

# Surviving in a cosexual world: a cost-benefit analysis of dioecy in tropical trees Appendices

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These appendices contain detailed information on used methodology and results.

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# S1 Lists of species included in each vital rate analysis

Table S1.1: List of used species per vital rate analysis.

Abbreviation	Family	Genus	Species	$P_{\text{reproduction}}$	fecundity	$P_{\text{establishment}}$	Recruit distribution	Seedling survival	Seedling growth	$C_{\text{seedling}}$	Tree survival	Tree growth
ade1tr	Euphorbiaceae	<i>Adelia</i>	<i>triloba</i>								X	X
alchco	Euphorbiaceae	<i>Alchornea</i>	<i>costaricensi</i>	X		X	X	X	X	X	X	X
alibed	Rubiaceae	<i>Alibertia</i>	<i>edulis</i>			X		X	X	X	X	X
alsebl	Rubiaceae	<i>Alseis</i>	<i>blackiana</i>			X	X	X	X	X	X	X
andiin	Fabaceae	<i>Andira</i>	<i>inermis</i>								X	X
annoac	Annonaceae	<i>Annona</i>	<i>acuminata</i>								X	X
annosp	Annonaceae	<i>Annona</i>	<i>spraguei</i>								X	X
apeime	Tiliaceae	<i>Apeiba</i>	<i>membranacea</i>	X		X	X				X	X
apeiti	Tiliaceae	<i>Apeiba</i>	<i>tibourbou</i>	X								
aspicr	Apocynaceae	<i>Aspidosperma</i>	<i>spruceanum</i>	X		X		X	X	X	X	X
ast2gr	Anacardiaceae	<i>Astronium</i>	<i>graveolens</i>								X	X
beilpe	Lauraceae	<i>Beilschmiedia</i>	<i>pendula</i>			X	X	X	X	X	X	X
brosal	Moraceae	<i>Brosimum</i>	<i>alicastrum</i>	X		X	X	X	X	X	X	X
cappfr	Capparaceae	<i>Capparis</i>	<i>frondosa</i>			X	X	X	X	X	X	X
caseac	Flacourtiaceae	<i>Casearia</i>	<i>aculeata</i>								X	X
casear	Flacourtiaceae	<i>Casearia</i>	<i>arborea</i>								X	X
cassel	Rhizophoraceae	<i>Cassipourea</i>	<i>elliptica</i>			X	X	X	X	X	X	X
cecrin	Cecropiaceae	<i>Cecropia</i>	<i>insignis</i>	X	X	X	X	X	X	X	X	X
cecro	Cecropiaceae	<i>Cecropia</i>	<i>obtusifolia</i>	X							X	X
ceibpe	Bombacaceae	<i>Ceiba</i>	<i>pentandra</i>				X					
chr2ar	Sapotaceae	<i>Chrysophyllum</i>	<i>argenteum</i>			X	X	X	X	X	X	X
chr2ca	Sapotaceae	<i>Chrysophyllum</i>	<i>cainito</i>			X	X	X	X	X	X	X
cocco	Polygonaceae	<i>Coccoloba</i>	<i>coronata</i>								X	X
cocma	Polygonaceae	<i>Coccoloba</i>	<i>manzinellens</i>								X	X
cordal	Boraginaceae	<i>Cordia</i>	<i>alliodora</i>	X	X	X	X	X	X	X	X	X
cordbi	Boraginaceae	<i>Cordia</i>	<i>bicolor</i>	X	X	X	X	X	X	X	X	X
cou2cu	Rubiaceae	<i>Coussarea</i>	<i>curvigemma</i>	X	X	X	X	X	X	X	X	X
dendar	Araliaceae	<i>Dendropanax</i>	<i>arboreus</i>			X	X					
des2pa	Annonaceae	<i>Desmopsis</i>	<i>panamensis</i>	X	X	X	X	X	X	X	X	X
diptpa	Fabaceae	<i>Dipteryx</i>	<i>oleifera</i>	X	X			X	X			
drypst	Euphorbiaceae	<i>Drypetes</i>	<i>standleyi</i>			X	X	X	X	X	X	X
ery2pa	Erythroxylaceae	<i>Erythroxylum</i>	<i>panamense</i>								X	X
eugeco	Myrtaceae	<i>Eugenia</i>	<i>coloradoensis</i>			X		X	X	X	X	X
eugega	Myrtaceae	<i>Eugenia</i>	<i>galalonensis</i>				X	X	X	X	X	X
eugene	Myrtaceae	<i>Eugenia</i>	<i>nesiotica</i>			X		X	X	X	X	X
eugeoe	Myrtaceae	<i>Eugenia</i>	<i>oerstediana</i>	X		X	X	X	X	X	X	X
faraoc	Rubiaceae	<i>Faramea</i>	<i>occidentalis</i>	X		X	X	X	X	X	X	X
gar2in	Clusiaceae	<i>Garcinia</i>	<i>intermedia</i>	X		X	X	X	X	X	X	X
geniam	Rubiaceae	<i>Genipa</i>	<i>americana</i>			X	X					
guapst	Nyctaginaceae	<i>Guapira</i>	<i>standleyana</i>			X	X				X	X
guargu	Meliaceae	<i>Guarea</i>	<i>guidonia</i>	X		X	X	X	X	X	X	X
guatdu	Annonaceae	<i>Guatteria</i>	<i>dumetorum</i>			X	X				X	X
gustsu	Lecythidaceae	<i>Gustavia</i>	<i>superba</i>	X		X	X	X	X	X	X	X
hameax	Rubiaceae	<i>Hamelia</i>	<i>axillaris</i>								X	X

Table S1.1: List of used species per vital rate analysis.

