

1 Capturing juvenile tree dynamics from count data using Approximate Bayesian Computation

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3 E. R. Lines<sup>1\*</sup>, M. A. Zavala<sup>2</sup>, P Ruiz-Benito<sup>3</sup> and D. A. Coomes<sup>4</sup>

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5 <sup>1</sup>School of Geography, Queen Mary University of London, Mile End Road, London, UK

6 <sup>2</sup>Forest Ecology and Restoration Group, Universidad de Alcala, Madrid, Spain.

7 , Madrid, Spain.

8

9 <sup>4</sup>Department of Plant Sciences, University of Cambridge, Downing Street, Cambridge, UK

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11 \*Corresponding author: e.lines@qmul.ac.uk

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25

26 **Abstract**

27 The juvenile life stage is a crucial determinant of forest dynamics and a first indicator of changes to  
28 species' ranges under climate change. However, paucity of detailed re-measurement data of  
29 seedlings, saplings and small trees means that their demography is not well understood at large  
30 scales, and rarely represented in forest models in detail. In this study we quantify the effects of  
31 climate and density dependence on recruitment and juvenile growth and mortality rates of thirteen  
32 species measured in the Spanish Forest Inventory. Single-census sapling count data is used to  
33 constrain demographic parameters of a simple forest juvenile dynamics model based on the Perfect  
34 Plasticity Approximation model (PPA) within a likelihood-free parameterisation method, Approximate  
35 Bayesian Computation. Our results highlight marked differences between species, and the important  
36 role of climate and stand structure, in controlling juvenile dynamics. Recruitment had a hump-shaped  
37 relationship with conspecific density, and for most species conspecific competition had a stronger  
38 negative effect than heterospecific competition. Mediterranean species showed on average higher  
39 mortality and lower growth rates than temperate species, and in low density stands recruitment and  
40 mortality rates were positively correlated. Under climate change our model predicted declines in  
41 recruitment rates for almost all species. Reliable predictive models of forest dynamics should include  
42 realistic representation of critical early life-stage processes and our approach demonstrates that  
43 existing coarse count data can be used to parameterise such models. Approximate Bayesian  
44 Computation may have wide application in many fields of ecology to unlock information about past  
45 processes from single survey observations.

46

47 Key-words: Approximate Bayesian Computation; forest inventory; growth; juvenile dynamics;  
48 mortality; recruitment; predictive modelling.

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50

## 51 **Introduction**

52

53 Understanding the processes driving juvenile tree dynamics is crucial to making defensible, long-  
54 term predictions of forest dynamics and distribution shifts (Kobe et al. 1995, Ibáñez et al. 2007)  
55 because filtering at early life stages is a critical determinant of long-term composition (Kobe 1996,  
56 Metz et al. 2010, Green et al. 2014). Tree species' distributions have been observed to be shifting  
57 under climate change (e.g. Peñuelas et al. 2007), and climate-induced shifts may halve the value of  
58 European forests by 2100 (Hanewinkel et al. 2013). The increased availability of large scale, long-  
59 term forest inventory datasets has led to dramatic improvements in the understanding of adult tree  
60 growth and mortality, but such datasets rarely contain multi-temporal information on individual  
61 juveniles. Instead, studies of juveniles have typically involved tracking stems in small plots and/or at  
62 only a few sites (e.g. Clark et al. 1998, Ibáñez et al. 2007, Metz et al. 2010, Matías et al. 2011),  
63 providing few insights into critical landscape-level dynamics.

64 Forest dynamics models applied at large scales typically use simplistic approaches to  
65 incorporate information about early life stages (e.g. Vanderwel et al. 2013). The most basic approach  
66 is to assume that recruitment into the smallest size class is unlimited (Clark et al. 1998); treat  
67 recruitment as a function of asymmetric competition for light and shade tolerance (Pacala et al.  
68 1996), a function of stand basal area characteristics (Kolbe et al. 1999), or parameterise recruitment  
69 according to ingrowth into a minimum inventory data size class (Vanderwel et al. 2013). In contrast,  
70 smaller scale spatially-explicit individual-based models typically use seed dispersal kernels, with  
71 seedling establishment in locations with probability dependent on the distance to conspecific adults,  
72 species, adult size and shading (e.g. SORTIE, Pacala et al. 1996; TROLL, Jérôme 1999).  
73 Parameterisation of this approach requires large amounts of fine-scale multi-temporal data that is  
74 often not available at landscape-scales.

75 Competitive and facilitative processes strongly influence juvenile dynamics, and the  
76 presence and density of conspecific and heterospecific adults are well-recognised determinants of  
77 seedling establishment and sapling success in reaching the canopy (e.g. Gomez-Aparicio et al.  
78 2008, Comita et al. 2014). These biotic interactions may influence recruitment success and range  
79 shifts under climate change (McCarthy-Neumann and Ibáñez 2012, Katz and Ibáñez 2016, Ettinger

80 and HilleRisLambers 2017) but remain under-studied. In addition, seedling recruitment is affected  
81 by canopy gaps and competition from understory shrubs (Beckage et al. 2000), soil moisture,  
82 drought and precipitation (Urbieto et al. 2008, Gomez-Aparicio et al. 2008, Mendoza et al. 2009),  
83 and facilitation through protection from water and radiation stress by 'nurse' plants (Gómez-Aparicio  
84 et al. 2004, Gomez-Aparicio et al. 2008, Plieninger et al. 2010).

85         This study presents a new method to unlock information on recruitment, growth and survival  
86 rates of juveniles from large-scale plot networks. Such datasets, though increasingly available to  
87 researchers, are not collected with the aim of understanding juvenile dynamics, such as the annual  
88 recruitment rates required by many forest dynamics models. In order to use traditional likelihood  
89 methods to fit an annual recruitment rate model we would require annual recruitment observations  
90 that is typically not available at large scales – so new statistical techniques are needed to extract  
91 this information. We use data from two Spanish Forest Inventories (IFN, MMA 1996, 2007) which  
92 systematically and periodically re-samples millions of trees with diameter breast height (DBH) > 7.5  
93 cm across the country. Only counts of smaller stems, without tagging or re-measurement, are  
94 recorded, so whilst the dynamics of adult trees can be tracked through re-measurement, those of  
95 small stems may be viewed a hidden process with no recruitment rate data available to constrain a  
96 model to through a likelihood approach. Here, we used a simple forest dynamics simulator based on  
97 the Perfect Plasticity Approximation, PPA, model (Purves et al. 2008) to model juvenile dynamics  
98 and compare the number of juveniles predicted by the model with actual numbers recorded in the  
99 inventory, using the likelihood-free approach, Approximate Bayesian Computation (ABC), to find the  
100 best fit juvenile recruitment, growth and mortality model parameters. ABC is unlike other model fitting  
101 methods because it does not require the computation of a likelihood function calculated from  
102 response data (data on individual juvenile stem recruitment or dynamics) for models, and can  
103 parameterise a model using summary data only (such as our stem count data). ABC has huge  
104 promise as a method in systems where the data needed to accurately describe processes is  
105 unavailable or not practical to collect (Beaumont, 2010). ABC is increasingly used in areas including  
106 epidemiology and genetics (Bertorelle et al. 2010) and, to a lesser extent, ecology (Jabot and Chave  
107 2009, Csilléry et al. 2010, Clarke et al. 2016).

108           The Mediterranean is a biodiversity hotspot highly vulnerable to the effects of climate change  
109 (Thuiller et al. 2005) and defensible projections of species' distribution changes is a pressing need.  
110 Climate change may be accelerating low regeneration in some Spanish forests, and concerning  
111 mismatches between juvenile and adult distributions have been observed (e.g. Plieninger et al.,  
112 2010; Urbieto et al., 2011). Our results quantify the variation in recruitment and juvenile growth and  
113 mortality between species and functional groups, trade-offs in rates at the juvenile life stage, test the  
114 influence of climate and con- and hetero-specific competition on juvenile performance, and predict  
115 changing rates under climate change.

116

## 117 **Materials and methods**

### 118 *The Approximate Bayesian Computation (ABC) approach*

119 ABC methods represent a significant statistical advance in fitting models when the likelihood cannot  
120 be formulated or is computationally prohibitive to analyse (Sisson et al. 2007). ABC estimates model  
121 parameters for complex processes where only coarse-scale, aggregated data are available (as here,  
122 where annual recruitment rates are not known but total numbers of small stems are observed). To  
123 fit the particle (parameter set)  $p$  of a given model  $f$  (the forest simulation model in our application),  
124 which predicts an quantity  $y$ . Without observed data of  $y$ ,  $y_0$ , we cannot use a likelihood approach  
125 to estimate the posterior of  $p$ . However, with data on one or more observed summary statistics of  $y$ ,  
126  $S(y_0)$ , we can use ABC to infer best-fit values  $p$  using a rejection algorithm, thereby approximating  
127 the posterior.

128 Here, we used an ABC Sequential Monte Carlo algorithm (ABC-SMC; Sisson et al. 2007, Beaumont  
129 et al. 2009). ABC-SMC repeatedly resamples from previous sets of particles with decreasing  
130 tolerance levels, producing a series of sets of particles representing improving approximations to the  
131 true posterior. ABC-SMC works as follows: for iterations  $t=1\dots T$ ,  $N$  independent particles are  
132 sampled from the distribution  $\pi(p|d(S(y_0), S(\hat{y})) \leq \epsilon_t)$ , with  $\epsilon_1 > \epsilon_2 > \dots > \epsilon_T \geq 0$ . If  $t > 1$ , particles are  
133 sampled from the previous distribution ( $t-1$ ), using weighted sampling (weights  $\omega_i^{(t-1)}$ ) particles that  
134 better approximate  $\pi(p|y)$  are re-sampled more often:

### 135 **ABC-SMC**

136 1. When  $t=1$ , for  $i=1\dots N$

137 a. Sample particles from the prior,  $p_i^{(1)} \sim \pi(p)$ , and generate  $\hat{y} \sim f(y|p_i^{(1)})$  until  
138  $d(S(y_0), S(\hat{y})) < \varepsilon_1$ ,

139 b. Set all weights equal, as  $\omega_i^{(1)} = 1/N$ ,

140 c. Set  $\Sigma_1$  to be twice the empirical variance of particles  $\{p_j^{(1)}\}$ .

141 2. For  $t=2\dots T$

142 a. For  $i=1\dots N$

143 i. Sample particle  $p^*$  from the previous particle distribution, denoted  $\{p_j^{(t-1)}\}$ , with  
144 weights  $\omega_j^{(t-1)}$ ,

145 ii. Perturb  $p^*$  according to a transition kernel,  $p^{**} \sim N(p^*|\Sigma_{t-1})$ ,

146 iii. Use the simulation model  $f$  to generate  $y^{**} \sim f(y|p^{**})$ . If  $d(S(y_0), S(y^{**})) < \varepsilon_t$ , set

147  $p_i^{(t)} = p^{**}$ , otherwise return to 2ai.

148 b. For  $i=1\dots N$

149 Calculate the weight of each particle according to:

150 
$$\omega_i^{(t)} \propto \frac{\pi(p_i^{(t)})}{\sum_{j=1}^N \omega_j^{(t-1)} K_t(p_i^{(t)}|p_j^{(t-1)})}$$

151 where  $K_t(p_i^{(t)}|p_j^{(t-1)})$  is the multivariate normal density with variance  $\Sigma_{t-1}$ .

152 c. Set  $\Sigma_t$  to be twice the empirical variance of particles  $\{p_j^{(t)}\}$ . (1)

153

154 The ABC-SMC algorithm described in eqn 1 fit our model's parameters, but suffered low acceptance  
155 rates (frequent rejection at 2aiii), and was slow to deliver the full particle sample. We therefore used  
156 a modified ABC-SMC with adaptive weighting, ABC-SMC-AW (Bonassi and West 2015). ABC-SMC-  
157 AW alters the weighting  $\omega_j$  of each particle  $p_j$  according to the value of the metric  
158  $d(S(y_0), S(f(y|p_j)))$ , drawing particles with new weights  $v_j$  at step 2ai in eqn 1, calculated as  
159 follows:

160

161 for  $j=1\dots N$   $\hat{v}_j^{(t-1)} \propto \omega_j^{(t-1)} K_t \left( S(y_0) | S \left( f(y|p_j^{(t-1)}) \right) \right)$

162 for  $j=1\dots N$   $v_j^{(t-1)} = \frac{\hat{v}_j^{(t-1)}}{\sum_{i=1}^N \hat{v}_i^{(t-1)}}$

163 (2)

164 Here,  $K_t$  is a multivariate normal distribution with variance equal to the empirical variance of  
 165  $S \left( f(y|p_j^{(t-1)}) \right)$ .

166

167 *Forest Inventory Data*

168 Data came from the second and third Spanish Forest inventories (IFN2 and IFN3; MMA, 1996, 2007),  
 169 which sampled over 70,000 re-measured plots systematically on a 1 km<sup>2</sup> grid across Spain. IFN plots  
 170 were sampled using a variable radius concentric plots. All trees DBH > 7.5 cm were measured in a  
 171 plot of radius 5 m, DBH > 12.5 cm in a plot radius 10 m, DBH > 22.5 cm in a plot radius 15 m and  
 172 DBH > 42.5 cm in a plot radius 25 m. In the central 5 m radius plot, counts of ‘large saplings’ with  
 173 heights > 130 cm and DBH in the range 2.5 - 7.5 cm were recorded, along with a categorical measure  
 174 of the presence/absence of ‘small saplings’ (heights > 130 cm and DBH < 2.5 cm). Here we refer to  
 175 all stems between 1 cm and 7.5 cm DBH as ‘juveniles’.

176 We used plots with no recorded management or unnatural source of regeneration recorded  
 177 in the IFN3, and without planted pines stems, following Ruiz- Benito et al. (2012). We selected 13  
 178 species to parameterise models of juvenile dynamics for; all had at least 300 plots containing at least  
 179 one adult tree (Fig. 1). These comprised seven conifers and six angiosperms; temperate conifers  
 180 (*Pinus sylvestris*, *Pinus uncinata*), Mediterranean conifers (*Pinus pinea*, *Pinus halepensis*, *Pinus*  
 181 *nigra*, *Pinus pinaster*, *Juniperus thurifera*), temperate angiosperms (*Quercus petraea*, *Quercus*  
 182 *pyrenaica*, *Fagus sylvatica*) and Mediterranean angiosperms (*Quercus faginea*, *Quercus ilex*,  
 183 *Quercus suber*.). Small stems may be either saplings or resprouts (a common feature of some  
 184 Mediterranean oaks; Grove and Rackham, 2001), but we were unable to differentiate between these  
 185 in the data.

186

187 *Overview of the modelling approach*

188 The number of juvenile stems occurring in an inventory-plot is the result of both establishment and  
 189 demographic processes. We characterised four key processes - the probability of occurrence of  
 190 juveniles in a plot, the annual rate of recruitment of new stems, and the growth and mortality rates  
 191 of juveniles. We used a multi-step Bayesian model-fitting approach describe below to parameterise  
 192 these from the inventory data, separating climate and forest structural effects on recruitment. The  
 193 first and second processes relate to recruitment: we chose to determine the *probability* of juvenile  
 194 occurrence by climate, and the annual recruitment *rate* using conspecific density and competitive  
 195 factors. Fitting these two separately (following Zhu et al. 2015) avoided overfitting and allowed us to  
 196 make best use of the data available by incorporating all inventory information on stems < 7.5 cm  
 197 DBH. The probability of juvenile occurrence was estimated using an MCMC approach on inventory  
 198 presence/absence data, and recruitment, growth and mortality rates were estimated using the ABC  
 199 approach with a forest simulator (the PPA) and inventory juvenile count data.

