represented by
205 parameter $Y_{\text{pheno}_{k,g}}$, and assumed to follow a normal distribution:

$$Y_{\text{pheno}_{k,g}} \sim \mathcal{N}(\mu_{k,g}, \sigma_d^2) \quad (5)$$

206 with

$$\mu_{k,g} = \alpha_{\text{pheno}_k} + \beta_{\text{chilling}_k} \cdot c_g + \beta_{\text{forcing}_k} \cdot f_g + \beta_{\text{photoperiod}_k} \cdot p_g \quad (6)$$

207 and

$$\begin{aligned} \beta_{\text{chilling}_k} &= \alpha_{\text{chilling}_k} + \beta_{\text{trait.chilling}} \cdot \alpha_{\text{trait}_k} \\ \beta_{\text{forcing}_k} &= \alpha_{\text{forcing}_k} + \beta_{\text{trait.forcing}} \cdot \alpha_{\text{trait}_k} \\ \beta_{\text{photoperiod}_k} &= \alpha_{\text{photoperiod}_k} + \beta_{\text{trait.photoperiod}} \cdot \alpha_{\text{trait}_k} \end{aligned} \quad (7)$$

208 where α_{pheno_k} , $\alpha_{\text{chilling}_k}$, $\alpha_{\text{forcing}_k}$, and $\alpha_{\text{photoperiod}_k}$ are elements of the normal random vectors:

$$\boldsymbol{\alpha}_{\text{pheno}} = \{\alpha_{\text{pheno}_1}, \dots, \alpha_{\text{pheno}_n}\}^T \text{ such that } \boldsymbol{\alpha}_{\text{pheno}} \sim \mathcal{N}(\mu_{\text{pheno}}, \sigma_{\text{pheno}}^2) \quad (8)$$

$$\boldsymbol{\alpha}_{\text{chilling}} = \{\alpha_{\text{chilling}_1}, \dots, \alpha_{\text{chilling}_n}\}^T \text{ such that } \boldsymbol{\alpha}_{\text{chilling}} \sim \mathcal{N}(\mu_{\text{chilling}}, \sigma_{\text{chilling}}^2)$$

$$\boldsymbol{\alpha}_{\text{forcing}} = \{\alpha_{\text{forcing}_1}, \dots, \alpha_{\text{forcing}_n}\}^T \text{ such that } \boldsymbol{\alpha}_{\text{forcing}} \sim \mathcal{N}(\mu_{\text{forcing}}, \sigma_{\text{forcing}}^2)$$

$$\boldsymbol{\alpha}_{\text{photoperiod}} = \{\alpha_{\text{photoperiod}_1}, \dots, \alpha_{\text{photoperiod}_n}\}^T \text{ such that } \boldsymbol{\alpha}_{\text{photoperiod}} \sim \mathcal{N}(\mu_{\text{photoperiod}}, \sigma_{\text{photoperiod}}^2)$$

209 The model partitions day of budburst for species (k) as a combination of the overall mean day of
 210 budburst without the influence of chilling, forcing, or photoperiod treatments ($\alpha_{\text{pheno},k}$, normally dis-
 211 tributed with a mean of μ_{pheno} and variance σ_{pheno}^2) combined with the effects of treatments both
 212 dependent and independent of trait values. The parameters $\alpha_{\text{chilling}_k}$, $\alpha_{\text{forcing}_k}$, and $\alpha_{\text{photoperiod}_k}$
 213 represent the trait-independent responses of species k to chilling, forcing, and photoperiod treat-
 214 ments respectively, each with an associated mean (μ_{chilling} , μ_{forcing} , $\mu_{\text{photoperiod}}$) and variance ($\sigma_{\text{chilling}}^2$,
 215 $\sigma_{\text{forcing}}^2$, $\sigma_{\text{photoperiod}}^2$) across species. The shared parameter between the trait and phenology sub-model,
 216 α_{trait_k} , represents the effect of the species trait value on its responses to chilling ($\beta_{\text{trait.chilling}}$), forcing
 217 ($\beta_{\text{trait.forcing}}$), and photoperiod ($\beta_{\text{trait.photoperiod}}$). Finally, σ_d^2 is the variance arising from measurement
 218 error for the observed day of budburst.