Abbreviation	Family	Genus	Species	<i>P<sub>preproduction</sub></i>	fecundity	<i>P<sub>establishment</sub></i>	Recruit distribution	Seedling survival	Seedling growth	<i>C<sub>seedling</sub></i>	Tree survival	Tree growth
hampap	Malvaceae	<i>Hampea</i>	<i>appendiculata</i>			X	X				X	X
hassfl	Flacourtiaceae	<i>Hasseltia</i>	<i>floribunda</i>			X	X				X	X
heisac	Olacaceae	<i>Heisteria</i>	<i>acuminata</i>			X	X				X	X
heisco	Olacaceae	<i>Heisteria</i>	<i>concinna</i>			X	X	X	X	X	X	X
herrpu	Sterculiaceae	<i>Herrania</i>	<i>purpurea</i>								X	X
hirttr	Chrysobalanaceae	<i>Hirtella</i>	<i>triandra</i>	X	X	X	X	X	X	X	X	X
hybapr	Violaceae	<i>Hybanthus</i>	<i>prunifolius</i>			X	X	X	X	X	X	X
hyeral	Euphorbiaceae	<i>Hieronyma</i>	<i>alchorneoides</i>	X							X	X
ingago	Fabaceae	<i>Inga</i>	<i>goldmanii</i>								X	X
ingama	Fabaceae	<i>Inga</i>	<i>marginata</i>			X	X	X	X	X	X	X
ingaqu	Fabaceae	<i>Inga</i>	<i>nobilis</i>								X	X
ingasa	Fabaceae	<i>Inga</i>	<i>sapindoides</i>								X	X
ingaum	Fabaceae	<i>Inga</i>	<i>umbellifera</i>								X	X
jac1co	Bignoniaceae	<i>Jacaranda</i>	<i>copaia</i>	X	X	X	X				X	X
laciag	Flacourtiaceae	<i>Lacistema</i>	<i>aggregatum</i>				X	X	X	X	X	X
lacmpa	Apocynaceae	<i>Lacmellea</i>	<i>panamensis</i>			X	X				X	X
laetth	Flacourtiaceae	<i>Laetia</i>	<i>thamnia</i>								X	X
licahy	Chrysobalanaceae	<i>Licania</i>	<i>hypoleuca</i>								X	X
licapl	Chrysobalanaceae	<i>Licania</i>	<i>platypus</i>								X	X
loncla	Fabaceae	<i>Lonchocarpus</i>	<i>heptaphyllus</i>			X	X				X	X
luehse	Tiliaceae	<i>Luehea</i>	<i>seemannii</i>	X	X	X	X	X	X	X	X	X
malmsp	Annonaceae	<i>Mosannonna</i>	<i>garwoodii</i>	X							X	X
maquco	Moraceae	<i>Maquira</i>	<i>guianensis</i>								X	X
mourmy	Melastomataceae	<i>Mouriri</i>	<i>myrtilloides</i>	X	X	X	X	X	X	X	X	X
nectci	Lauraceae	<i>Nectandra</i>	<i>cissiflora</i>								X	X
ocotce	Lauraceae	<i>Ocotea</i>	<i>cernua</i>					X	X	X	X	X
olmeas	Moraceae	<i>Trophis</i>	<i>caucana</i>				X	X	X	X	X	X
ormoma	Fabaceae	<i>Ormosia</i>	<i>macrocalyx</i>								X	X
ouralu	Ochnaceae	<i>Ouratea</i>	<i>lucens</i>			X		X	X	X	X	X
paligu	Rubiaceae	<i>Palicourea</i>	<i>guianensis</i>			X	X	X	X	X	X	X
pentma	Rubiaceae	<i>Pentagonia</i>	<i>macrophylla</i>								X	X
perexa	Moraceae	<i>Perebea</i>	<i>xanthochyma</i>								X	X
phoeci	Lauraceae	<i>Cinnamomum</i>	<i>triplinerne</i>			X	X	X	X	X		
picrla	Simaroubaceae	<i>Picramnia</i>	<i>latifolia</i>			X	X	X	X	X	X	X
pipeco	Piperaceae	<i>Piper</i>	<i>cordulatum</i>				X					
pla1pi	Fabaceae	<i>Platymiscium</i>	<i>pinnatum</i>					X	X	X	X	X
pla2el	Fabaceae	<i>Platypodium</i>	<i>elegans</i>								X	X
poular	Moraceae	<i>Poulsenia</i>	<i>armata</i>		X							
poutre	Sapotaceae	<i>Pouteria</i>	<i>reticulata</i>	X	X	X	X	X	X	X	X	X
pri2co	Fabaceae	<i>Prioria</i>	<i>copaifera</i>	X						X	X	X
protpa	Burseraceae	<i>Protium</i>	<i>panamense</i>					X	X	X	X	X
protte	Burseraceae	<i>Protium</i>	<i>tenuifolium</i>	X	X	X	X	X	X	X	X	X
psycac	Rubiaceae	<i>Psychotria</i>	<i>acuminata</i>			X	X	X	X	X		
psycde	Rubiaceae	<i>Psychotria</i>	<i>deflexa</i>				X	X	X	X		
psycho	Rubiaceae	<i>Psychotria</i>	<i>horizontalis</i>			X	X	X	X	X	X	X
psycli	Rubiaceae	<i>Psychotria</i>	<i>limonensis</i>				X					
psycma	Rubiaceae	<i>Psychotria</i>	<i>marginata</i>			X	X	X	X	X	X	X

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Abbreviation	Family	Genus	Species	$P_{\text{production}}$	fecundity	$P_{\text{establishment}}$	Recruit distribution	Seedling survival	Seedling growth	$C_{\text{seedling}}$	Tree survival	Tree growth
psycra	Rubiaceae	<i>Psychotria</i>	<i>racemosa</i>			X	X	X	X	X		
pterro	Fabaceae	<i>Pterocarpus</i>	<i>rohrrii</i>								X	X
quaras	Bombacaceae	<i>Quararibea</i>	<i>asterolepis</i>	X	X	X	X	X	X	X	X	X
quasam	Simaroubaceae	<i>Quassia</i>	<i>amara</i>								X	X
randar	Rubiaceae	<i>Randia</i>	<i>armata</i>	X		X	X	X	X	X	X	X
simaam	Simaroubaceae	<i>Simarouba</i>	<i>amara</i>	X	X	X	X	X	X	X	X	X
sloate	Elaeocarpaceae	<i>Sloanea</i>	<i>terniflora</i>	X							X	X
soroaf	Moraceae	<i>Sorocea</i>	<i>affinis</i>			X	X	X	X	X	X	X
sponmo	Anacardiaceae	<i>Spondias</i>	<i>mombin</i>				X				X	X
sponra	Anacardiaceae	<i>Spondias</i>	<i>radlkoferi</i>					X	X	X	X	X
stylst	Myrsinaceae	<i>Stylogyne</i>	<i>turbacensis</i>				X	X	X	X	X	X
swars2	Fabaceae	<i>Swartzia</i>	<i>simplex</i> var					X	X	X		
sympgl	Clusiaceae	<i>Symphonia</i>	<i>globulifera</i>								X	X
tab1gu	Bignoniaceae	<i>Tabebuia</i>	<i>guayacan</i>			X	X					
tab1ro	Bignoniaceae	<i>Tabebuia</i>	<i>rosea</i>			X	X	X	X	X	X	X
tab2ar	Apocynaceae	<i>Tabernaemont</i>	<i>arborea</i>			X	X	X	X	X	X	X
tachve	Fabaceae	<i>Tachigali</i>	<i>versicolor</i>					X	X	X	X	X
termam	Combretaceae	<i>Terminalia</i>	<i>amazonia</i>	X								
termob	Combretaceae	<i>Terminalia</i>	<i>oblonga</i>	X	X							
tet2pa	Burseraceae	<i>Tetragastris</i>	<i>panamensis</i>	X		X	X	X	X	X	X	X
thevah	Apocynaceae	<i>Thevetia</i>	<i>ahouai</i>								X	X
tratas	Burseraceae	<i>Trattinnicki</i>	<i>aspera</i>	X								
tri2pa	Meliaceae	<i>Trichilia</i>	<i>pallida</i>	X		X	X				X	X
tri2tu	Meliaceae	<i>Trichilia</i>	<i>tuberculata</i>	X		X	X	X	X	X	X	X
tripcu	Polygonaceae	<i>Triplaris</i>	<i>cumingiana</i>	X	X	X	X				X	X
turpoc	Staphyleaceae	<i>Turpinia</i>	<i>occidentalis</i>								X	X
unonpi	Annonaceae	<i>Unonopsis</i>	<i>pittieri</i>	X		X	X	X	X	X	X	X
virose	Myristicaceae	<i>Virola</i>	<i>sebifera</i>	X	X	X	X	X	X	X	X	X
virosu	Myristicaceae	<i>Virola</i>	<i>surinamensis</i>								X	X
vochfe	Vochysiaceae	<i>Vochysia</i>	<i>ferruginea</i>			X	X					
xyllma	Annonaceae	<i>Xylopia</i>	<i>macrantha</i>	X				X	X		X	X
zantp1	Rutaceae	<i>Zanthoxylum</i>	<i>panamense</i>			X	X				X	X
total:				40	18	65	69	62	62	61	105	105