200

201 *MCMC-derived estimates of probability of occurrence of juveniles*

202 First, we quantified the probability of the occurrence of juveniles of any size of each species as a  
 203 function of climatic conditions. We extracted annual precipitation (AP, mm), mean annual  
 204 temperature (AVT, °C) and drought length (DL, months) from Gonzalo Jiménez (2010). We used  
 205 inventory information on large and small saplings to calculate presence/absence information for  
 206 58,616 unmanaged plots in IFN3. We used MCMC to fit the probability of the occurrence of juveniles,  
 207 tested logistic models with climatic predictors in quadratic form in all possible permutations, and  
 208 compared models using AIC (see supporting information, Tables S8 – S10). The best-fit model was:

209 
$$P(\text{occurrence}) = \frac{1}{1 + \exp(-k)}, \text{ where}$$

210 
$$k = a_0 + a_1 a_2 AVT - a_2 AVT^2 + a_3 a_4 AP - a_4 AP^2 + a_5 a_6 DL - a_6 DL^2 \quad (3)$$

211

212 We assigned positive priors for parameters  $a_1 - a_6$ , resulting in prior quadratic maxima within the  
 213 climatic ranges of the data.

214

215 *Annual juvenile recruitment rate*



216 We hypothesis that recruitment rates increase with conspecific adult density (potential parent trees),  
 217 and are impacted by con- and hetero-specific competition. We used crown area index (CAI, projected  
 218 crown area per unit of ground) to represent both. CAI has been used within several forest models  
 219 (e.g. Bohlman and Pacala 2011, Coomes et al. 2012, Vanderwel et al. 2013) and was a good  
 220 predictor for our data in growth and mortality functions (see below, and supporting information Tables  
 221 S1 – S7). We applied species-specific crown width allometric equations to calculate CAI of all adults  
 222 (>7.5 cm DBH) ( $CAI_{all}$ ) and of conspecifics only ( $CAI_{sp}$ ) in each inventory plot (allowing for the  
 223 variable-radius plot structure), for both inventories to calculate temporal changes in competitive  
 224 environment within the simulations (see supporting information text and Tables S1-S3, Fig. S1).

225 We define and model recruitment rate as:

$$\begin{aligned}
 & \# \text{ new stems growing through a 1 cm DBH threshold per year} \\
 & = p_0 CAI_{sp} \exp(-p_1(CAI_{all} - CAI_{sp}) - p_2 CAI_{sp}) \quad (4)
 \end{aligned}$$

228

229 Where  $p_0 - p_2$  are parameters fit by the ABC-SMC-AW algorithm. We define the *expected annual*  
 230 *rate of recruitment* of a species in a given 5 m radius subplot as the probability of recruitment  
 231 occurring (eqn 3) multiplied by the rate of recruitment (eqn 4).

232

233 *Juvenile growth and mortality rates constrained by informative priors*

234 Many different recruitment, growth and mortality rates could combine to give the observed stem  
 235 counts, yet not all are reasonable given ecological knowledge of demographic processes. We  
 236 constructed priors for growth and mortality rates of juveniles small adult tree data in the inventories.  
 237 We fitted species-specific growth and mortality functions to data from re-measured trees 7.5 - 10 cm  
 238 DBH within an MCMC framework, comparing alternative models containing size and competition  
 239 effects using AIC. The best-fit models were:

$$\text{Annual growth rate (cm/year)} = p_3 DBH / (1 + p_4 CAI_{all}) \quad (5)$$

$$\text{Annual mortality rate} = \text{logit}(k) ; k = p_5 + p_6 DBH + p_7 CAI_{all} \quad (6)$$

242 (see supporting information text and Tables S4 – S8, Figs S2 and S3 for a full methodology and  
 243 results). These functional forms were used within the simulation model (eqn 7 below), with juvenile

244 growth and mortality parameter values  $p_3 - p_7$  fit within the ABC-SMC-AW framework. Parameter  
245 values from the small adult data were used as strong priors for parameters  $p_3 - p_7$  within the ABC-  
246 SMC-AW framework.

247

#### 248 *Simulation model*

249 We used a simple cohort-based forest dynamics model to generate juvenile tree densities that were  
250 compared with the inventory count data using the ABC-SMC-AW framework (eqns 2, 3). The model  
251 simulated size structure and density of juveniles in each plot from their recruitment, growth and  
252 mortality rates, taking plot data on climate and competitive environment as inputs. Our simulator was  
253 based on the PPA model of Purves et al. (2008) which simulates cohorts rather than tracking  
254 individual stems, reducing complexity whilst retaining the ability to reproduce many of the features  
255 of spatially explicit models (Strigul et al. 2008). We simulated dynamics over 100 years (time steps)  
256 using annual time steps to reduce census interval-dependence of results (Kohyama et al. 2018), with  
257 species fitted separately. For each cohort  $i$  at time  $t$  we recorded the density  $den_{i,t}$  (#stems / 5 m  
258 radius plot) and diameter  $DBH_{i,t}$  (cm). After 100 time steps densities for all cohorts in the range 2.5  
259 cm < DBH < 7.5 cm were summed to give a model-predicted density directly comparable to the  
260 inventory count data. The simulation model ran independently on each plot, as follows:

#### 261 **Forest dynamics simulation model (based on PPA):**

262 For each time step ( $t=1...T$ )

263 1. Calculate plot conditions ( $CAI_{all}$  and  $CAI_{sp}$ ) for time  $t$ .

264 2. For all existing juvenile cohorts ( $i=1...N$ )

265 a. Reduce stem density according to the mortality rate (eqn 6):

$$266 \quad den_{i,t} = (1 - P(\text{mortality}_{i,t-1})) \times den_{i,t-1}$$

267 b. Increase stem size according to the growth rate (eqn 5):

$$268 \quad DBH_{i,t} = DBH_{i,t-1} + \text{growth}$$

269 3. With probability according to climatic conditions (eqn 3), create a new cohort of stems with  
270 DBH = 1 cm, with density according to the recruitment rate (eqn 4).

271

(7)

272

273 *Implementation of ABC-SMC-AW to derive juvenile demographic rates*

274 We set wide uniform positive prior distributions for recruitment parameters (eqn 4):  $p_0 \sim U[0,50]$ ,  
275  $p_1 \sim U[0,5]$  and  $p_2 \sim U[0,5]$ . Note that the ABC-SMC-AW algorithm could select negative values for  $p_1$   
276 and  $p_2$  –for example to represent a facilitation– if data support was strong. For parameters  $p_3$ - $p_7$   
277 (eqns 6 and 7) we used Gaussian priors with means set to the means fitted on small adult growth  
278 and mortality data (supporting information Tables S6 and S7) and standard deviations set as 10%  
279 of the MCMC posterior estimate. Prior distributions were used as initial sampling distributions for all  
280 parameters.

281 We chose two summary statistics, the observed mean and standard deviation of the count of  
282 juvenile stems, and used absolute difference as the metric of comparison for both ( $d$  in eqn 1). We  
283 simulated 1000 particles in 9 SMC steps, with tolerance levels starting at 4 and reduced to 0.02 for  
284 both statistics (reduction of tolerance by 25% for the first two steps, 50% for the next two, and 75%  
285 for the last five).

286 Temporal variation in competitive environment ( $CAI_{sp}$  and  $CAI_{all}$ ) was simulated using IFN2  
287 values for the first 90 steps of the simulation, and altering values during the final 10 time steps  
288 (corresponding to a 10-year time interval between inventories) using a linear relationship between  
289 IFN2 and IFN3 values. All algorithms (MCMC, ABC-SMC-AW and forest simulation model) were  
290 coded in C and compiled in a CentOS 7.3 environment with compiler GCC 4.8.5. Statistical packages  
291 for a range of different ABC algorithms are available for use 'off-the-shelf', including several R  
292 packages (such as abc; Csilléry et al., 2012).

293

## 294 **Results**

295 *ABC model implementation and fit*

296 Time to convergence of each ABC-SMC-AW iteration varied between species, with all but one (*P.*  
297 *halepensis*, Fig. 2) species' fits completing 10 iterations. Final estimate model particles' simulations  
298 had mean and standard deviation of juvenile counts within 0.02 of observations, or 0.06 for *P.*  
299 *halepensis* (observed means were 0.16 - 2.40 stems/5 m radius plot, standard deviations 0.63 -

300 4.58). We compared model predictions with data graphically and analysed posterior particle values  
301 to examine model performance. For all species, the fitted model was able to predict stem counts  
302 within the range of observations along gradients of conspecific and heterospecific crown area (Figs  
303 2 and supporting information S4). However, model predictions did not capture all variability observed  
304 in the data for all species. Predictions are shown using mean parameter values taken from the final  
305 iteration, however for some parameters, credible intervals contained zero (Table 1), though these  
306 may be inflated as a result of the ABC approach (Csilléry et al. 2010).

307

### 308 *Climatic controls on probability of occurrence of juveniles*

309 The best-fit model probability of occurrence was the full model (eqn 3) for all but one species, and  
310 was used for all species within the simulation model (eqn 7) (details in supporting information text  
311 and Tables S9 and S10). Probability of occurrence of juveniles was strongly controlled by climate for  
312 all species, with large variation in the peak of juvenile occurrence for each species (Fig. 3). The  
313 model predicted maximum recruitment probability at higher mean annual temperatures, lower annual  
314 rainfall rates and longer droughts for Mediterranean species than temperate species (average  
315 13.0°C vs 8.3°C, 685 mm vs 1086 mm and 0.9 months vs 0.4 months, respectively, see Fig. 3).  
316 Maximum probability of occurrence and probability predicted at the centre of each species' climatic  
317 range were higher for conifers than angiosperms (maximum 0.20 vs 0.14, average 0.10 vs 0.03),  
318 and for temperate than Mediterranean species (maximum 0.18 vs 0.14, average 0.08 vs 0.05).

319

### 320 *Predicted recruitment, growth and mortality rates of juveniles*

321 Expected recruitment rate varied strongly between species (fitted parameters Table 1), and was  
322 strongly affected by competitive environment (parameters  $p_1$  and  $p_2$  in Table 1 and Fig. 4). In their  
323 average climatic and competitive conditions (supporting information Table S12), conifer species  
324 showed higher rates than angiosperms (19.5 vs 8.3 new 1 cm stems/ha/year) and temperate species  
325 showed higher rates than Mediterranean species (17.1 vs 12.6 stems/ha/year). Species' predicted  
326 recruitment rates in monospecific stands ( $CAI_{all}=CAI_{sp}$ ) in their average climate were on average  
327 higher for temperate conifers than Mediterranean conifers, but lower for temperate angiosperm than  
328 Mediterranean angiosperms, in both low and higher density stands (Table 2). For most species,

329 recruitment rate showed an overall hump-shaped relationship with conspecific density, with  
330 increases at low levels and declines at higher (Figs 2 and 4). Comparing from low to mid-density  
331 monospecific stands, most Mediterranean species showed a decline and most temperate species  
332 an increase in recruitment rates, but with large differences between species' rates (Table 2). Most  
333 species' recruitment rates showed a stronger negative effect of increases in conspecific than  
334 heterospecific crown area ( $p_1 < p_2$  for 10 of 13 species), with on average stronger effects in higher  
335 competition (higher  $p_1$  and  $p_2$ ) for temperate than Mediterranean species.

336 Predicted growth and mortality rates were highly variable between species, and between  
337 groups of species (Fig. 4, supporting information Table S11). In all conditions simulated in Table 2  
338 conifer juveniles had higher growth and mortality rates than angiosperm juveniles, and  
339 Mediterranean species had lower growth and higher mortality rates than temperate species. Growth  
340 rates of conifer species showed more rapid decline in higher competition than angiosperms (higher  
341 average  $p_4$ , eqn 5, Fig. 4), though there was little difference between average mortality responses,  
342 or between temperate and Mediterranean species. In species' average environments and in low  
343 monospecific stands (Table 2), mortality and recruitment rates were significantly positively correlated  
344 to each other, and to the probability of occurrence of juveniles ( $p < 0.05$ ).

345 Under a simple climate change scenario of +2 °C AVT, -20% AP and +20% DL, most species'  
346 probability of occurrence of recruitment and expected recruitment rates at the centre of their climate  
347 ranges showed substantial decline (Table 3). Temperate species showed a stronger decline,  
348 averaging 65%, whilst Mediterranean species had average decline of 19%. Three Mediterranean  
349 species, *P. pinea*, *P. halepensis* and *Q. ilex* showed increases in this changed climate (of 84%, 43%  
350 and 3% respectively).

351

## 352 **Discussion**

### 353 *Drivers of recruitment, growth and mortality: implications for modelling*

354 This study demonstrates the ability of ABC to quantify annual recruitment rates and juvenile  
355 dynamics from summarised data (Figs 2 and supporting information S4). Coarse juvenile data is  
356 widely available in national forest inventory datasets and permanent plot networks and our  
357 statistically rigorous approach could be used to both unlock understanding of processes affecting

358 regeneration across large regions, and improve large-scale demographic model accuracy. Our  
359 approach using annual time steps accounted for time-variation in plot structure, reducing the bias in  
360 rate estimation (Kohyama et al. 2018).

361 We quantified the influence of climate, conspecific and heterospecific competition on juvenile  
362 processes, and found strong differences among species, even within groupings (Figs 3 and 4).  
363 Conifer species showed higher probability of occurrence and recruitment rates than angiosperms  
364 growing under similar conditions, in agreement with comparisons between Mediterranean pine and  
365 oak regeneration levels (Urbieto et al. 2011). Increasing conspecific density had a stronger effect in  
366 reducing overall recruitment rates than heterospecific competition for most species, consistent with  
367 the Janzen–Connell hypothesis and findings in plant communities worldwide (Comita et al. 2014).

368 We found that canopy density strongly and negatively affected juvenile recruitment and  
369 growth, and positively affected mortality rates for all species. This negative effect was on average  
370 smaller for Mediterranean species. Competition for light may be less intense in Mediterranean  
371 ecosystems due to lower leaf densities (Coomes and Grubb 2000) and facilitative effects from  
372 neighbouring trees and shrubs are known to aid seedling survival and growth, preventing desiccation  
373 by reducing water stress and protecting leaves from high levels of irradiance. Recruitment facilitation  
374 benefits reported for deciduous and Mediterranean evergreen species are stronger than those for  
375 temperate and montane *Pinus* species (Gómez-Aparicio et al. 2004, Mendoza et al. 2009).

376 This approach reveals recruitment patterns on scales large enough to understand and predict  
377 impacts of climate change. Although long recognised as critical for understanding forest diversity  
378 and dynamics (Kobe et al. 1995, Kobe 1996, Metz et al. 2010), studies of *rates* rather than *patterns*  
379 of recruitment have often been limited to small scales by data requirements, making predictions of  
380 change difficult. Here, we predict declines in recruitment for all species under longer drought  
381 conditions, and most under hotter temperatures, which is of particular concern given existing  
382 observed recruitment limitations (Mendoza et al. 2009) although under these conditions we predict  
383 some species may experience increases in recruitment in the cooler parts of their ranges. Warming-  
384 induced changes in recruitment rates have been observed in Spain (Peñuelas et al. 2007, Camarero  
385 and Gutiérrez 2007), and species-specific responses may be important in predicting range shifts  
386 under climate change. For example, higher rainfall has been found to increase regeneration rates of

387 the deciduous *Q. pyrenaica* but decrease rates of the evergreen *Q. ilex* (Plieninger et al. 2010),  
388 whilst temperature is an important determinant of differential regeneration rates between species  
389 (Gómez-Aparicio et al. 2009), and seasonal drought and waterlogging may negatively affect  
390 establishment of Mediterranean oaks (Urbieta et al. 2008).

391 Under an scenario of increasing aridity and the frequency of climatic extremes, recruitment  
392 dynamics might be key for properly describing ecosystem responses under climate change (Matías  
393 et al. 2011, 2012). Our results show strong interspecific differences in recruitment that are likely to  
394 be critically important to robust predictions of ecosystem responses to climate change. In Spain,  
395 growth of some species may increase in a hotter future climate (Benito- Garzón et al. 2013), but our  
396 results indicate that recruitment may decrease with increasing aridity. These mismatches in  
397 demographic responses could result in ecosystem time-delayed responses and legacy effects  
398 resulting in a delayed ecosystem collapse.