219

220 The model was coded in the Stan (Stan Development Team, 2024), which is a probabilistic program-
 221 ming language enabling for building Bayesian models. We used the rstan package (Stan Development
 222 Team, 2018) to interface with and run the Stan code in R version 3.3.6 (R Development Core Team,
 223 2017). For our model, we chose weakly informative priors, and validated them using a series of prior
 224 predictive checks. The model was fit with 1,000 iterations per chain across 4 chains (4,000 total sam-
 225 pling iterations), and all models met basic diagnostic checks, including no divergences, high effective
 226 sample size (n_{eff}), and \hat{R} close to 1, fitting the data well (Fig S4). Here we present our model
 227 estimates as the means and 90% posterior uncertainty intervals (UI), with the 50% UI included in the
 228 supplementary tables and figures to allow for comparison and to assess the strength of relationships.
 229 We consider parameters with UI that overlap to be similar to each other and those that include zero
 230 in the 90% UI to have small effects.

231 Results

232 Across traits, height, SLA, and LNC were related to one or more environmental cue ($\beta_{\text{chilling}_k}$, β_{forcing_k} ,
 233 or $\beta_{\text{photoperiod}_k}$, Fig 2 a-f & j-l), with only LNC showing a relationship with all three cues (Fig. 2 j-l).
 234 As we predicted, height was negatively related to chilling ($\beta_{\text{chilling}_k}$) and photoperiod ($\beta_{\text{photoperiod}_k}$),
 235 with taller species having larger responses to high chilling and longer photoperiod conditions (-0.5 m

236 per standardized chilling; 90% uncertainty interval (UI): -1.0, -0.1 and -0.2 m per standardized pho-
237 toperiod; 90% UI: -0.5, 0.0, Fig 2 a-c, Table S2). We found height to have a larger relationship with
238 the timing of budburst (as estimated by $\mu_{k,g}$), with later budburst estimated for taller trees under
239 increasing chilling and photoperiods (Fig. S5). In contrast, seed mass had a negligible relationship
240 with budburst and all three cues (Fig. 2 g-i & Table S4).

241

242 Of our leaf traits, we found that SLA related to photoperiod ($\beta_{\text{photoperiod}_k}$, -0.2 mm²/mg per stan-
243 dardized photoperiod; 90% UI: -0.5, 0.0, Fig. 2 f, Table S3), but did not strongly predict responses
244 to chilling ($\beta_{\text{chilling}_k}$) or forcing treatments (β_{forcing_k} , Fig. 2 d & e). Contrary to our predictions,
245 species with high SLA—indicative of larger, thin leaves and a lower investment in leaf mass and asso-
246 ciated with more acquisitive growth strategies—exhibited larger responses to photoperiod commonly
247 observed in late budbursting species (Fig. 2 f). The relationship between LNC and budburst cues,
248 were in line with our predictions, with high LNC species being less responsive to chilling (0.7 mg/g
249 per standardized chilling; 90% UI: 0.2, 1.2, Table S5), forcing (0.5 mg/g per standardized forcing; 90%
250 UI: 0.1, 0.8, and photoperiod (0.3 mg/g per standardized photoperiod; 90% UI: 0.0, 0.6), Fig 2 j-l &
251 Fig S5 d-f). This suggests that species that produce leaves with high nitrogen content, which relates
252 generally to high photosynthetic rates and acquisitive growth, are likely to budburst early based on
253 the relationships between this trait and environmental cues.

254

255 We found that the species-level variation across traits (σ_{trait}^2) were comparable to, or greater than
256 variation across studies (using our model that partitions the measurement error in the trait values
257 from variation from species and study-level effects, σ_{study}^2 , Fig 3). For height, variation across studies
258 (σ_{study}^2) was greater (7.5 m; 90% UI: 5.8, 9.7), than the variation caused by species (σ_{trait}^2 , 5.9 m;
259 90% UI: 4.8, 7.3, Fig 3a). For seed mass and LNC, study-level variation was less than that of the
260 species-level variation, with variation in seed mass observations of 1 mg (90% UI: 0.8, 1.1) and 1.6 mg
261 (90% UI: 0.8, 1.1) for study-level and species-level variation respectively and for LNC 3.6 mg g⁻¹ (90%
262 UI: 2.2, 5.3) for study-level variation and 5.1 mg g⁻¹ for the species-level variation (90% UI: 2.2, 5.3,
263 Fig 3c and d). Study-level variation was smallest for SLA, with the estimate of 3.3 mm² mg⁻¹ (90% UI:
264 2, 5.1) for study-level variation being approximately half that of the estimated species-level variation
265 of 7.8 mm² mg⁻¹ (90% UI: 6.4, 9.4, Fig 3b). Across all traits, the effect of study-level variation (σ_{study}^2)
266 made a considerable contribution to the overall variation observed in our trait values and suggests that
267 models using large trait databases that fail to separate out study from species-level variation (σ_{trait}^2)
268 may poorly estimate species traits.