## S2 Trait distributions for each breeding system and each vital rate analysis

To ensure that that estimated effects of breeding system were not biased by differing trait or size distributions between breeding systems, we compared distributions of wood density (WD), seed mass (SM), adult stature ( $D_{max}$ ) and individual size between breeding systems for each vital rate. Recall that trait values were normalized accross all species in the BCI 50-ha FDP database, and seed mass and maximum size were log-transformed before normalization. Prior to normalization, mean seed mass was 0.0512 g, mean wood density was 0.548 g/cm<sup>3</sup>, and maximum size was 158 mm. Standard deviations were 0.95 (log-transformed), 0.15 and 0.51 (log transformed) for seed mass, wood density and maximum size respectively (Fig. S2.1).

In the figures below (Figs. S2.2-S2.7), the cumulative density distributions are given for seed mass, wood density, maximum DBH and size ranges, for each vital rate analysis for dioecious (thick lines) and hermaphroditic (thin lines) species. A summary of the differences in normalized trait values for the 25%, 50% and 75% quantiles of included species, for all vital rate analyses, is given in Table S2.1.

Table S2.1: Differences in normalized trait values between hermaphroditic and dioecious species, given for the 25%, 50% and 75% quantiles, for the species included in each vital rate analysis.  $p_{reproduction}$  is reproduction probability,  $p_{establishment}$  is seedling establishment,  $f_{dist}$  is recruit size distribution,  $p_{sdlgrowth}$  and  $p_{treegrowth}$  is seedling and tree growth,  $p_{sdlsurvival}$  and  $p_{treesurvival}$  is seedling and tree survival,  $x_{dbh}$  is the relation between seedling DBH and height.

Vital rate	Trait	25%	50%	75%
$f_{dist}$	WD	-0.464	-0.097	-0.027
$f_{dist}$	SM	-0.849	-0.395	-0.274
$f_{dist}$	$D_{max}$	-0.535	-0.154	0.088
$p_{establishment}$	WD	-0.22	-0.012	0.018
$p_{establishment}$	SM	-0.784	-0.075	-0.151
$p_{establishment}$	$D_{max}$	-0.384	-0.165	0.07
$p_{repr}$	WD	-0.3	0.287	0.337
$p_{repr}$	SM	-0.568	-0.066	-0.023
$p_{repr}$	$D_{max}$	-0.229	0.005	0.258
$p_{sdlgrowth}$ and $p_{sdlsurvival}$	WD	-0.045	-0.031	0.3
$p_{sdlgrowth}$ and $p_{sdlsurvival}$	SM	-0.709	-0.022	-0.116
$p_{sdlgrowth}$ and $p_{sdlsurvival}$	$D_{max}$	-0.341	-0.2	0.122
$p_{sdlgrowth}$ and $p_{sdlsurvival}$	size	0.018	0.031	0.017
$p_{treegrowth}$ and $p_{treesurvival}$	WD	-0.316	-0.056	0.101
$p_{treegrowth}$ and $p_{treesurvival}$	SM	-0.097	0.098	0.164
$p_{treegrowth}$ and $p_{treesurvival}$	$D_{max}$	-0.267	-0.099	-0.005
$p_{treegrowth}$ and $p_{treesurvival}$	size	-0.026	-0.067	-0.138
$x_{dbh}$	WD	-0.088	-0.157	-0.076
$x_{dbh}$	SM	-0.753	-0.051	-0.113
$x_{dbh}$	$D_{max}$	-0.402	-0.183	0.125
$x_{dbh}$	size	0.001	0.006	0.016