#### 399 400 *The potential of the ABC approach to exploit existing ecological data*

401 There are many exciting applications of ABC in ecology, for example to infer unobserved historical  
402 processes that have led to an observed state of a system (this study), or for stochastic models for  
403 which likelihoods cannot be constructed such as the neutral model of biodiversity (Jabot and Chave  
404 2009), and these methods have been widely adopted in many areas of biological research (see  
405 Bertorelle et al. 2010). A major advantage of ABC when applied to ecological situations is that it  
406 allow the inclusion of partial knowledge of a system, whether as functional forms within a simulation  
407 model structure or as prior distributions for parameters, as demonstrated here. Whilst direct  
408 measurements of some processes may be lacking, it is unlikely that nothing is known about the  
409 direction or magnitude of *any* process within an ecological system, and the inclusion of good prior  
410 information will improve the speed of convergence of estimated parameters, and ensure ecologically  
411 reasonable output.

412 Despite its potential, ABC requires care in application. The multiple elements involved in  
413 calibration of the method can make it challenging to ensure that the true posterior distribution of  
414 parameters is estimated. Our choice of forest simulator (based on the PPA) was pragmatic given the  
415 structure of data available to us, but the underlying simulation model will influence ABC output and

416 is therefore an additional source of uncertainty to consider. Model performance and validity may be  
417 influenced by the choice of summary statistics (Marin et al. 2014), but sufficiency of chosen summary  
418 statistics is difficult to establish (Marjoram et al. 2003) and optimal statistics are dataset specific  
419 (Nunes and Balding 2010). Moreover, credible intervals on posterior parameter estimates arising  
420 from ABC simulation models are likely to be inflated due to an information loss from summarised  
421 data (Csilléry et al. 2010), and ABC posterior values may not represent true probabilities (Templeton  
422 2010). We found that, although mean trends in data were well captured by the model, predicted  
423 variability in juvenile counts was often smaller than observations (Figs 2 and supporting information  
424 S4). This is likely in part due to both the stochastic nature of recruitment, and to the fact that juvenile  
425 data was collected in a small plot size in the inventory (circular, 5 m radius), meaning microsite  
426 conditions, which may be important drivers of spatial patterns of juvenile dynamics (Vilà-Cabrera et  
427 al. 2013), are not captured within the modelling approach.

428         Compared to likelihood-based methods, there is less agreement on methods for ABC model  
429 comparison and goodness-of-fit (Lemaire et al. 2016), leading us to employ a pragmatic graphical  
430 approach to evaluate model performance. ABC parameterisation may be slow: the most  
431 computationally expensive element in this application was model simulation, and particle rejection  
432 rate varied strongly with species and iteration number though individual particle acceptance is  
433 independent so model simulations could be parallelised. Adoption of the ABC-SMC-AW approach  
434 (eqn 2) reduced simulations required before acceptance by an average of 27%: a figure similar to  
435 that found in Bonassi and West (2015).

436

## 437 **Conclusions**

438 Our results highlight the role of juvenile stage as a driver of forest species distributions along  
439 environmental gradients. We observed strong interspecific differences, within and between  
440 functional groupings, and quantified life-history strategies and competitive effects driving species  
441 segregation. Mediterranean species had on average higher recruitment rates and maximum  
442 recruitment in warmer and drier locations, but also higher mortality of juveniles and lower growth  
443 rates than cool temperate species. The juvenile life stage is likely to be the first indicator of changes  
444 to species distributions and structural and successional dynamics in a changing climate, making best



445 use of data on early life history crucial for defensible predictive modelling as well as designing forest  
446 restoration and adaptation strategies. Importantly, our results predict a widespread recruitment  
447 decline for most studied species, along with a few 'winners' in the ecosystem; all Mediterranean  
448 species. However, whether this pattern will be reflected in adult diversity may depend critically on  
449 feedbacks between species demography and interspecific interactions (e.g. Matías and Jump 2012),  
450 so models that do not capture these feedbacks may give misleading results when projecting species  
451 distributions under climate change.

452 The ABC method used here incorporates partial knowledge of the systems to infer critical  
453 unmeasured processes, and thus fully parameterise complex models that previously could not be  
454 fully specified. Without such an approach expensive and time-consuming repeat measurements  
455 would have been needed to understand juvenile dynamics in this system. This study demonstrates  
456 the power of the ABC approach for understanding ecological processes and highlights its potential  
457 for revealing critical unrecorded processes from existing information.

458

#### 459 **Data Accessibility**

460 The second and third Spanish Forest Inventory data is available in the MAPAMA

461 <https://www.mapama.gob.es/>). The climate data used is available in Gonzalo Jiménez (2010).

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589 **Tables and figures**

590

591 **Table 1** Fitted mean and 95% credible interval of recruitment parameters, from eqn 4: # new stems592 growing through a 1 cm DBH threshold per year=  $p_0 CAI_{sp} \exp(-p_1(CAI_{all} - CAI_{sp}) - p_2 CAI_{sp})$ .

Species	$p_0$	$p_1$	$p_2$
<i>P. sylvestris</i>	75.65 (48.78, 108.79)	3.84 (2.68, 5.04)	26.34 (14.40, 39.21)
<i>P. uncinata</i>	48.02 (25.68, 73.14)	2.56 (0.45, 4.36)	2.77 (-3.07, 8.99)
<i>P. pinea</i>	57.69 (23.52, 97.88)	2.06 (-1.26, 5.23)	-0.06 (-2.75, 2.96)
<i>P. halepensis</i>	23.53 (3.45, 65.58)	-0.21 (-2.94, 3.11)	7.00 (-2.50, 16.36)
<i>P. nigra</i>	116.76 (55.77, 187.17)	1.11 (0.03, 1.77)	14.46 (6.45, 23.09)
<i>P. pinaster</i>	62.48 (23.54, 108.18)	0.73 (-1.51, 2.26)	2.74 (-3.66, 11.82)
<i>J. thurifera</i>	59.21 (34.03, 91.01)	2.20 (-2.00, 6.00)	5.65 (-6.74, 18.73)
<i>Q. petraea</i>	32.77 (11.01, 60.46)	2.38 (0.29, 4.37)	-0.05 (-1.94, 2.44)
<i>Q. pyrenaica</i>	59.93 (28.95, 91.15)	1.23 (0.12, 2.17)	1.86 (-1.33, 6.29)
<i>Q. faginea</i>	78.48 (24.72, 135.83)	2.66 (-1.32, 4.79)	10.68 (3.02, 17.02)
<i>Q. ilex</i>	37.19 (8.22, 88.39)	0.05 (-1.13, 0.95)	13.15 (2.70, 23.33)
<i>Q. suber</i>	44.91 (20.14, 77.41)	2.25 (-0.90, 4.76)	0.55 (-3.38, 4.94)
<i>F. sylvatica</i>	51.76 (21.02, 90.42)	1.17 (-1.01, 2.68)	5.25 (1.45, 9.03)

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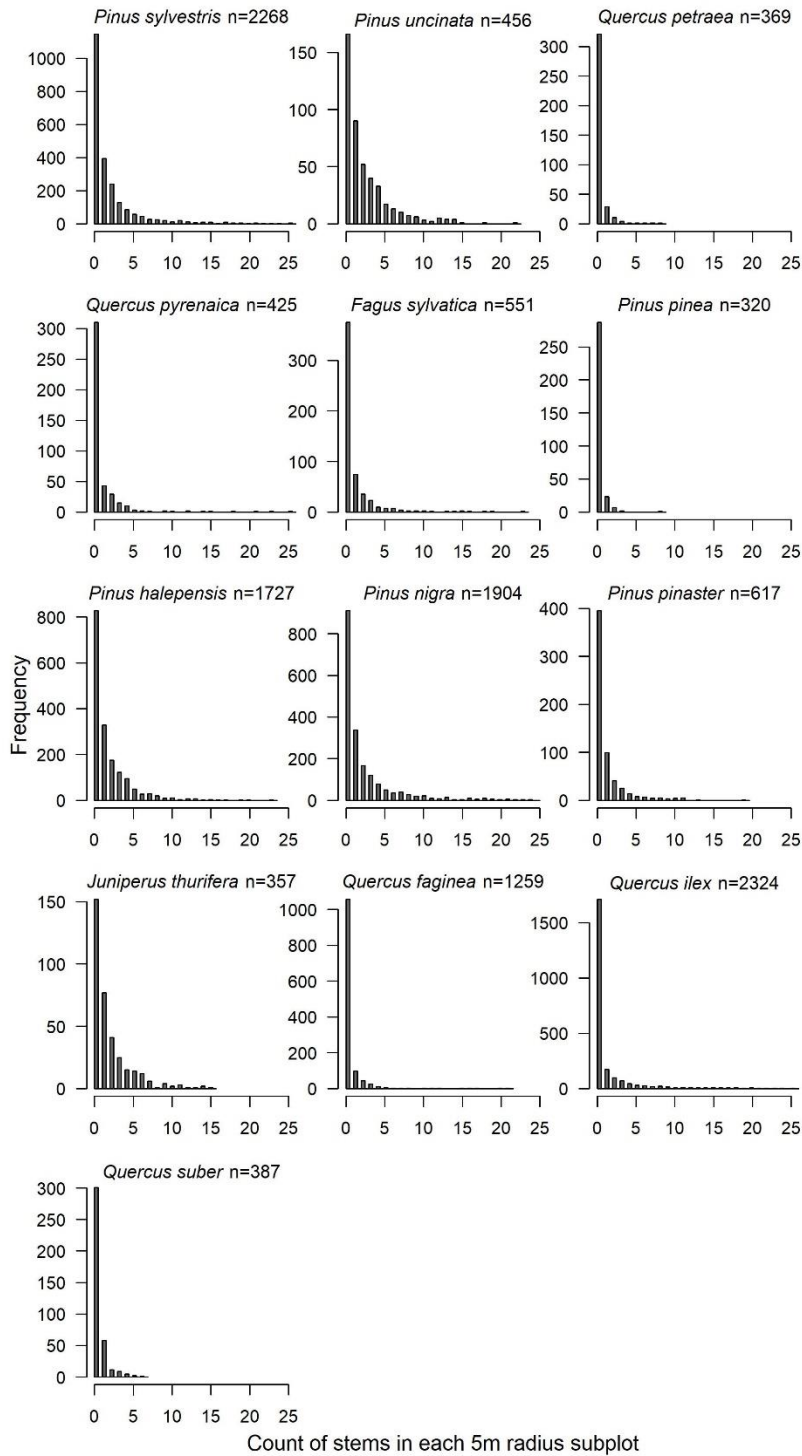


595 **Table 2** Predicted probability of occurrence (eqn 3) in the average environment encountered by a  
596 species, and under a scenario of 2°C increase in AVT, 20% decrease in MAP, 20% increase in DL.  
597 Expected rates of recruitment (RR, eqn 3 and eqn 4: 1 cm DBH stems/ha/year), growth (GR, eqn  
598 5: cm/year for 1 cm DBH stem) and mortality (MR, eqn 6: annual probability of mortality of 1 cm  
599 DBH stem). Rates are calculated at the centre of each species' climatic ranges in the average  
600 competitive environment ( $CAI_{all}$  and  $CAI_{sp}$ ) and monospecific stands; a low density ( $CAI_{all} =$   
601  $CAI_{sp} = 0.2$  ha/ha) and a higher density stand ( $CAI_{all} = CAI_{sp} = 1$  ha/ha).

Species	Probability of occurrence	Probability of occurrence under climate change	Average competitive environment			$CAI_{all} = CAI_{sp} = 0.2$			$CAI_{all} = CAI_{sp} = 1$		
			RR	GR	MR	RR	GR	MR	RR	GR	MR
<i>P. sylvestris</i>	1.12E-01	4.95E-02	0.43	0.314	0.016	8.13	0.413	0.012	0.00	0.184	0.030
<i>P. uncinata</i>	1.56E-01	8.11E-03	66.33	0.225	0.049	22.66	0.275	0.066	59.72	0.109	0.205
<i>P. pinea</i>	2.99E-03	5.51E-03	1.54	0.250	0.042	0.63	0.232	0.048	23.31	0.097	0.079
<i>P. halepensis</i>	8.45E-02	1.21E-01	13.64	0.232	0.022	7.92	0.251	0.030	0.23	0.121	0.097
<i>P. nigra</i>	1.35E-01	6.17E-02	28.99	0.214	0.085	37.64	0.250	0.103	0.00	0.101	0.208
<i>P. pinaster</i>	2.97E-02	9.73E-03	19.10	0.373	0.032	7.54	0.409	0.044	15.23	0.141	0.142
<i>J. thurifera</i>	2.48E-02	3.66E-03	6.24	0.104	0.028	4.20	0.083	0.045	0.66	0.034	0.253
<i>Q. petraea</i>	4.08E-03	2.49E-03	1.71	0.189	0.003	0.47	0.216	0.004	17.90	0.098	0.019
<i>Q. pyrenaica</i>	9.34E-03	3.72E-03	7.48	0.153	0.006	2.17	0.178	0.007	11.12	0.096	0.015
<i>Q. faginea</i>	1.88E-02	7.41E-03	4.54	0.174	0.008	3.21	0.179	0.009	0.00	0.114	0.016
<i>Q. ilex</i>	3.81E-02	3.93E-02	4.20	0.153	0.011	4.23	0.156	0.013	0.00	0.117	0.023
<i>Q. suber</i>	4.49E-02	3.74E-02	22.23	0.163	0.032	7.01	0.169	0.042	148.21	0.074	0.122
<i>F. sylvatica</i>	3.50E-02	8.24E-03	9.34	0.194	0.022	6.20	0.308	0.026	1.21	0.148	0.047

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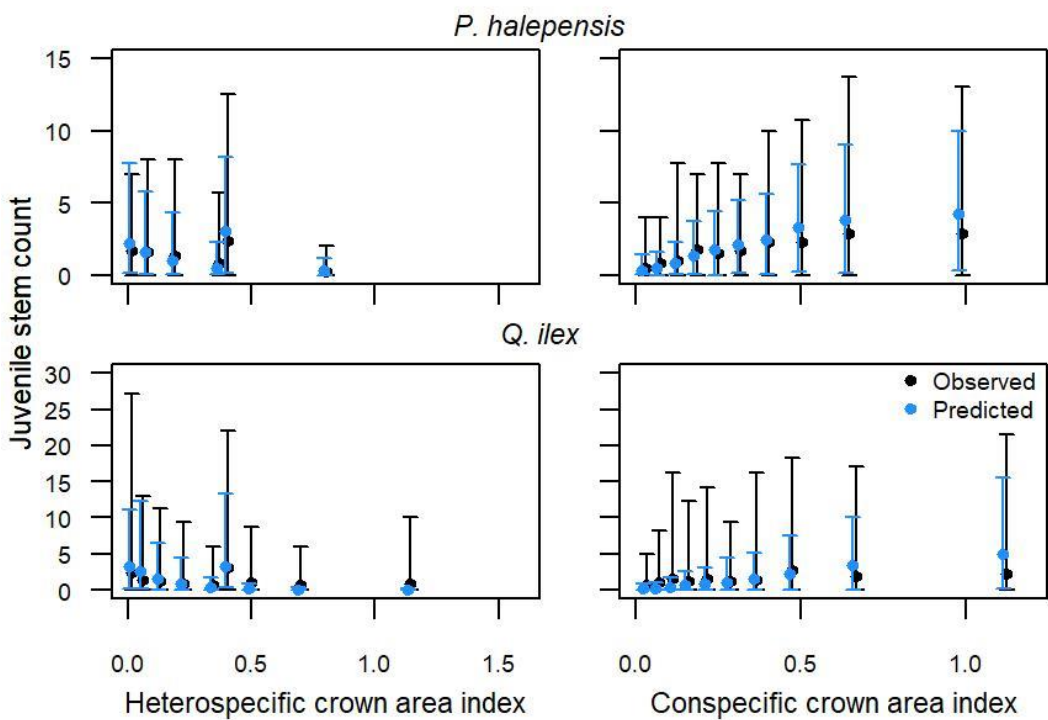
603 **Figure 1** Histograms of juvenile stem counts in inventory plots used for the analysis, for the 13  
 604 study species. Juveniles are here defined as trees with DBH in the range 2.5 – 7.5 cm. Plots with  
 605 more than 25 observed juveniles are not shown for visual clarity, but account for no more than 1%  
 606 of plots for any species.