269

270 Discussion

271 We found several species traits influenced the timing of budburst in response to one or more of the
272 three primary cues of spring phenology: chilling, forcing and photoperiod. While the relationships
273 between SLA and seed mass with phenological cues differed from our predictions, the trait effects of
274 height and LNC were associated with earlier or later phenology, following well-established gradients in
275 growth strategies predicted by functional trait frameworks (Chave *et al.*, 2009; Díaz *et al.*, 2016; West-
276 oby, 1998; Westoby & Wright, 2006; Wright *et al.*, 2004). Early species—which generally budburst
277 given small levels of forcing, chilling, and shorter photoperiod—exhibited relationships with several
278 traits associated with fast and acquisitive growth strategies, while later budbursting species—that
279 require larger levels of forcing, chilling, and longer photoperiods to initiate growth—did exhibit traits
280 indicative of conservative, slower growth strategies. We found the largest budburst responses occurred
281 for traits related to resource acquisition and structure, with SLA, LNC, and height all showing large
282 responses to at least one of our three cues. In contrast, our one reproductive trait—seed mass—showed
283 the smallest response. Our results provide a major step forward in integrating phenology into broader
284 trait syndromes that shape species growth strategies, and support previous findings from more local
285 scales that found large relationships between height and species phenology (Osada & Hiura, 2019;
286 Seiwa, 1999). Our more global analysis supports previous studies of plant phenological events, which
287 found no relationship between phenology and seed mass in woody plants (Bolmgren & D. Cowan, 2008;
288 Ettinger *et al.*, 2018).

289

290 In addition to identifying trait-phenology relationships shaping the timing of spring budburst, our
291 results also provide important insights into the use of data from large databases to estimate ecological
292 processes. By partitioning the different sources of variation that contribute to observed trait values,
293 we found considerable effects of study-level variation. For one of our traits, the differences due to
294 study exceeded those due to species. Such study-level variation is likely the result of myriad factors,
295 including observer error and differences in methodologies, that are present in any dataset that pools
296 data from diverse sources. Our findings thus highlight that analyses using data from aggregate trait
297 databases may need to account for this variation to make the most accurate predictions.

298 Effects of phenology-trait relationships on community assembly

299 Our findings suggest the changing pressures across the early growing season may affect the temporal
300 assembly of communities. Species with small cue responses, an indication of earlier budburst, had
301 some traits indicative of acquisitive growth strategies (shorter heights and high LNC) that allow faster
302 return on resource investments (Chave *et al.*, 2009; Grime, 1977; Westoby, 1998). These traits should

allow early species to benefit from greater light availability in the open forest canopy in the early spring and withstand the low light conditions later in the season. In contrast, later-budbursting species had traits associated with slower, more conservative, growth (Chave *et al.*, 2009; Grime, 1977; Westoby, 1998), which may help them compete for the more limited soil and light resources later in the growing season. Similar trait-phenology relationships have also been linked to other ecological processes and species characteristics that define community structure and diversity, such as species successional position (Laube *et al.*, 2014b), providing support to the differences we observed for height and LNC in our example comparing *Alnus incana* (a pioneer species) and *Quercus rubra* (a later successional species; Fig 2).

312

The trait by cue relationships that deviated from our expectations also offer novel insights into the tradeoffs between traits and environmental cues. All of our traits are associated with multiple aspects of species growth, and may be adaptive for reasons other than those we predicted. Contrary to our predictions, we found large responses to forcing for short trees, which could prevent frost damage or xylem cavitation under a late spring frost (Clements *et al.*, 1972; Marquis *et al.*, 2020) and influence annual cambial meristem growth (Lenz *et al.*, 2016). Similarly, the lack of a relationship between SLA and chilling and forcing could be driven by other physiological constraints or tradeoffs with selection by other cues—as variation in SLA also reflects differences in species relative growth rates or leaf longevity—and not just photosynthetic potential (Reich, 2014; Westoby, 1998). These findings highlight the complexity of determining the drivers of species trait profiles, and further our understanding of how traits affect community dynamics under variable environments.