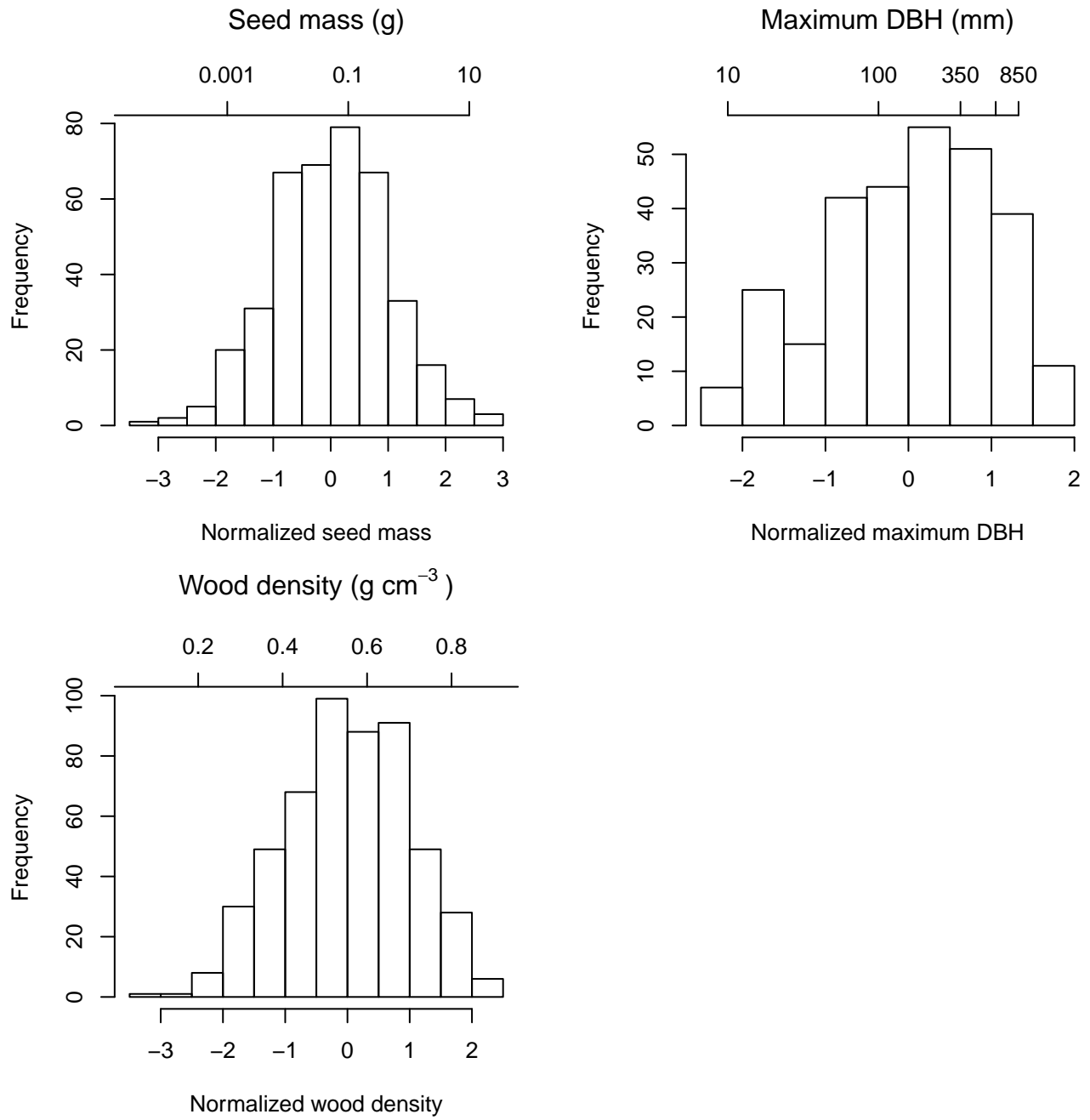


Figure S2.1: Histogram showing the distribution of each functional trait, combining all species.

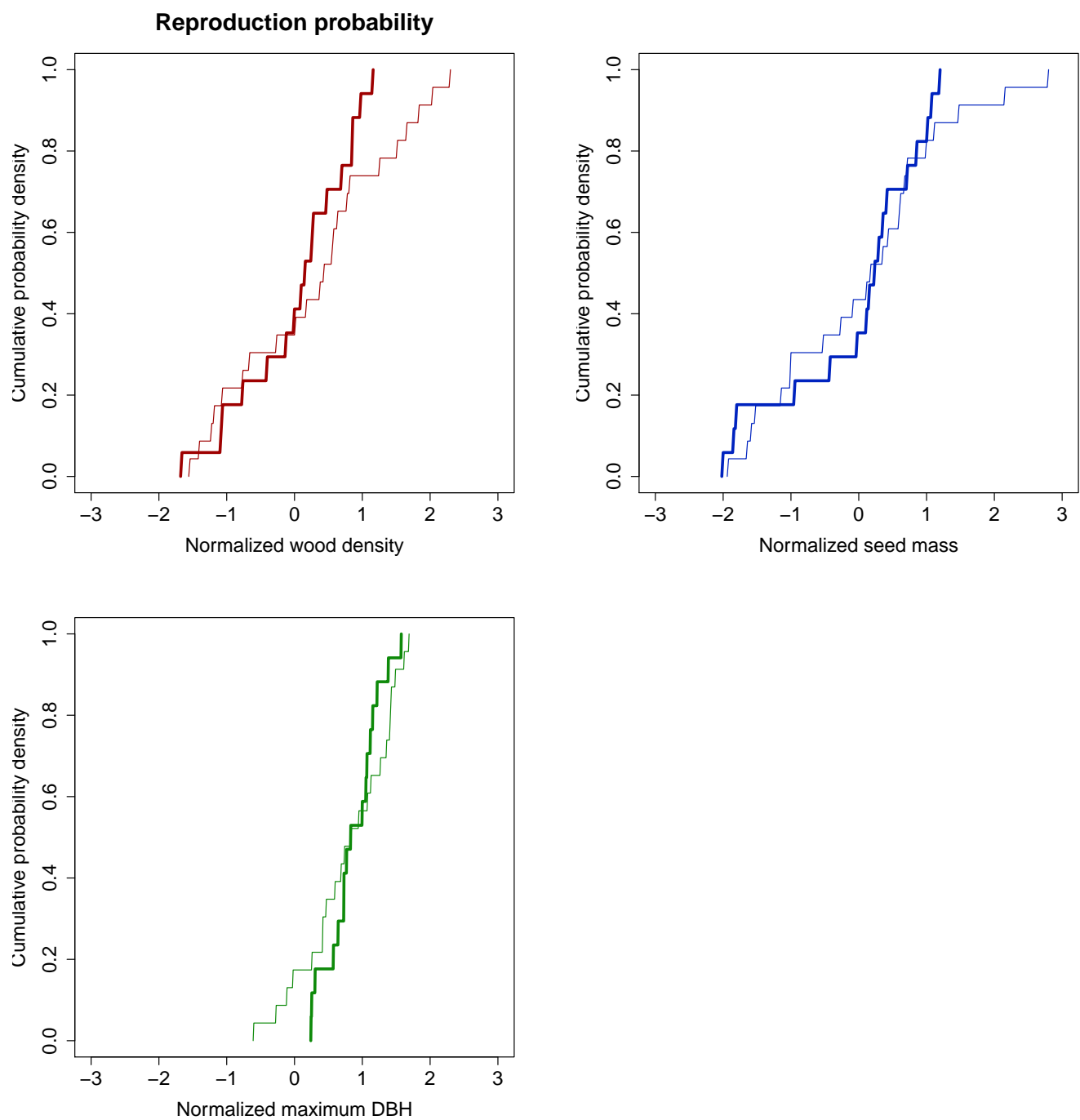


Figure S2.2: Cumulative density distributions for normalized seed mass, wood density and maximum DBH across species included in the reproduction probability models for dioecious (thick lines) and hermaphroditic (thin lines) species.