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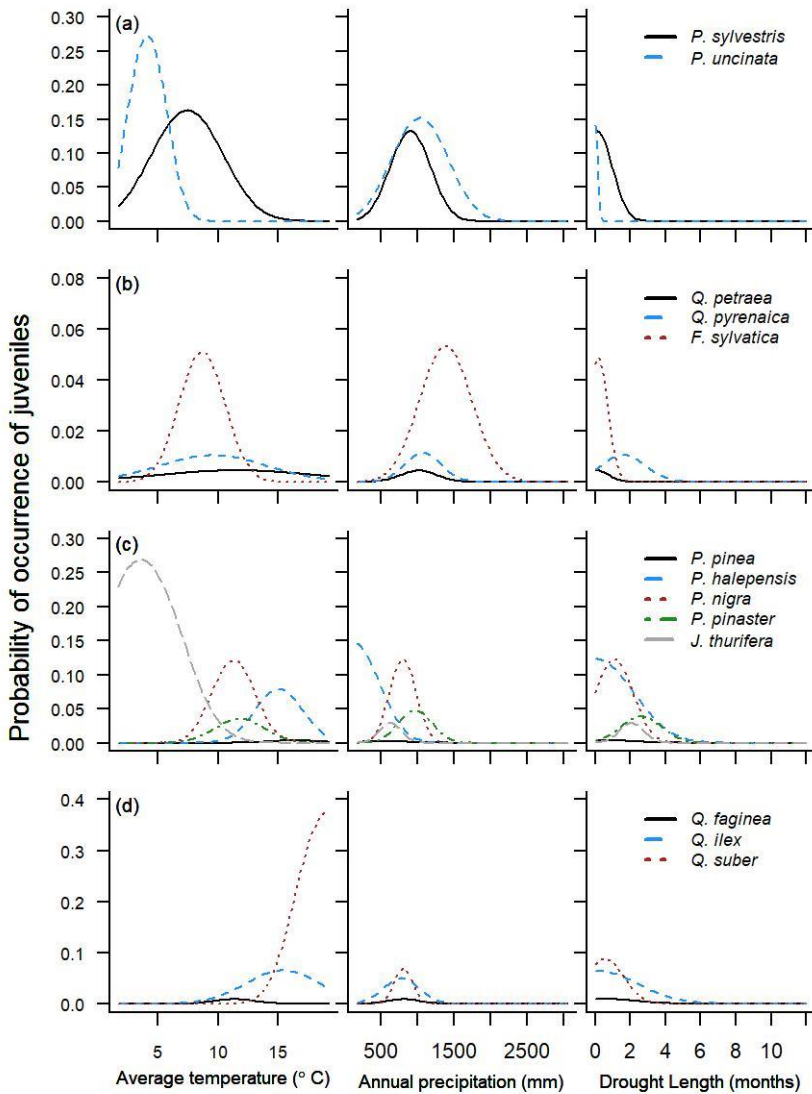
609 **Figure 2** Model observed (black) versus predicted (blue, offset 0.01 to the left for visual clarity)  
 610 juvenile stem counts, shown along gradients of conspecific and heterospecific crown area index  
 611 ( $CAI_{sp}$  and  $CAI_{all} - CAI_{sp}$ , eqn 4), for *P. halepensis* and *Q. ilex*. Model output and data plotted in  
 612 bins representing 10% of plots, except where bins overlapped (for species with high numbers of  
 613 monospecific plots), where bins are combined. Error bars represent 95% range (all species are  
 614 shown in supporting information Fig. S4).



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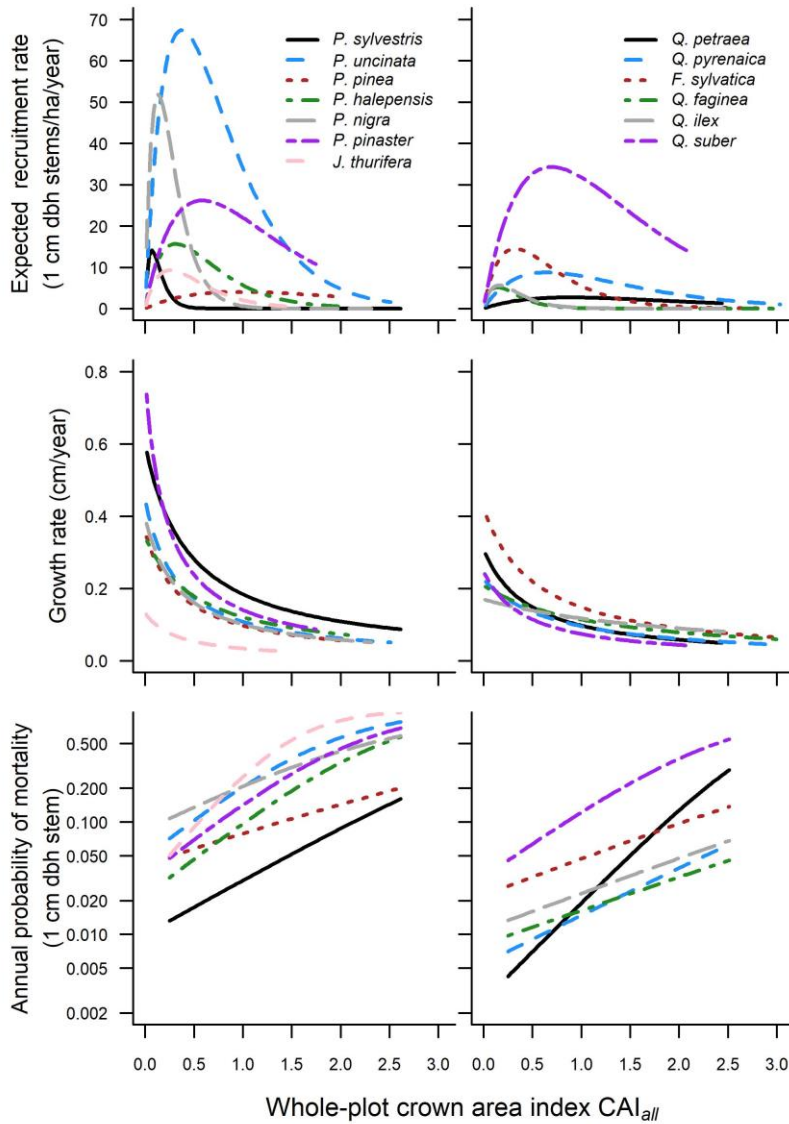
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617 **Figure 3** Fitted probability of occurrence of juveniles across whole-data gradients of predictor  
 618 variables for species of (a) temperate conifer, (b) temperate angiosperm, (c) Mediterranean conifer  
 619 and (d) Mediterranean angiosperm (note differences in y-axis ranges for different species  
 620 groupings). For each variable, species' probabilities of recruitment are plotted using constant  
 621 values for the other two variables, which are set at the species' average values (supporting  
 622 information Table S12).



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627 **Figure 4** Predicted rate of recruitment, growth and mortality for stems of 1 cm DBH across the  
 628 observed range of total plot crown area for the species, for (column 1) conifer, and (column 2)  
 629 angiosperm species. For each species, rates are calculated in the centre of the observed climatic  
 630 range (calculated from the central 90% of the data see supporting information Table S12), with  
 631 fixed conspecific canopy area set at the mean observed conditions.



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635 **Supplementary materials**

636

637 *MCMC algorithm for fitting crown allometry and small adult growth and mortality rates*

638

639 We estimated parameters and credible intervals (CIs) of models of crown diameter, individual tree  
640 growth and annual mortality (described below) using an adaptive MCMC Metropolis algorithm (Lee  
641 1997; Gelman, Roberts & Gilks 1999). We fitted several different functional forms for each model  
642 and compared them using the Akaike information criterion (Akaike, 1974). The MCMC algorithm  
643 compares parameter values using the log-likelihood of the data given the model. At each iteration  
644 the algorithm selects a parameter to alter and recalculates the likelihood. If the new parameter  
645 improves the likelihood then it is accepted by the algorithm. If not, it is accepted with probability of  
646 the ratio of the new and old likelihoods. In this way it returns not only a best-fit value for each  
647 parameter given the data but also estimates its distribution. The algorithm has two periods: burn-in  
648 and sampling. During the burn-in period the algorithm alters the search range ("jumping distance")  
649 of each parameter value to achieve an optimal acceptance ratio of 25% (Gelman, Roberts & Gilks  
650 1999). After the burn-in period, the jumping distance is fixed (separately for each parameter). During  
651 sampling parameter values are recorded every 100 iterations and the resulting parameter samples  
652 are taken as samples from the posterior distribution of each parameter. The resulting samples are  
653 then used to calculate mean and 95% confidence intervals for each parameter. We used uniform  
654 priors on all parameters, setting bounds much wider than expected parameter values, so that the  
655 MCMC algorithm needed to refer to the log-likelihood only (at U[-250, 250]). We used normalised  
656 mean annual temperature and mean annual precipitation values (taken from Gonzalo Jiménez,  
657 2008). All models were fitted using an adaptive Metropolis algorithm written in C. Convergence was  
658 checked using the Geweke diagnostic statistic (Geweke 1992), using a sampling period of 500,000  
659 iterations of the algorithm and testing means of the initial 10% and final 50% of the chain.

660

661 *Competitive environment: crown diameter allometry and calculation of crown metric CAI*

662

663 We expected recruitment to be positively correlated with conspecific adult density (potential parent  
664 trees) and negatively with aboveground competition for light, so we generated metrics to describe  
665 these factors, choosing crown area to represent both. For each plot we defined two values to  
666 represent conspecifics adult density and aboveground competition for light; the crown cover of adults  
667 of all species of interest ( $CAI_{sp}$ , m<sup>2</sup>/ha) and of all adults on the plot ( $CAI_{all}$ ), using species-specific  
668 crown width allometric equations derived from data collected from the second inventory. We  
669 calculated  $CAI_{all}$  and  $CAI_{sp}$  for all plots in both inventories, to quantify change in canopy area over  
670 time.

671 We parameterised models of crown diameter (CD) as a function of stem size (DBH) and  
672 climate for each species in order to calculate the crown area of adults in each plot, both in total and  
673 of each species individually, and checked convergence using the Geweke diagnostic statistic  
674 (Geweke 1992). We used a subset of the IFN2 database in which two measurements of crown  
675 diameter were recorded for around four trees of particular silvicultural interest in each plot. The  
676 number of measurements for each species is shown in Table S1. We parameterised DBH-CD  
677 equations using adaptive MCMC for the 30 species with more than 50 trees measurements in the  
678 data (in total >200,000 measurements), which accounted for >90% of the data. We tested a set of  
679 models (see Table S2 for functional forms tested) for crown diameter as a function of stem size and  
680 climate and selected the best model as the best for the most species and data (model 10, see Table  
681 S2).

682 For each tree we used these functions to use to calculate the total crown area of all taller  
683 trees in each plot,  $CAI_h$ , and the crown area of all conspecifics,  $CAI_{sp}$  in the plot. We also calculated

684 the crown area of all trees in each plot,  $CAI_{all}$ . Observed and predicted crown diameters are shown  
 685 for each of the 30 fitted species in Fig. S1. For species lacking allometric data we estimated the  
 686 crown diameter-stem diameter relationship by either using the allometric equation of the single most  
 687 closely related species or by averaging the allometric parameters of all the most closely related  
 688 species if there was more than one at the closest distance (determined according to a phylogenetic  
 689 tree created using the software Phylomatic, Webb & Donoghue 2005, see Table S3).

690  
 691 *Construction of priors for growth and mortality functions*

692  
 693 To construct priors for the growth and mortality functions within the ABC algorithm we fitted models  
 694 to data of small trees from the Spanish Forest Inventory. We selected plots that had been measured  
 695 in both the second (IFN2) and third (IFN3) inventories and fitted models to trees that had stem  
 696 diameter (DBH) < 10 cm in the IFN2, excluding individuals whose mortality was human induced. We  
 697 fitted models to 16 species with >100 individual stems for both growth and mortality. All models were  
 698 species specific, with parameters fitted separately for each species.

699 Growth and mortality rates of trees are strongly size dependent, with growth increasing and  
 700 mortality decreasing with size (e.g. Kunstler et al., 2009; Lines et al., 2010; Coomes et al., 2012).  
 701 We compared three candidate models for growth and three candidate models for mortality using  
 702 initial stem size (DBH<sub>1</sub>) and competition measured as crown area of all taller trees, CAI<sub>h</sub>, in the plot  
 703 (see Tables S4 and S5 for the model functional forms). For both growth and mortality, we tested a  
 704 constant rate model, a size dependent model and a size and competition dependent model. We  
 705 tested whether the effect of competition was important for growth using a functional form from  
 706 Coomes et al. (2012) and a simple linear model for mortality. We modelled annual growth by fitting  
 707 a model for the stem diameter measured in the IFN3 (DBH<sub>2</sub>) as a function of the initial stem diameter  
 708 measured in the IFN2 (DBH<sub>1</sub>) and the growth rate using:

709 
$$DBH_2 \sim N(DBH_1 + tGR, \omega_0^2) \quad (\text{eqn S1})$$

710 where GR is the predicted annual growth rate, t is the time interval (average 9 years) and  $\omega_0$  is the  
 711 standard deviation, estimated by the model.

712 We modelled the annual probability of mortality using a logistic function:

713 
$$P(\text{mortality}) = 1 / (1 + \exp(-k)) \quad (\text{eqn S2})$$

714 with corresponding likelihood:

715 
$$\text{likelihood of data given model} = \begin{cases} [1 - P(\text{mortality})]^t & \text{if tree survived} \\ 1 - [1 - P(\text{mortality})]^t & \text{if tree died} \end{cases}$$

716 We compared a set of models with different functional for k and selected the best fit model according  
 717 to AIC (see Tables S4 and S5, for model functional forms and AIC scores for growth and mortality  
 718 respectively).

720 *Model fit results of growth and mortality model MCMC parameterisation*

721  
 722 We compared three models for both annual growth and annual mortality rates (Tables S4 and S5),  
 723 and checked convergence using the Geweke diagnostic statistic (Geweke 1992). We calculated AIC  
 724 values to compare models for each species individually. For both growth and mortality the best fit  
 725 models for all species included the effects of both stem size and competition (model 2 in Tables S4  
 726 and S5), so we used these functional forms in the recruitment model. Individual species' parameter  
 727 values and their corresponding 95% CIs for these two models are shown in Table S6 and S7.  
 728 Predicted and observed values for DBH<sub>2</sub>, fitted using model 2 in Table S4, are shown in Fig. S2.  
 729 Predicted and observed values for annual mortality rate, fitted using model 2 in Table S5, are shown  
 730 in Fig. S3. Predicted growth and mortality rates for each species plotted against DBH and against  
 731 the range of values of  $CAI_{all}$  in which it is found are shown in Fig. 3.





733 **Table S1** Amount of field data for each species used to estimate DBH-crown diameter allometric  
 734 equations.

<b>Species Name</b>	<b>Count</b>
<i>Abies alba</i>	631
<i>Abies pinsapo</i>	63
<i>Castanea sativa</i>	4659
<i>Chamaecyparis lawsoniana</i>	177
<i>Eucalyptus camaldulensis</i>	1972
<i>Eucalyptus globules</i>	7127
<i>Eucalyptus nitens</i>	143
<i>Fagus sylvatica</i>	10292
<i>Larix spp.</i>	409
<i>Picea abies</i>	59
<i>Pinus halepensis</i>	30046
<i>Pinus nigra</i>	18455
<i>Pinus pinaster</i>	38086
<i>Pinus pinea</i>	8970
<i>Pinus radiata</i>	6609
<i>Pinus sylvestris</i>	28093
<i>Pinus uncinata</i>	2720
<i>Platanus spp.</i>	115
<i>Populus alba</i>	97
<i>Populus nigra</i>	1817
<i>Pseudotsuga menziesii</i>	172
<i>Quercus canariensis</i>	417
<i>Quercus faginea</i>	7845
<i>Quercus ilex</i>	36945
<i>Quercus petraea</i>	3660
<i>Quercus pyrenaica</i>	11832
<i>Quercus robur</i>	7958
<i>Quercus rubra</i>	304
<i>Quercus suber</i>	8693
<i>Robinia pseudoacacia</i>	214

735

736

737 **Table S2** Tested models of crown diameter (CD) as a function of stem size (DBH), drought length  
738 (DL), average annual temperature (AvT) and annual precipitation (PA), and the number of  
739 parameters in each model. Parameters fitted are denoted p0-p6. Average temperature and annual  
740 precipitation were normalised to aid convergence (using annual precipitation mean = 862, standard  
741 deviation = 378, average temperature mean = 12, standard deviation = 3). The number of parameters  
742 of each model, its AIC score, rank, and the number of species and percentage of the data for which  
743 it was the best model are shown. The model selected for use is shown in bold.