324

325 Phenology-trait relationships under future climates

Incorporating phenology within broader trait syndromes could aid forecasting of species and community responses to climate change. While decades of research have documented phenological shifts with anthropogenic climate change (Fitter & Fitter, 2002; Menzel *et al.*, 2006), increasing research suggests a potential connection between phenological responses to warming and performance with warming, where species that shift their phenology more also perform better (Cleland *et al.*, 2012; Macgregor *et al.*, 2019).

332

Our results suggest this phenology-performance relationship could be driven in part by a suite of traits that covary with phenological cues to determine how responsive species are to warming. Species with smaller responses to all cues, especially chilling and photoperiod, would tend to advance more with

336 warming (Guy, 2014). Our results suggest that these same species are likely to have acquisitive traits,
337 such as short heights and high LNC that allow them to grow quickly and benefit from the greater
338 availability of nutrients in the early spring. Understanding these trait-phenology relationships may
339 provide insight into how climate change may alter species coexistence (Rudolf, 2019; Wolkovich &
340 Donahue, 2021). A greater understanding of trait-phenology relationships may also improve our abil-
341 ity to manage species invasions, as invasive species to have earlier phenologies (Alexander & Levine,
342 2019; Polgar *et al.*, 2014; Zettlemoyer *et al.*, 2019), but possibly a unique suite of traits that facilitate
343 fast growth (Fridley *et al.*, 2022).

344

345 Our analytical approach and results may be especially useful to help forecast changes in forest dy-
346 namics. Identifying the varying trait syndromes of forest communities over a spring season can aid
347 predictions of how climate change will alter species growth and productivity. For example, our results
348 suggest that, by favoring more phenologically responsive species (i.e., with small chilling and pho-
349 toperiod responses), warming may also favor species with acquisitive growth strategies. In contrast,
350 conservative species, which appear less phenologically responsive to changes in temperature (due to
351 larger chilling and photoperiod responses) could face greater abiotic and biotic stress (Guy, 2014).

352

353 Our results could further help identify which species are most likely to be negatively impacted under
354 future climates, and develop better strategies for climate change mitigation and conservation. Species
355 that fail to advance phenologically with warming might experience more competition (Alexander &
356 Levine, 2019; Carter *et al.*, 2018), as species that begin growth increasingly earlier with warming have
357 more time to deplete resources. In addition to altering the timing and interactions between species
358 within a season, species trait syndromes have the potential to further redefine the environmental
359 conditions under which growth occurs, and as a result, shape community assembly and productivity
360 within ecological communities (Rudolf, 2019; Wolkovich & Donahue, 2021). By identifying the species
361 most vulnerable to climate change impacts, we can develop more effective management practices that
362 prevent the loss of critical ecosystem services and preserve community diversity under future conditions.

363

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³⁶⁷ **Author Contributions Statement**

³⁶⁸ DL, FAMJ, GL, MG, DS, and EMW planned and designed the study. All authors conducted the
³⁶⁹ literature review and cleaned the database. DL, FAMJ, GL, and EMW performed the data analysis
³⁷⁰ and contributed code. DL, FAMJ, and GL created the figures. DL and EMW wrote the initial draft
³⁷¹ and all authors reviewed and revised the manuscript.

³⁷² **Competing Interests Statement**

³⁷³ The authors declare no competing interests.

³⁷⁴ **Data availability statement**

³⁷⁵ The phenological data used for this manuscript is a subset of the existing OSPREE dataset (doi:10.5063/F1CZ35KB)
³⁷⁶ and the trait data a subset of the the TRY database (doi:10.1111/gcb.14904) and the BIEN database
³⁷⁷ (doi: 10.1111/2041-210X.1286).