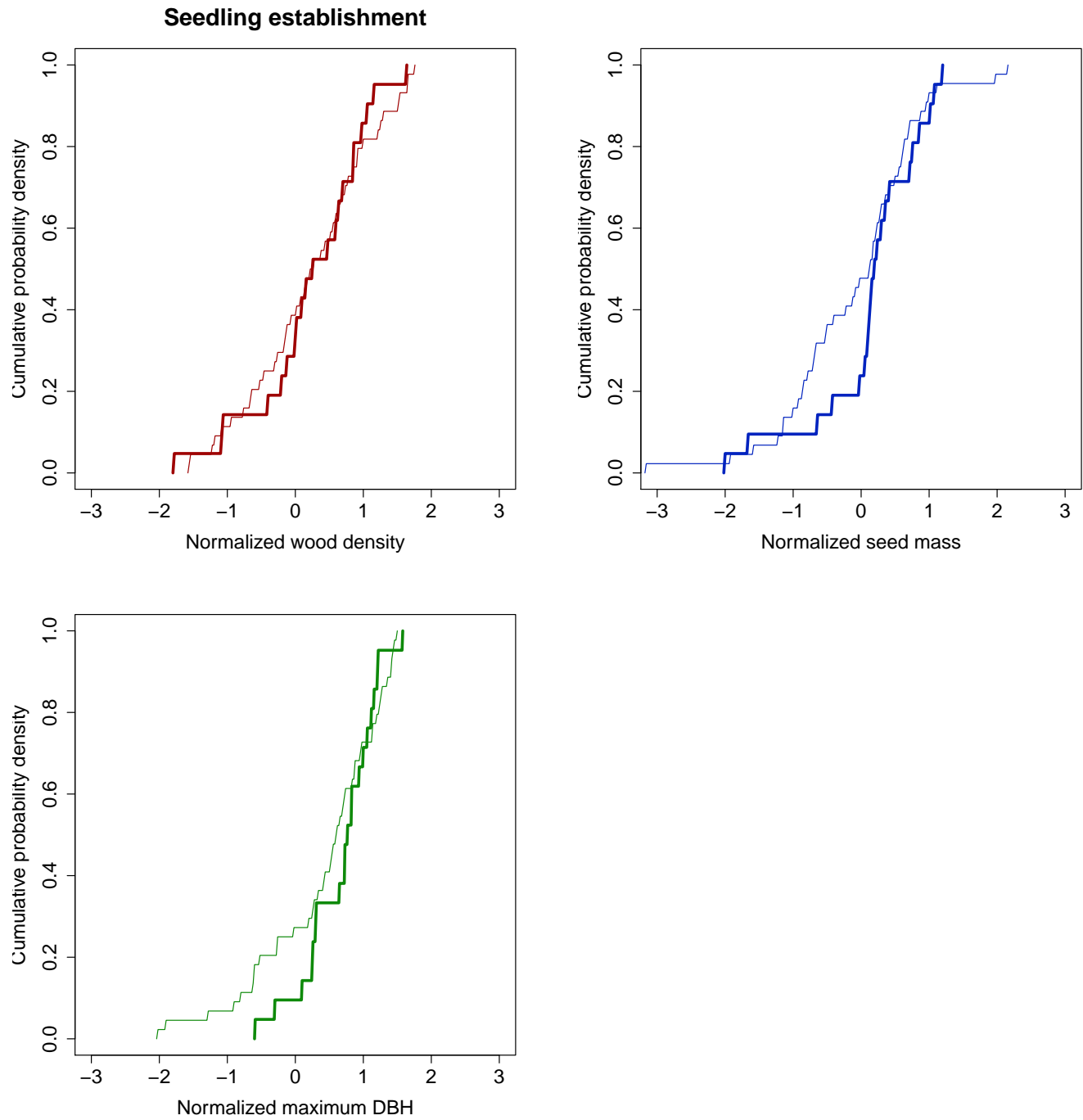


Figure S2.3: Cumulative density distributions for normalized seed mass, wood density and maximum DBH across species included in the seedling establishment models for dioecious (thick lines) and hermaphroditic (thin lines) species.