Model	Description	# parameters	AIC	AIC rank	# species' best model	% data best model
<b>0</b>	<b>CD ~ N(p<sub>1</sub>+p<sub>2</sub>DBH, p<sub>0</sub>)</b>	3	5593348	11	1	0.07
1	CD ~ N(p <sub>2</sub> +p <sub>3</sub> DBH, p <sub>0</sub> +p <sub>1</sub> DBH)	4	5481178	7	5	16.92
2	CD ~ N(p <sub>1</sub> +p <sub>2</sub> DBH+p <sub>3</sub> DL, p <sub>0</sub> )	4	5584746	8	0	0.00
3	CD~N(p <sub>2</sub> +p <sub>3</sub> DBH+p <sub>4</sub> DL,p <sub>0</sub> +p <sub>1</sub> DBH)	5	5472071	3	0	0.00
4	CD~N(p <sub>1</sub> +p <sub>2</sub> DBH+p <sub>3</sub> AvT,p <sub>0</sub> )	4	5588356	9	0	0.00
5	CD~N(p <sub>2</sub> +p <sub>3</sub> DBH+p <sub>4</sub> AvT,p <sub>0</sub> +p <sub>1</sub> DBH)	5	5474664	5	2	1.98
6	CD~N(p <sub>1</sub> +p <sub>2</sub> DBH +p <sub>3</sub> PA,p <sub>0</sub> )	4	5590359	10	0	0.00
7	CD~N(p <sub>2</sub> +p <sub>3</sub> DBH+p <sub>4</sub> PA, p <sub>0</sub> +p <sub>1</sub> DBH)	5	5478742	6	4	3.34
8	CD~N(p <sub>2</sub> +p <sub>3</sub> DBH+p <sub>4</sub> DL+p <sub>5</sub> AvT, p <sub>0</sub> +p <sub>1</sub> DBH)	6	5466517	2	2	2.90
9	CD~N(p <sub>2</sub> +p <sub>3</sub> DBH+p <sub>4</sub> PA+p <sub>5</sub> AvT, p <sub>0</sub> +p <sub>1</sub> DBH)	6	5472122	4	5	19.92
<b>10</b>	<b>CD~N(p<sub>2</sub>+p<sub>3</sub>DBH+p<sub>4</sub>PA+p<sub>5</sub>AvT+p<sub>6</sub>DL, p<sub>0</sub>+p<sub>1</sub>DBH)</b>	7	5464760	1	12	54.87

744  
745

746 **Table S3** IFN species code, species genus and family, the number of plots the species was found  
 747 in, and the code of the species' crown diameter allometric equations used to calculate crown area  
 748 for the species (in bold if the species had its own equation), assigned using nearest phylogenetic  
 749 neighbour or neighbours, if there was more than one at the closest distance. If more than one  
 750 species' code is listed then the average of those species' parameters was used. For 93% of the data  
 751 we were able to use crown diameter equations fitted to the individual species' crown measurements.

IFN code	Species	Family	#Plots	IFN code(s) of species' allometric equation used to fit crown area.
31	<i>Abies alba</i>	Pinaceae	293	31
32	<i>Abies pinsapo</i>	Pinaceae	42	32
7	<i>Acacia spp.</i>	Mimosaceae	37	92
76	<i>Acer campestre</i>	Aceraceae	902	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,79,92
54	<i>Alnus glutinosa</i>	Betulaceae	618	41,42,43,44,45,46,47,48,71,72
88	<i>Apollonias barbujana</i>	Lauraceae	4	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,79,92
68	<i>Arbutus unedo</i>	Ericaceae	743	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,92
73	<i>Betula spp.</i>	Betulaceae	1424	41,42,43,44,45,46,47,48,71,72
91	<i>Buxus sempervirens</i>	Buxaceae	29	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,92
98	<i>Carpinus betulus</i>	Coryloideae	5	41,42,43,44,45,46,47,48,71,72
72	<i>Castanea sativa</i>	Fagaceae	2396	72
17	<i>Cedrus atlantica</i>	Pinaceae	17	21,22,23,24,25,26,28,31,32,33,34,35
13	<i>Celtis australis</i>	Ulmaceae	18	41,42,43,44,45,46,47,48,71,72
67	<i>Ceratonia siliqua</i>	Fabaceae	218	92
18	<i>Chamaecyparis lawsoniana</i>	Cupressaceae	76	18
9	<i>Cornus sanguinea</i>	Cornaceae	1	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,92
74	<i>Corylus avellana</i>	Betulaceae	433	41,42,43,44,45,46,47,48,71,72
15	<i>Crataegus spp.</i>	Rosaceae	328	41,42,43,44,45,46,47,48,71,72
36	<i>Cupressus sempervirens</i>	Cupressaceae	71	18
83	<i>Erica arborea</i>	Ericaceae	183	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,92
62	<i>Eucalyptus camaldulensis</i>	Myrtaceae	691	62
61	<i>Eucalyptus globulus</i>	Myrtaceae	3006	61
64	<i>Eucalyptus nitens</i>	Myrtaceae	69	64
5	<i>Euonymus europaeus</i>	Celastraceae	1	51,58
71	<i>Fagus sylvatica</i>	Fagaceae	3549	71
3	<i>Frangula alnus</i>	Rhamnaceae	7	41,42,43,44,45,46,47,48,71,72
55	<i>Fraxinus angustifolia</i>	Oleaceae	761	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,92
1	<i>Heberdenia bahamensis</i>	Myrsinaceae	2	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,79,92

65	<i>Ilex aquifolium</i>	Aquifoliaceae	446	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,92
82	<i>Ilex canariensis</i>	Aquifoliaceae	114	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,92
75	<i>Juglans regia</i>	Juglandaceae	98	41,42,43,44,45,46,47,48,71,72
37	<i>Juniperus communis</i>	Cupressaceae	832	18
39	<i>Juniperus phoenicea</i>	Cupressaceae	203	18
38	<i>Juniperus thurifera</i>	Cupressaceae	1588	18
35	<i>Larix spp.</i>	Pinaceae	173	35
94	<i>Laurus nobilis</i>	Lauraceae	139	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,79,92
12	<i>Malus sylvestris</i>	Rosaceae	32	41,42,43,44,45,46,47,48,71,72
81	<i>Myrica faya</i>	Myricaceae	202	41,42,43,44,45,46,47,48,71,72
87	<i>Ocotea phoetens</i>	Lauraceae	2	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,79,92
66	<i>Olea europaea</i>	Oleaceae	743	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,92
63	<i>Other/unknown eucalyptus species</i>	Myrtaceae	1	61,62,64
89	<i>Other/unknown laurel species</i>	Lauraceae	6	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,79,92
29	<i>Other/unknown pine species</i>	Pinaceae	7	21,22,23,24,25,26,28
59	<i>Other/unknown riparian species</i>	Unknown (Angiosperm Average)	6	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,79,92
90	<i>Other/unknown small trees</i>	Unknown (Angiosperm Average)	1	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,79,92
99	<i>Other/unknown species</i>	Unknown (Angiosperm Average)	252	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,79,92
84	<i>Persea indica</i>	Lauraceae	43	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,79,92
8	<i>Phillyrea latifolia</i>	Oleaceae	96	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,92
69	<i>Phoenix spp.</i>	Arecaceae	12	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,79,92
86	<i>Picconia excelsa</i>	Oleaceae	16	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,92
33	<i>Picea abies</i>	Pinaceae	34	33
27	<i>Pinus canariensis</i>	Pinaceae	1448	23,24,26
24	<i>Pinus halepensis</i>	Pinaceae	10893	24
25	<i>Pinus nigra</i>	Pinaceae	6988	25
26	<i>Pinus pinaster</i>	Pinaceae	12372	26
23	<i>Pinus pinea</i>	Pinaceae	3288	23
28	<i>Pinus radiata</i>	Pinaceae	2368	28
21	<i>Pinus sylvestris</i>	Pinaceae	9221	21
22	<i>Pinus uncinata</i>	Pinaceae	929	22
93	<i>Pistacia terebinthus</i>	Anacardiaceae	39	61,62,64

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79	<i>Platanus hispanica</i>	Platanaceae	72	79
51	<i>Populus alba</i>	Salicaceae	51	51
58	<i>Populus nigra</i>	Salicaceae	658	58
52	<i>Populus tremula</i>	Salicaceae	158	51,58
95	<i>Prunus spp.</i>	Rosaceae	324	41,42,43,44,45,46,47,48,71,72
34	<i>Pseudotsuga menziesii</i>	Pinaceae	80	34
16	<i>Pyrus spp.</i>	Rosaceae	30	41,42,43,44,45,46,47,48,71,72
47	<i>Quercus canariensis</i>	Fagaceae	220	47
44	<i>Quercus faginea</i>	Fagaceae	4373	44
45	<i>Quercus ilex</i>	Fagaceae	15714	45
42	<i>Quercus petraea</i>	Fagaceae	1695	42
43	<i>Quercus pyrenaica</i>	Fagaceae	4596	43
41	<i>Quercus robur</i>	Fagaceae	3821	41
48	<i>Quercus rubra</i>	Fagaceae	154	48
46	<i>Quercus suber</i>	Fagaceae	3537	46
4	<i>Rhamnus alaternus</i>	Rhamnaceae	11	41,42,43,44,45,46,47,48,71,72
96	<i>Rhus coriaria</i>	Anacardiaceae	4	61,62,64
92	<i>Robinia pseudoacacia</i>	Fabaceae	145	92
57	<i>Salix spp.</i>	Salicaceae	702	51,58
97	<i>Sambucus nigra</i>	Adoxaceae	47	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72, 92
78	<i>Sorbus spp.</i>	Rosaceae	492	41,42,43,44,45,46,47,48,71,72
53	<i>Tamarix spp.</i>	Tamaricaceae	7	41,42,43,44,45,46,47,48,51,58,61,62,64,71,72,92
14	<i>Taxus baccata</i>	Taxaceae	49	18
77	<i>Tilia spp.</i>	Malvaceae	123	61,62,64
56	<i>Ulmus minor</i>	Ulmaceae	246	41,42,43,44,45,46,47,48,71,72

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755 **Table S4** Set of species-specific growth models tested with corresponding maximum log-likelihoods  
 756 and AICs, and the number of species for which each model was the best fit (according to the AIC)  
 757 out of the thirteen in the analysis. Model 2 (shown in bold) provided the best fit for the largest number  
 758 of species, and was therefore chosen.

<b>Model number</b>	<b>Annual growth (GR in equation S1)</b>	<b>Max log likelihood</b>	<b># parameters</b>	<b>AIC</b>	<b># of species' best model</b>
<b>0</b>	$GR=\omega_1$	-54844.0	2	109740	0
<b>1</b>	$GR= \omega_1 DBH$	-54880.9	2	109813	0
<b>2</b>	$GR=\omega_1 DBH / (1+ \omega_2 CA/h)$	-52217.5	3	104513	13

759 **Table S5** Set of species-specific mortality models tested, with corresponding maximum log-  
 760 likelihoods and AICs, and the number of species for which each model was the best fit (according to  
 761 the AIC) out of the thirteen in the analysis. Model 2 (shown in bold) provided the best fit for the largest  
 762 number of species, and was therefore chosen.  
 763

<b>Model number</b>	<b>Annual probability of mortality P(mortality)=1/(1+exp(-k)) (equation S2)</b>	<b>Max log likelihood</b>	<b># of parameters</b>	<b>AIC</b>	<b># of species' best model</b>
<b>0</b>	$k=T_0$	-13147.1	1	26346.3	0
<b>1</b>	$k=T_0 +T_1 DBH$	-13127.5	2	26306.9	0
<b>2</b>	$k=T_0 +T_1 DBH +T_2 CA/h$	-12467.3	3	25012.6	13

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767 **Table S6** Parameter values and 95% confidence intervals for the chosen models for growth  
 768 (equation S1) for each of the thirteen species in the analysis (model 2 in table S4). Parameters  $\omega_1$   
 769 and  $\omega_2$  formed prior mean values for parameters  $p_3$  and  $p_4$  in eqn 7 (main manuscript).

<b>Species</b>	$\omega_0$	$\omega_1$	$\omega_2$
<i>Fagus sylvatica</i>	1.44 (1.39, 1.50)	0.0470 (0.0428, 0.0515)	0.000188 (0.000157, 0.000223)
<i>Juniperus thurifera</i>	1.32 (1.25, 1.40)	0.0215 (0.0191, 0.0241)	0.000311 (0.000176, 0.000475)
<i>Pinus halepensis</i>	2.10 (2.05, 2.15)	0.0387 (0.0369, 0.0405)	0.000180 (0.000154, 0.000207)
<i>Pinus nigra</i>	1.92 (1.88, 1.97)	0.0561 (0.0539, 0.0584)	0.000307 (0.000279, 0.000336)
<i>Pinus pinaster</i>	2.43 (2.43, 2.43)	0.0934 (0.0934, 0.0934)	0.000427 (0.000427, 0.000427)
<i>Pinus pinea</i>	2.52 (2.36, 2.69)	0.0670 (0.0600, 0.0747)	0.000279 (0.000205, 0.000366)
<i>Pinus sylvestris</i>	2.28 (2.24, 2.33)	0.0642 (0.0618, 0.0667)	0.000225 (0.000206, 0.000246)
<i>Pinus uncinata</i>	1.86 (1.75, 1.98)	0.0554 (0.0485, 0.0627)	0.000348 (0.000261, 0.000448)
<i>Quercus faginea</i>	1.10 (1.07, 1.13)	0.0203 (0.0195, 0.0212)	0.000084 (0.000069, 0.000101)
<i>Quercus ilex</i>	1.50 (1.48, 1.52)	0.0186 (0.0181, 0.0191)	0.000046 (0.000038, 0.000055)
<i>Quercus petraea</i>	1.98 (1.98, 1.98)	0.0364 (0.0364, 0.0364)	0.000201 (0.000201, 0.000201)
<i>Quercus pyrenaica</i>	1.42 (1.38, 1.45)	0.0268 (0.0257, 0.0280)	0.000133 (0.000115, 0.000151)
<i>Quercus suber</i>	1.58 (1.49, 1.69)	0.0347 (0.0287, 0.0414)	0.000228 (0.000136, 0.000339)

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771

772 **Table S7** Parameter values and 95% confidence intervals for the chosen models for mortality  
 773 (equation S2) for each of the thirteen species in the analysis (model 2 in table S5). Parameters  
 774 formed prior mean values for  $p_5$ ,  $p_6$  and  $p_7$  in eqn 8 (main manuscript).