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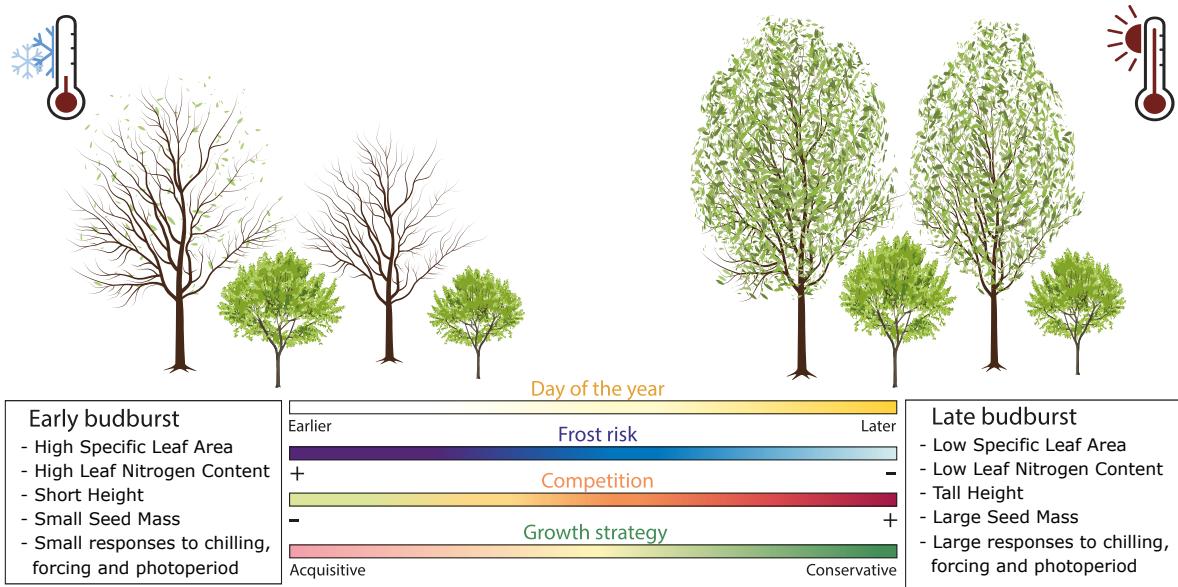


Figure 1: Leaf and wood traits follow a gradient that varies from acquisitive versus conservative growth strategies, which may also include phenology. We predicted early-budbursting species would have traits associated with acquisitive growth, as they are more likely to experience greater abiotic and biotic risk but reduced competition. In contrast, we expected later-budbursting species would have traits associated with conservative growth, as they experience greater competition but a more climatically benign environment. However previous studies looking at different phenological events, such as flowering, or suites of non-woody species, have found varying relationships between traits and phenology, highlighting the complexity that may shape species temporal niche.