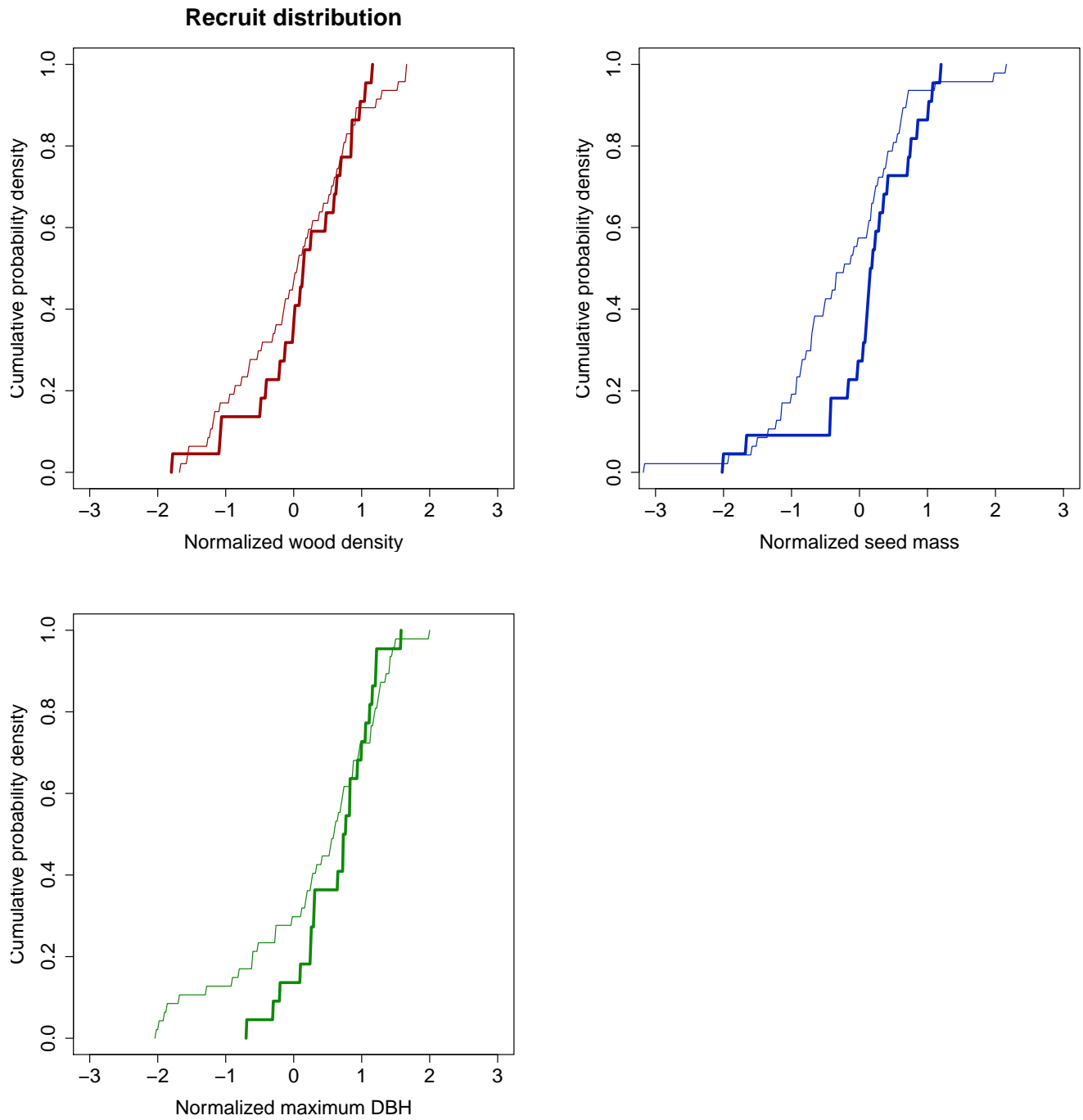


Figure S2.4: Cumulative density distributions for normalized seed mass, wood density and maximum DBH across species included in the new recruit size distribution models for dioecious (thick lines) and hermaphroditic (thin lines) species.

### Seedling survival and growth

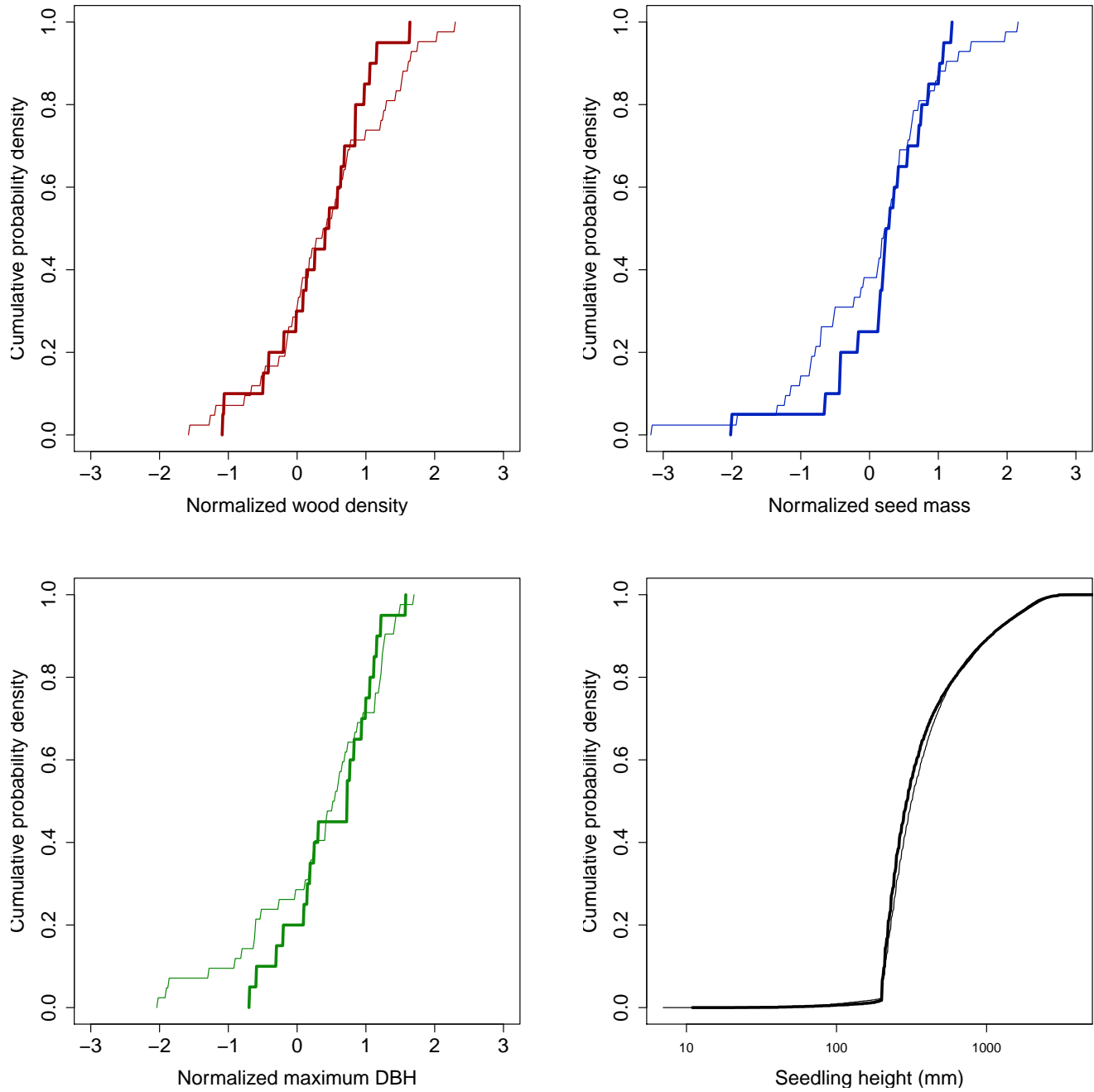


Figure S2.5: Cumulative density distributions for normalized seed mass, wood density and maximum DBH across species included in the seedling survival and growth analyses, as well as the cumulative density distribution of individual seedling heights (mm), for dioecious (thick lines) and hermaphroditic (thin lines) species.