Species	$T_0$	$T_1$	$T_2$
<i>Fagus sylvatica</i>	-3.645 (-5.460,-1.573)	-0.2528 (-0.4939,-0.0478)	0.000083 (0.000058,0.000106)
<i>Juniperus thurifera</i>	-2.973 (-5.782,-0.282)	-0.3757 (-0.6969,-0.0454)	0.000245 (0.000099,0.000371)
<i>Pinus halepensis</i>	-3.645 (-4.555,-2.653)	-0.1316 (-0.2457,-0.0273)	0.000158 (0.000131,0.000185)
<i>Pinus nigra</i>	-2.409 (-2.409,-2.409)	-0.3210 (-0.3210,-0.3210)	0.000076 (0.000076,0.000076)
<i>Pinus pinaster</i>	-3.028 (-3.817,-2.152)	-0.1128 (-0.2138,-0.0244)	0.000170 (0.000150,0.000189)
<i>Pinus pinea</i>	-2.243 (-3.786,-0.583)	-0.2087 (-0.3996,-0.0320)	0.000069 (0.000019,0.000120)
<i>Pinus sylvestris</i>	-4.743 (-5.352,-3.945)	-0.0726 (-0.1628,-0.0071)	0.000155 (0.000140,0.000170)
<i>Pinus uncinata</i>	-2.803 (-2.803,-2.803)	-0.1333 (-0.1333,-0.1333)	0.000175 (0.000175,0.000175)
<i>Quercus faginea</i>	-4.557 (-5.342,-3.337)	-0.0896 (-0.2312,-0.0053)	0.000086 (0.000053,0.000116)
<i>Quercus ilex</i>	-4.896 (-5.240,-4.357)	-0.0400 (-0.1027,-0.0021)	0.000079 (0.000062,0.000095)
<i>Quercus petraea</i>	-4.812 (-6.669,-1.669)	-0.2020 (-0.5699,-0.0126)	0.000198 (0.000140,0.000255)
<i>Quercus pyrenaica</i>	-3.933 (-4.577,-3.078)	-0.0820 (-0.1819,-0.0096)	0.000105 (0.000090,0.000120)
<i>Quercus suber</i>	-3.124 (-5.033,-0.849)	-0.2281 (-0.4831,-0.0199)	0.000141 (0.000071,0.000205)

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 776  
 777 **Table S8** Functional forms tested for the juvenile existence model, where  $P(\text{existence}) = \text{logistic}(k)$ .  
 778 Here AVT = average annual temperature (°C), AP = annual precipitation (mm/year) and DL = drought  
 779 length(months). (See main manuscript eqn 4).  
 780

Model	Number of parameters	Functional form
0	7	$k = a_0 + a_1 a_2 AVT - a_2 AVT^2 + a_3 a_4 AP - a_4 AP^2 + a_5 a_6 DL - a_6 DL^2$
1	3	$k = a_0 + a_1 a_2 AVT - a_2 AVT^2$
2	3	$k = a_0 + a_1 a_2 AP - a_2 AP^2$
3	3	$k = a_0 + a_1 a_2 DL - a_2 DL^2$
4	5	$k = a_0 + a_1 a_2 AVT - a_2 AVT^2 + a_3 a_4 AP - a_4 AP^2$
5	5	$k = a_0 + a_1 a_2 AVT - a_2 AVT^2 + a_3 a_4 DL - a_4 DL^2$
6	5	$k = a_0 + a_1 a_2 AP - a_2 AP^2 + a_3 a_4 DL - a_4 DL^2$

781



782 **Table S9** Number of parameters and AIC for all juvenile existence model forms (table S8). Lowest  
 783 values (best fit model) for each species are shown in bold. Model 0 (main manuscript eqn 4) was  
 784 chosen as it was judged the best for all but one species.  
 785

Model	0	1	2	3	4	5	6
Number of parameters	7	3	3	3	5	5	5
Species							
<i>P. sylvestris</i>	<b>10202.5</b>	11689.9	12091.7	11398.9	10949.8	10813.4	10606.4
<i>P. uncinata</i>	<b>1794.8</b>	1869.7	3339.1	3182.2	1835.5	1833.6	3025.3
<i>P. pinea</i>	<b>1156.3</b>	1172.0	1251.6	1273.3	1158.9	1181.3	1251.6
<i>P. halepensis</i>	<b>9656.1</b>	10291.3	10787.4	11651.1	9817.0	10343.6	10708.5
<i>P. nigra</i>	<b>9861.9</b>	11080.1	11099.2	11112.7	10054.0	10664.0	10314.5
<i>P. pinaster</i>	<b>5029.3</b>	5259.2	5387.2	5205.2	5216.6	5136.8	5099.3
<i>J. thurifera</i>	<b>2524.1</b>	2967.5	3090.1	2849.6	2658.9	2635.3	2748.9
<i>Q. petraea</i>	762.6	836.0	809.4	772.6	801.5	776.1	<b>758.8</b>
<i>Q. pyrenaica</i>	<b>1866.4</b>	1940.8	1903.6	1927.0	1878.7	1923.0	1867.4
<i>Q. faginea</i>	<b>3075.7</b>	3244.0	3290.3	3324.3	3084.4	3224.3	3177.9
<i>Q. ilex</i>	<b>7924.6</b>	8376.4	8224.8	8560.4	7997.8	8298.8	8206.2
<i>Q. suber</i>	<b>1209.9</b>	1653.0	1677.9	1822.4	1447.7	1315.9	1643.8
<i>F. sylvatica</i>	<b>2391.2</b>	2682.2	2673.0	2550.6	2481.3	2439.9	2509.1

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788 **Table S10.** Fitted parameter values (top) and standard deviations (bottom) for model 0 (see table  
789 S8), the chosen juvenile existence model.  
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Species	Posterior mean parameter value						
	$a_0$	$a_1$	$a_2$	$a_3$	$a_4$	$a_5$	$a_6$
<i>P. sylvestris</i>	-11.006	14.941	0.066	1.809	7.201	0.196	0.742
<i>P. uncinata</i>	-8.774	8.293	0.251	2.070	3.923	0.100	33.458
<i>P. pinea</i>	-36.531	32.838	0.113	1.077	4.156	1.347	0.186
<i>P. halepensis</i>	-30.870	30.143	0.133	0.241	4.350	0.052	0.120
<i>P. nigra</i>	-34.680	22.591	0.170	1.613	16.366	2.173	0.474
<i>P. pinaster</i>	-31.254	23.524	0.121	1.944	9.578	5.264	0.373
<i>J. thurifera</i>	-14.663	7.377	0.059	1.259	22.042	4.102	1.033
<i>Q. petraea</i>	-15.001	23.703	0.014	2.039	7.571	0.289	1.116
<i>Q. pyrenaica</i>	-16.825	18.828	0.024	2.155	8.116	3.254	0.313
<i>Q. faginea</i>	-33.643	22.715	0.180	1.628	9.944	0.691	0.151
<i>Q. ilex</i>	-20.592	30.710	0.054	1.565	8.600	0.102	0.095
<i>Q. suber</i>	-61.827	38.086	0.111	1.631	32.422	1.045	0.471
<i>F. sylvatica</i>	-21.784	17.370	0.141	2.792	4.062	0.361	1.829
Species	Posterior parameter standard deviation						
	$a_0$	$a_1$	$a_2$	$a_3$	$a_4$	$a_5$	$a_6$
<i>P. sylvestris</i>	0.392	0.382	0.004	0.024	0.439	0.082	0.049
<i>P. uncinata</i>	1.956	0.555	0.022	0.409	0.981	0.042	30.239
<i>P. pinea</i>	3.301	0.565	0.010	0.196	2.914	0.813	0.039
<i>P. halepensis</i>	1.180	0.314	0.006	0.043	0.258	0.044	0.008
<i>P. nigra</i>	1.101	0.143	0.009	0.013	0.583	0.097	0.039
<i>P. pinaster</i>	0.877	0.332	0.003	0.364	0.176	0.178	0.037
<i>J. thurifera</i>	0.922	2.341	0.011	0.040	3.623	0.167	0.129
<i>Q. petraea</i>	1.847	6.846	0.010	0.368	1.517	0.174	0.313
<i>Q. pyrenaica</i>	1.219	4.541	0.007	0.057	0.875	0.403	0.080
<i>Q. faginea</i>	0.950	0.224	0.007	0.044	0.885	0.394	0.037
<i>Q. ilex</i>	0.756	0.495	0.003	0.021	0.506	0.109	0.010
<i>Q. suber</i>	1.071	0.550	0.003	0.027	1.658	0.370	0.062
<i>F. sylvatica</i>	0.988	0.340	0.011	0.080	0.536	0.187	0.444

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793 **Table S11** Mean and 95% credible interval of juvenile growth and mortality parameters (eqn 6 and  
794 7) fitted by the ABC-SMC-AW method. Values for the recruitment parameters (eqn 5) are given in  
795 the main text.

Species	$p_3$	$p_4$	$p_5$	$p_6$	$p_7$
<i>P. sylvestris</i>	0.598 (0.343, 0.838)	2.247E-04 (1.329E-04, 3.098E-04)	-4.518 (-5.423, -3.537)	-0.077 (-0.112, -0.043)	1.126E-04 (4.189E-05, 1.841E-04)
<i>P. uncinata</i>	0.447 (0.282, 0.603)	3.122E-04 (1.845E-04, 4.370E-04)	-2.837 (-3.536, -2.237)	-0.192 (-0.192, -0.070)	1.615E-04 (9.611E-05, 2.259E-04)
<i>P. pinea</i>	0.356 (0.162, 0.576)	2.666E-04 (1.531E-04, 3.797E-04)	-2.901 (-3.599, -2.199)	-0.286 (-0.286, -0.162)	6.678E-05 (3.364E-05, 9.778E-05)
<i>P. halepensis</i>	0.343 (0.309, 0.379)	1.837E-04 (1.637E-04, 2.033E-04)	-3.668 (-4.049, -3.256)	-0.149 (-0.149, -0.118)	1.566E-04 (1.381E-04, 1.752E-04)
<i>P. nigra</i>	0.398 (0.248, 0.565)	2.942E-04 (1.628E-04, 4.358E-04)	-2.060 (-2.544, -1.587)	-0.447 (-0.447, -0.190)	1.040E-04 (7.225E-05, 1.364E-04)
<i>P. pinaster</i>	0.781 (0.446, 1.103)	4.551E-04 (2.810E-04, 6.326E-04)	-3.280 (-4.208, -2.474)	-0.158 (-0.158, -0.064)	1.595E-04 (9.098E-05, 2.344E-04)
<i>J. thurifera</i>	0.132 (0.073, 0.213)	2.913E-04 (1.827E-04, 4.001E-04)	-3.170 (-3.816, -2.541)	-0.529 (-0.529, -0.238)	2.466E-04 (1.300E-04, 3.624E-04)
<i>Q. petraea</i>	0.309 (0.182, 0.431)	2.162E-04 (1.347E-04, 2.967E-04)	-5.763 (-6.978, -4.407)	-0.289 (-0.289, -0.119)	2.019E-04 (1.130E-04, 2.852E-04)
<i>Q. pyrenaica</i>	0.226 (0.141, 0.312)	1.360E-04 (8.809E-05, 1.857E-04)	-5.115 (-6.052, -4.142)	-0.108 (-0.108, -0.054)	9.944E-05 (5.926E-05, 1.393E-04)
<i>Q. faginea</i>	0.208 (0.149, 0.265)	8.268E-05 (5.124E-05, 1.147E-04)	-4.720 (-6.917, -2.829)	-0.125 (-0.125, -0.032)	7.001E-05 (2.837E-05, 1.114E-04)
<i>Q. ilex</i>	0.170 (0.120, 0.215)	4.524E-05 (3.080E-05, 6.070E-05)	-4.452 (-6.055, -3.360)	-0.052 (-0.052, -0.030)	7.485E-05 (4.729E-05, 1.032E-04)
<i>Q. suber</i>	0.248 (0.141, 0.366)	2.334E-04 (1.285E-04, 3.310E-04)	-3.165 (-3.980, -2.490)	-0.331 (-0.331, -0.146)	1.428E-04 (8.702E-05, 1.967E-04)
<i>F. sylvatica</i>	0.422 (0.269, 0.572)	1.845E-04 (1.015E-04, 2.689E-04)	-3.504 (-4.747, -2.330)	-0.392 (-0.392, -0.157)	7.740E-05 (4.025E-05, 1.168E-04)

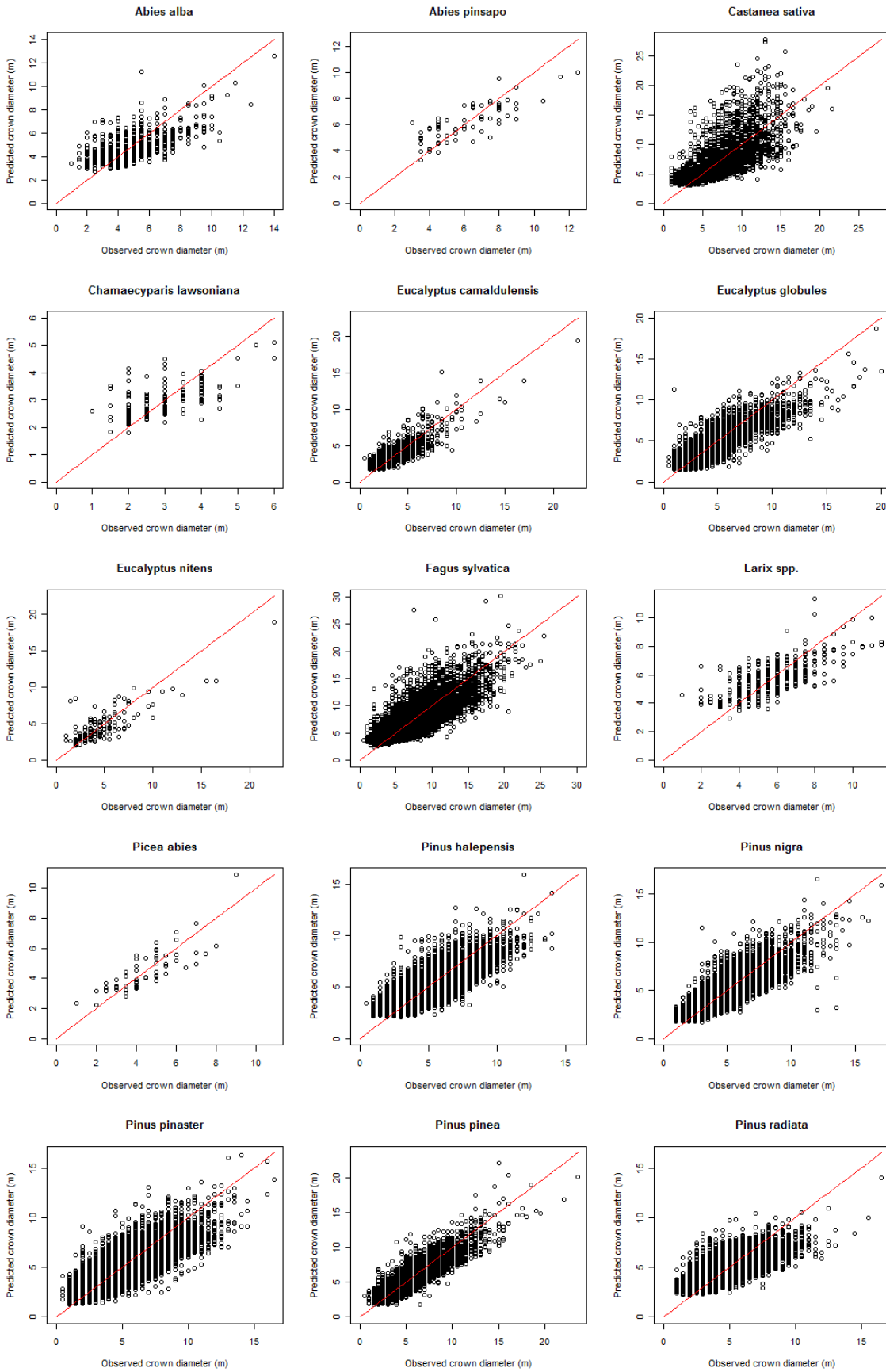
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798 **Table S12** Species average climatic conditions, calculated at the centre of the central 90% of their  
799 climatic ranges, and the average competitive conditions in the second forest inventory (average  
800  $CAI_{sp}$  and  $CAI_{all}$  in IFN2) from all plots used in the juvenile analysis.