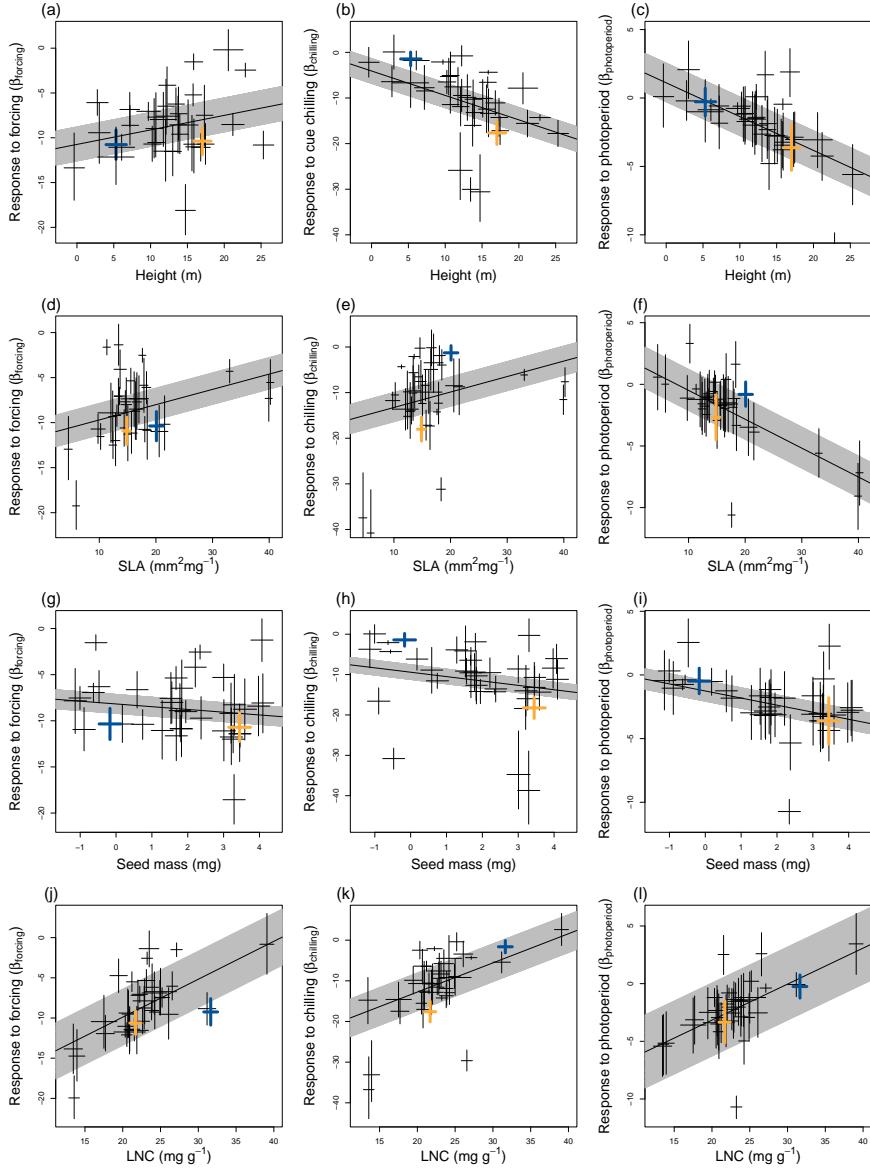


Figure 2: Estimated species-level responses to standardized forcing (left column: a, d, g & j), chilling (middle column: b, e, h & k), and photoperiod treatments (right column: c, f, i & l) predicted by estimated trait values for height (first row: a-c), SLA (second row: d-f), log10 Seed mass (third row: g-i), and LNC (fourth row: j-l). We estimated parameters using a joint trait-phenology model, with the black line depicting the mean linear relationship between estimated trait effects and the slope of the cue response (either β_{chilling} , β_{forcing} , $\beta_{\text{photoperiod}}$ for each respective trait) and the gray band the 50% uncertainty interval. Each set of crossed lines represents one species (with each line spanning the 50% uncertainty interval), depicting how well our model fits the data across all species. To illustrate the relationship between traits and the three phenological cues we highlight two example species that differ greatly in their architecture and life history—*Alnus incana*, shown in blue—a shorter, shrubby tree species with a growth strategy characteristic of an acquisitive species—and *Quercus rubra*, shown in yellow—a taller and characteristically conservative species (see also Fig S5).

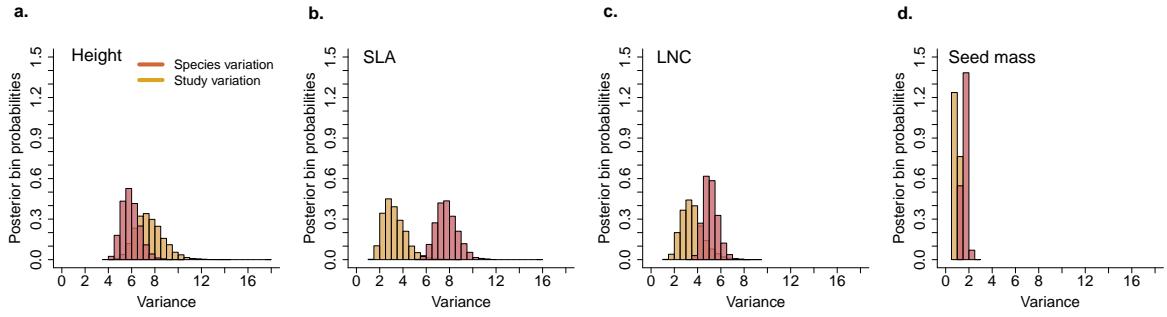


Figure 3: Traits differed in the relative magnitude of their species-level and study-level variation ($\sigma_{\text{species}}^2$ and σ_{study}^2 respectively), with only (a) the height model estimating greater study-level variation than species-level, while our (b) specific leaf area, (c) leaf nitrogen content, and (d) seed mass models all estimated higher species-level variation. Shown here are the posterior densities for the species-level variation, shown in red, and study-level variation, shown in yellow. For comparison, we show all x-axes spanning the minimum to maximum variances across all four traits. The histograms depict the full distribution of the study and species-level variance, where each bin is normalized by the total count of the posterior estimate.