### Tree survival and growth

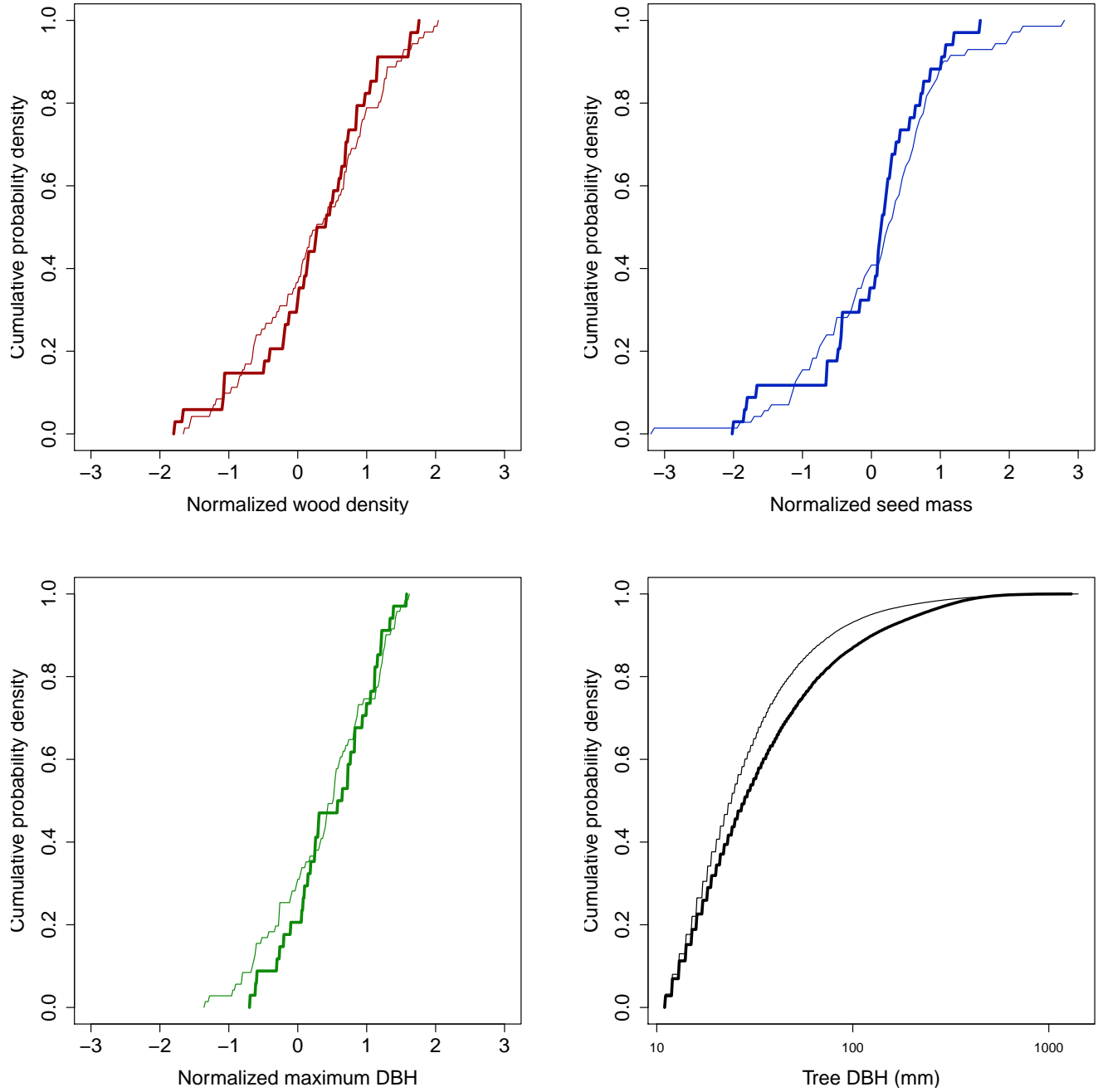


Figure S2.6: Cumulative density distributions for normalized seed mass, wood density and maximum DBH across species included in the tree survival and growth analyses, as well as the cumulative density distribution of individual tree DBHs (mm), for dioecious (thick lines) and hermaphroditic (thin lines) species.

**Relation seedling dbh~height**

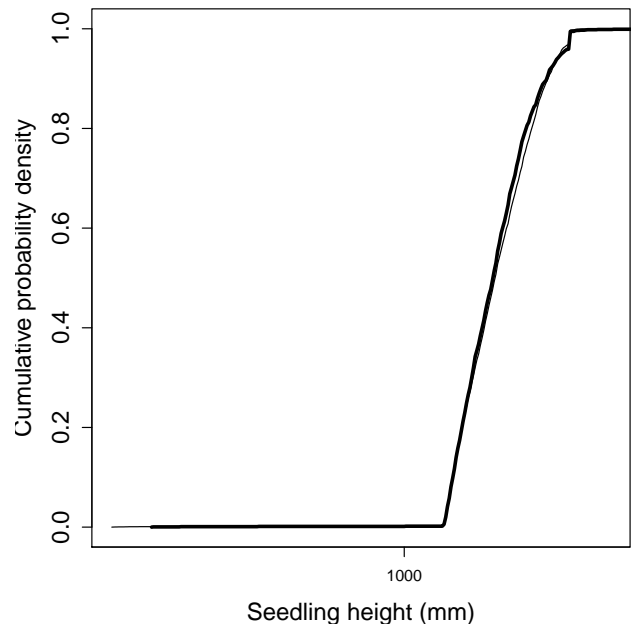
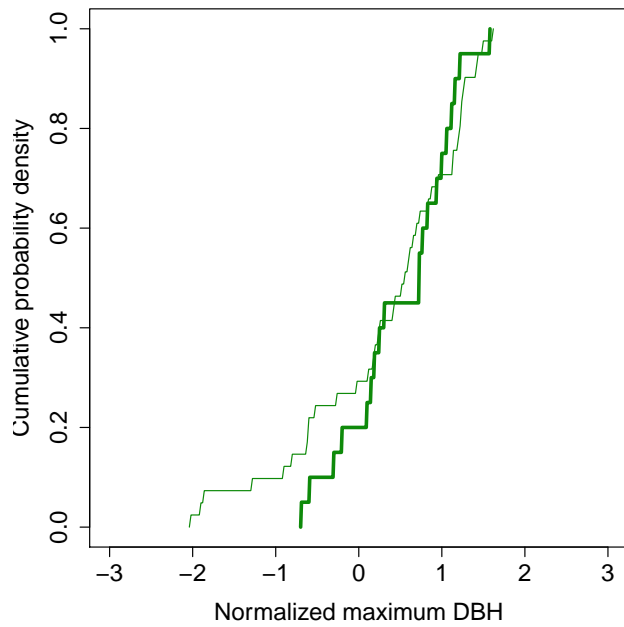
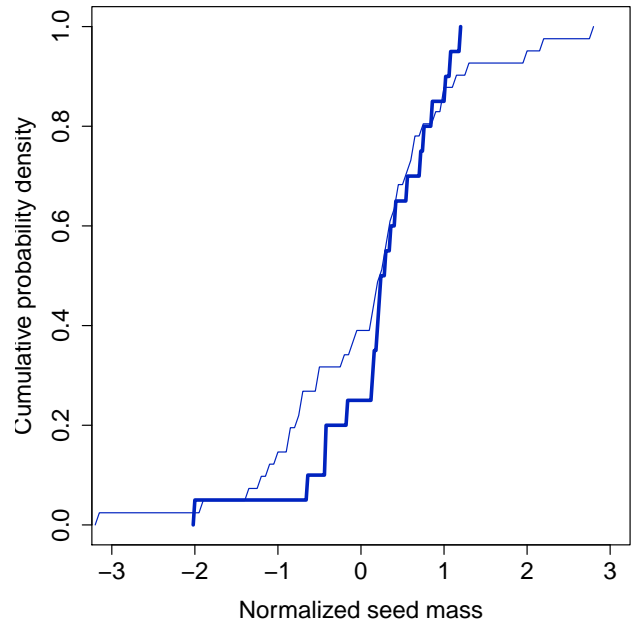
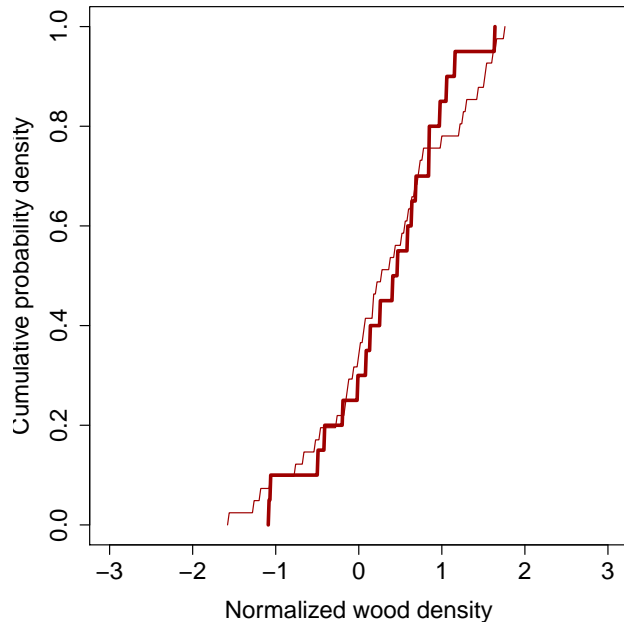