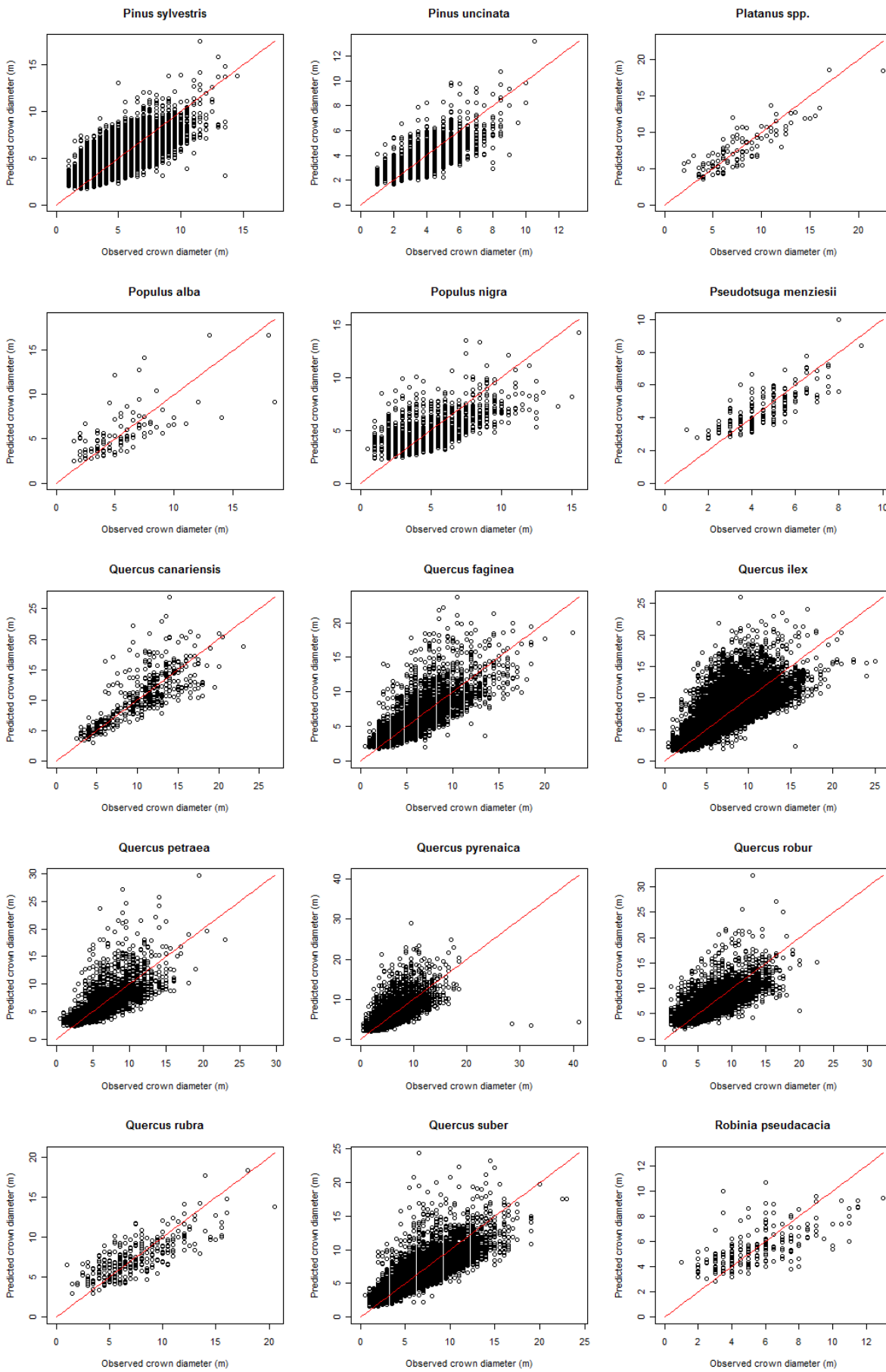
Species	Average annual temperature (°C)	Average annual precipitation (mm/year)	Average drought length (months)	Average $CAI_{sp}$	Average $CAI_{all}$
<i>P. sylvestris</i>	9.35	1022.33	0.76	0.21	0.40
<i>P. uncinata</i>	6.40	1233.13	0.00	0.16	0.32
<i>P. pinea</i>	13.80	678.53	1.91	0.08	0.16
<i>P. halepensis</i>	13.80	621.20	2.06	0.14	0.26
<i>P. nigra</i>	10.85	812.00	1.30	0.15	0.29
<i>P. pinaster</i>	12.20	860.30	1.60	0.12	0.24
<i>J. thurifera</i>	10.56	699.60	1.96	0.05	0.09
<i>Q. petraea</i>	10.80	1018.40	0.67	0.14	0.29
<i>Q. pyrenaica</i>	11.70	976.60	1.36	0.18	0.35
<i>Q. faginea</i>	11.40	870.60	1.33	0.12	0.24
<i>Q. ilex</i>	12.75	803.00	1.93	0.13	0.25
<i>Q. suber</i>	14.65	784.20	1.92	0.12	0.23
<i>F. sylvatica</i>	9.25	1271.50	0.38	0.34	0.64

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802 **Figure S1** Observed (black dots) and predicted (red line) crown diameters for each of the 30 species  
803 for which we had >50 measurements in the dataset.

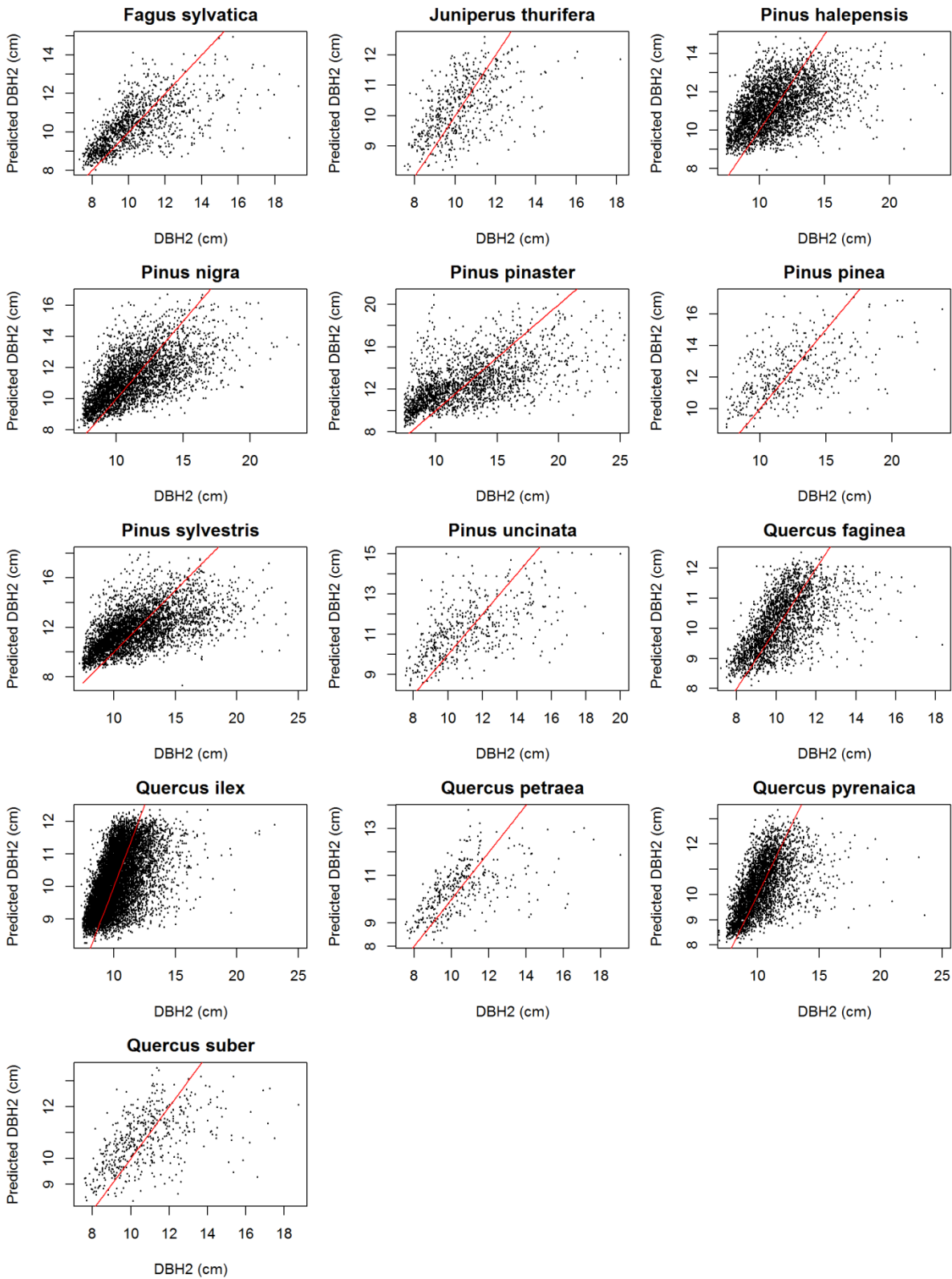


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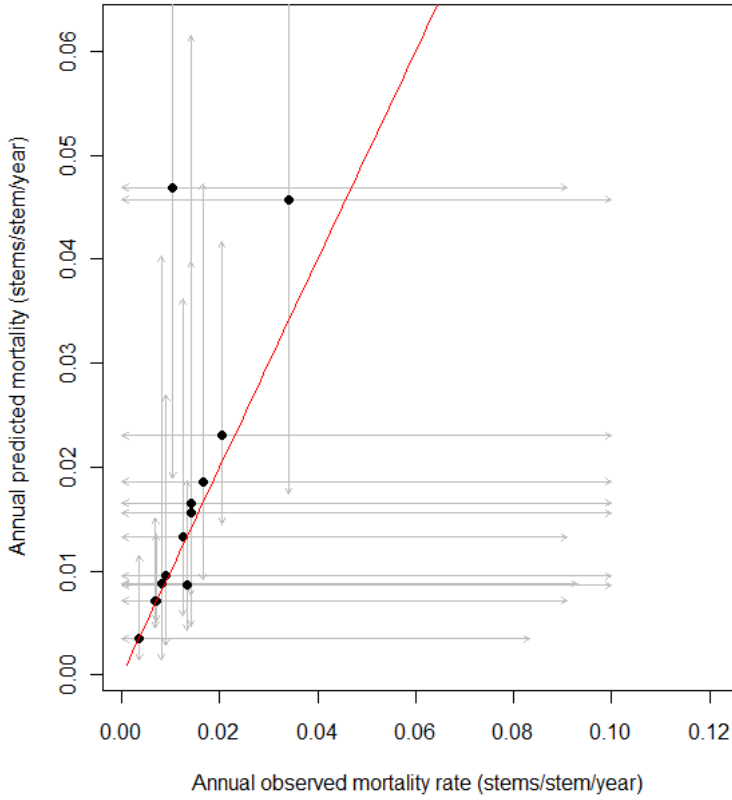
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807 **Figure S2** Predicted and observed diameters fitted using the chosen growth model (model 2 in table  
 808 S4). Growth was predicted separately for each species using initial stem size ( $DBH_1$ ) and  $CAI_{all}$ , and  
 809 final observed diameter ( $DBH_2$ ) is shown against predicted final diameter ( $pDBH_2$ ). The one to one  
 810 relationship is shown by the red line.



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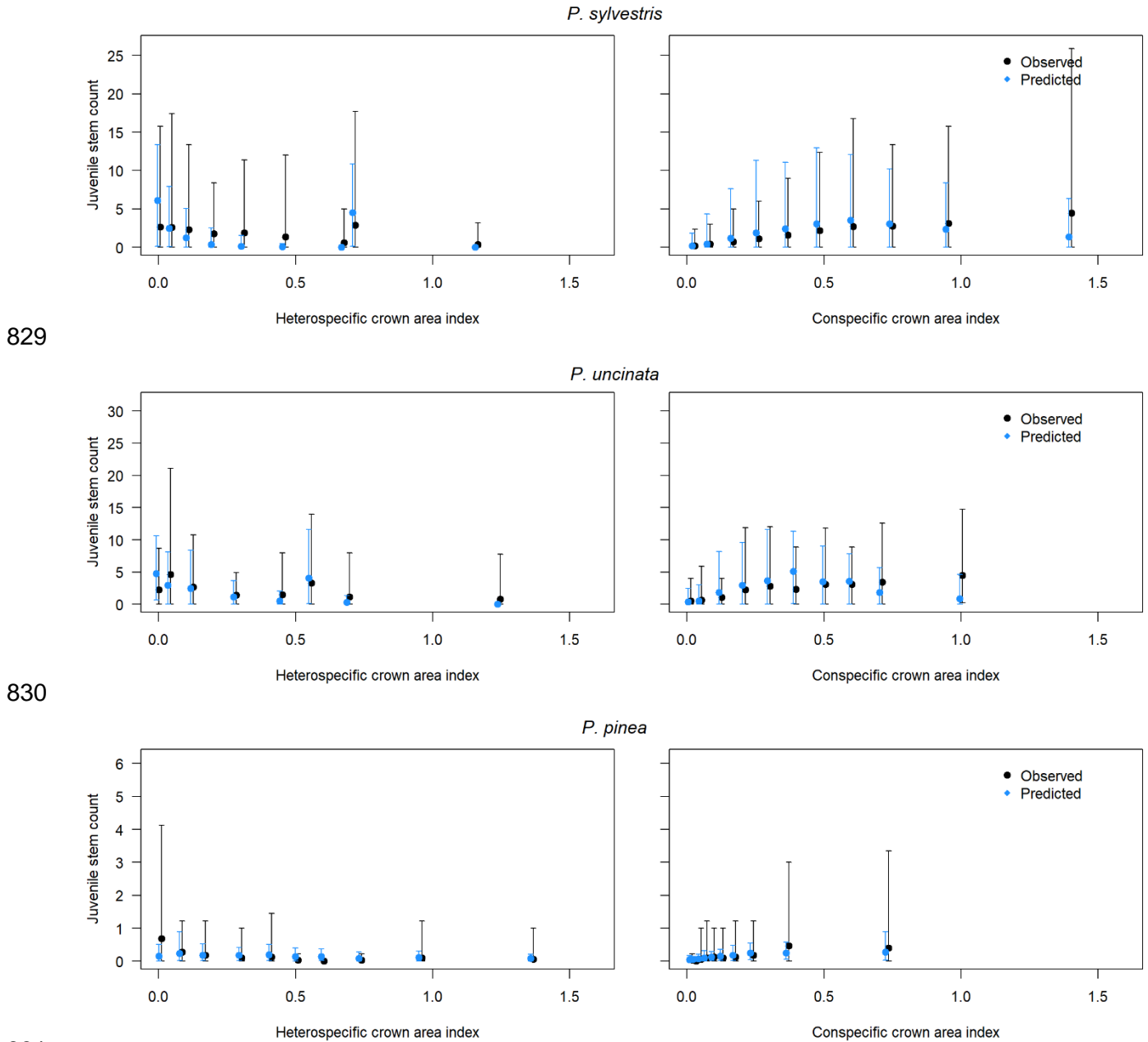
814 **Figure S3** Predicted and observed annual mortality fitted using the chosen mortality model (model  
815 2 in table S5). Mortality was predicted separately for each species using  $CAI_{all}$ , and average rates  
816 for each species are shown with their 95% credible intervals. The one to one relationship is shown  
817 by the red line.



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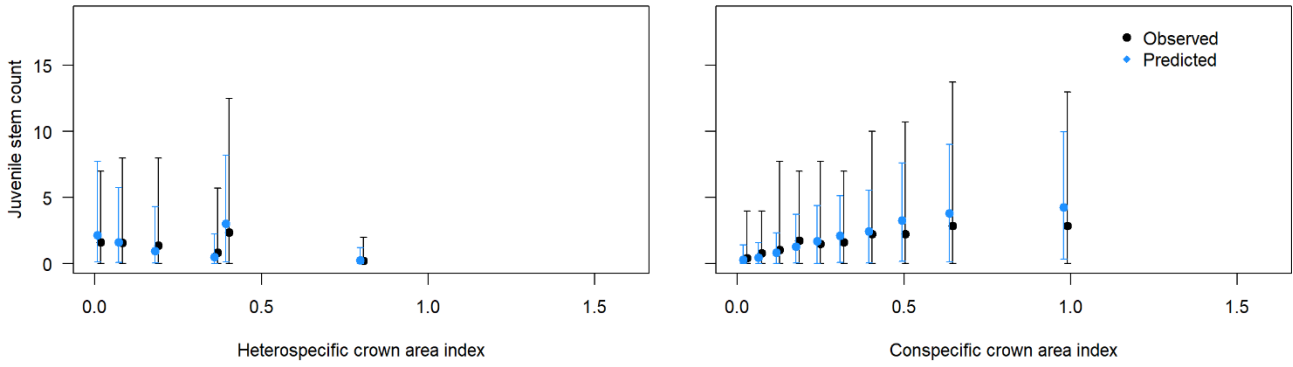


822 **Figure S4** Model predicted (blue) versus observed (black) juvenile stem counts, with data and  
 823 predictions shown along conspecific and heterospecific crown area index ( $CAI_{sp}$  and  $CAI_{all} - CAI_{sp}$  in  
 824 eqn 5 in the main manuscript). Both model and data are binned into even sized groups representing  
 825 10% of the plots, except where bins overlapped (for species with high numbers of monospecific  
 826 plots), where bins are combined, with model predictions (blue) offset by 0.01 to the left for visual  
 827 clarity. Error bars represent 95% range of observations and predictions.  
 828



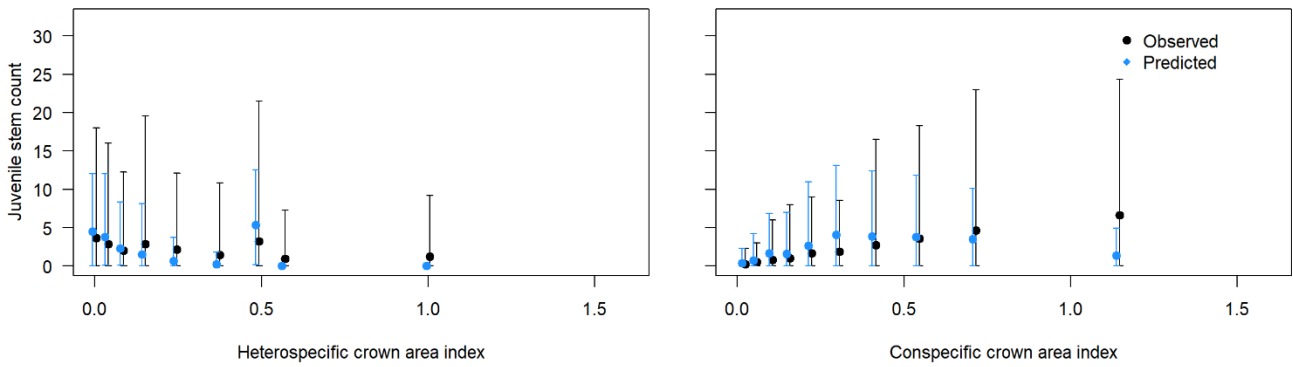
831

*P. halepensis*



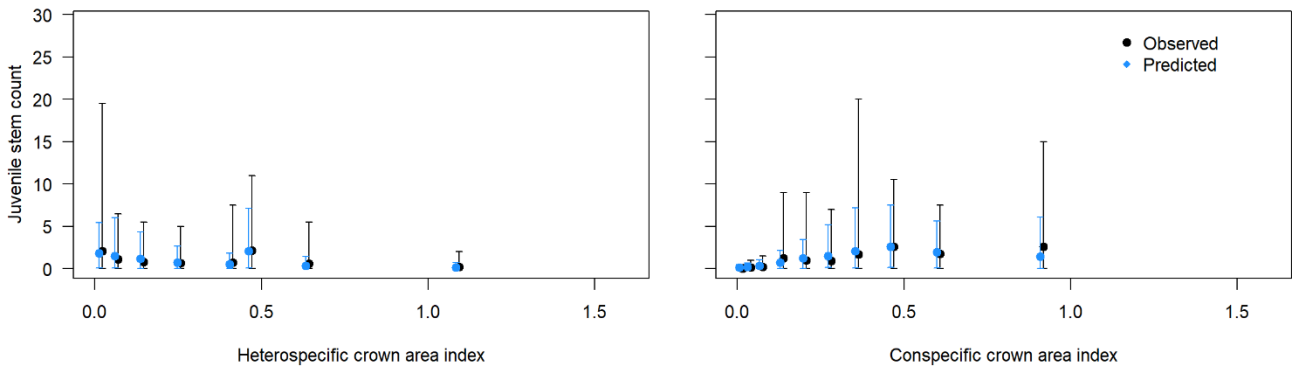
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*P. nigra*



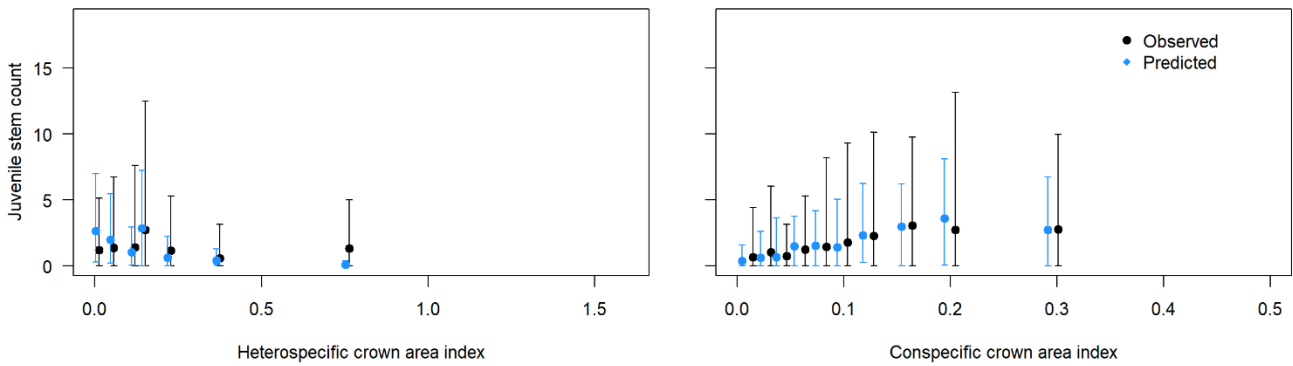
833

*P. pinaster*



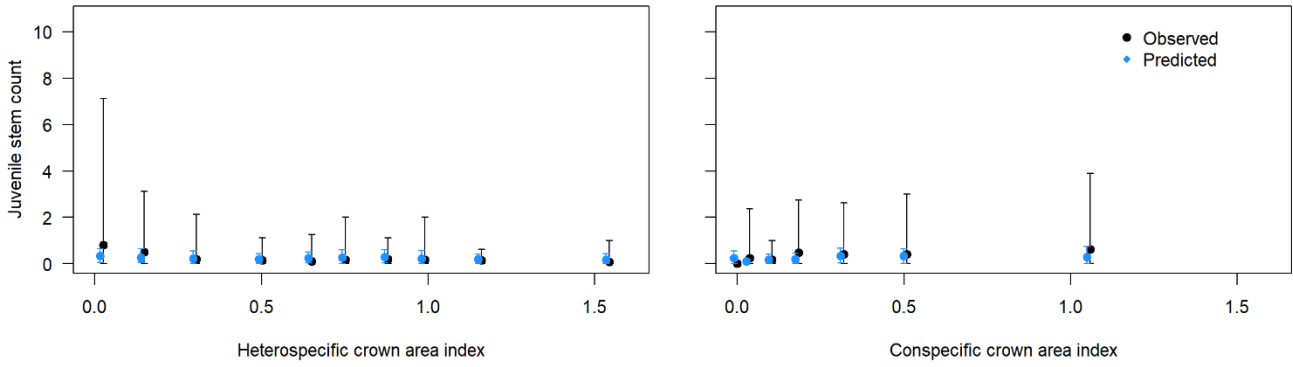
834

*J. thurifera*



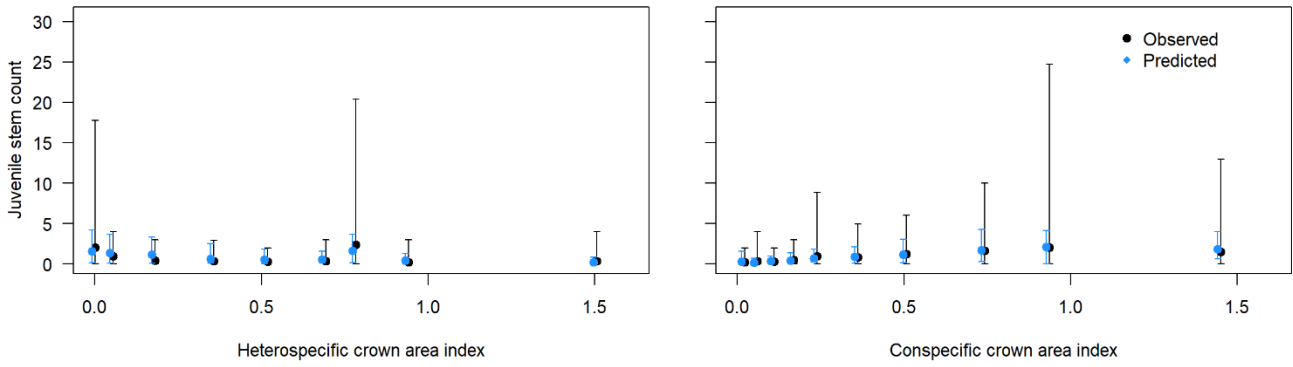
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*Q. petraea*



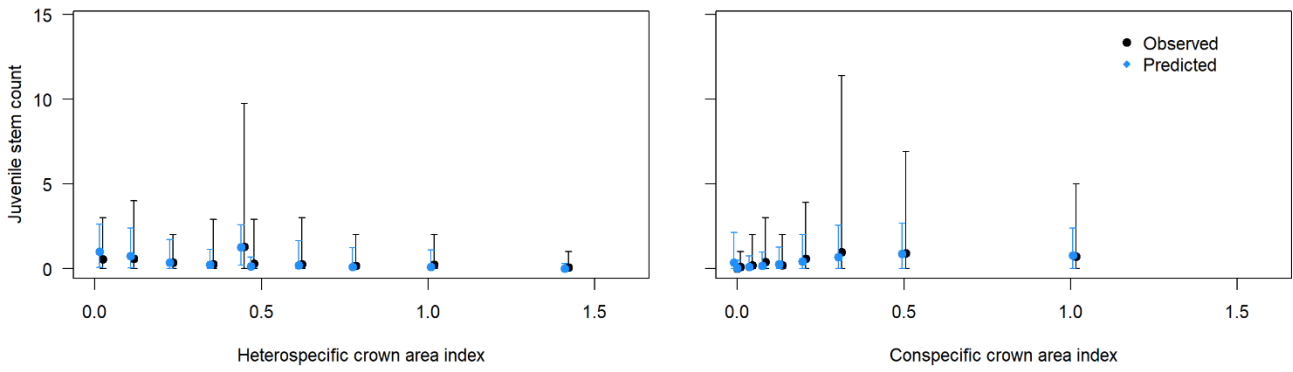
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*Q. pyrenaica*



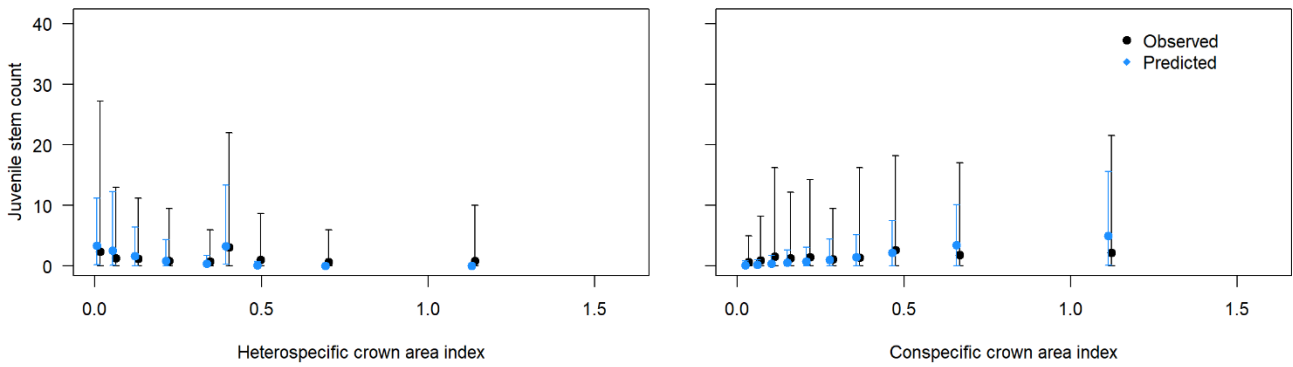
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*Q. faginea*



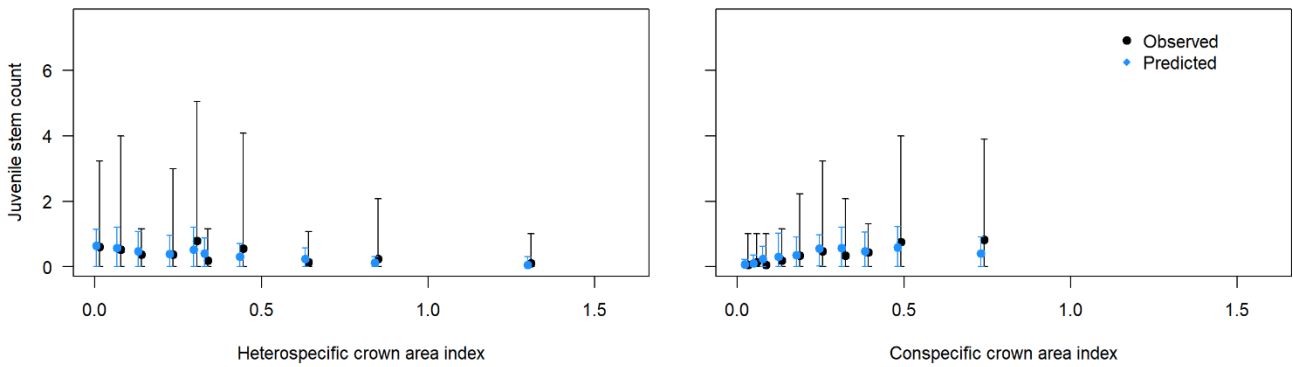
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*Q. ilex*



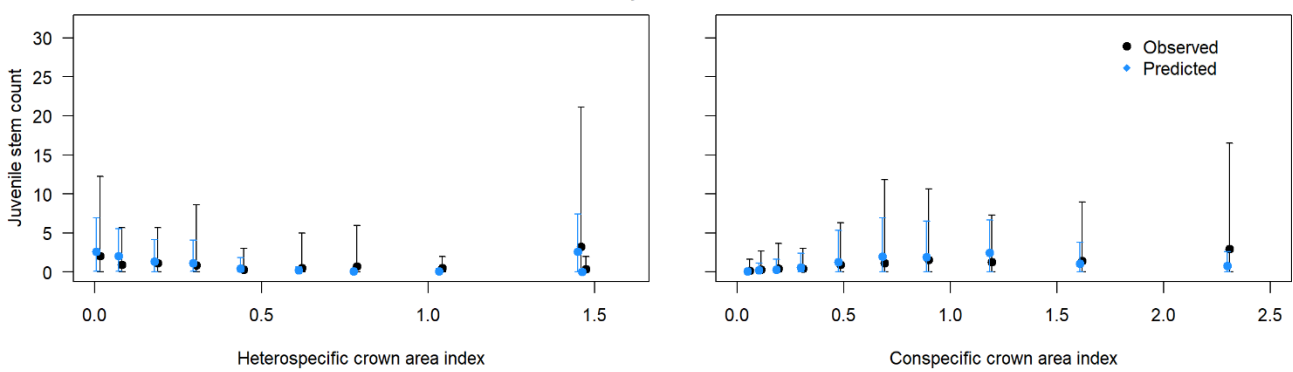
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*Q. suber*



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*F. sylvatica*



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