Figure S2.7: Cumulative density distributions for normalized seed mass, wood density and maximum DBH across species included in the models relating seedling DBH to seedling height, for dioecious (thick lines) and hermaphroditic (thin lines) species.

## S3 Supplementary methods

### S3.1 Seed production

Fecundity ( $f_{seeds}$ ) was estimated as a function of tree size by using inverse modeling (Ribbens et al., 1994; Clark et al., 1999; Muller-Landau et al., 2008). This technique estimates fecundity and dispersal parameters based on the spatial distribution of adult trees and arriving seeds. We assume the distribution of seeds around the mother tree, the seed shadow, is the product of two elements: (1) its estimated seed production, and (2) a dispersal kernel (i.e. the probability density function describing the distribution of seeds as a function of distance from the parent tree (Clark et al., 1999). The total expected number of seeds at a seed trap  $j$ ,  $\hat{H}_j$ , is calculated as the sum over expected seed rain from all  $T$  mature trees  $i$ :

$$\hat{H}_j = \alpha \cdot \sum_{i=1}^T Q(p_i b_i | \beta) \cdot F(r_{ij} | \mu, \sigma) \quad (1)$$

where  $\alpha$  is trap area (here  $0.5 \text{ m}^2$ ). For tree  $i$ , the seed rain is calculated by multiplying the fecundity  $Q$ , which is a function of basal area  $b_i$  (calculated as  $[DBH/2]^2 \pi$ ) and estimated probability of reproduction  $p_i$  (which is itself a function of tree diameter).  $F$  is a two-dimensional dispersal kernel, with  $r_{ij}$  being the distance between tree  $i$  and trap  $j$ .  $\beta$ , is a seed production parameter denoting the number of seeds produced per unit basal area. Parameters  $\mu$  and  $\sigma$  describe the shape and scale of the dispersal kernel.

For each hermaphroditic species,  $p_i$  was fitted as a function of size (DBH) using Generalized Linear Models. For the dioecious species, we used gender information collected in the field to identify fruiting female individuals. Here, observed females have a  $p_{female}$  of one, observed males have a  $p_{female}$  of zero. Individuals that were not reproductive at the time of the census are assigned a  $p_{female}$  using estimated relations between DBH and  $p_{female}$  estimated using logistic regression. Estimated coefficients of these regressions can be found in Appendix S10.

One challenge in calculating expected seed rain is that trees outside the plot could also contribute seeds. We omitted data from the traps within 20 meter from the edge of the plot in order to remove traps where seed rain might be dominated by off-plot contributions (Muller-Landau et al., 2008). Data from the remaining 188 traps and 45 gap traps were used. For each of these remaining traps, the contribution from unknown trees outside the plot was approximated under the assumption that tree density and seed production outside plot limits is equal to the mean within the plot (following Muller-Landau et al., 2008). Thus the total expected seed rain  $\hat{S}_j$  for trap  $j$  is then the sum of the expected contributions from trees inside the plot  $\hat{H}_j$  and the expected contributions from trees outside the plot  $\hat{I}_j$ .

$$\hat{S}_j = \hat{H}_j + \hat{I}_j \quad (2)$$

Seed numbers were predicted per trap and compared with observed seed numbers, whereby testing the different mentioned dispersal kernels. Observed seed rain was assumed to follow a negative binomial distribution around expected seed rain, in accordance with previous studies showing that seed arrival tends to be clumped (Muller-Landau et al., 2008). The likelihood of the data for  $N$  traps is thus

$$L(\beta, \mu, \sigma) = \prod_{j=1}^N \text{NegBinom}(S_j | \beta, \mu, \sigma, k) \quad (3)$$

where  $S_j$  is the total number of seeds that arrived in trap  $j$  between 2008 and 2012, and  $k$  is a negative binomial clumping parameter.

We tested several dispersal kernels, including the Exponential, the 2dt (Clark et al., 1999), 2dt1k (which is the 2dt distribution whereby the degrees of freedom parameter is set to 3) (Muller-Landau et al., 2008) and the Cauchy density distribution. Overall, the exponential distribution performed the best, so we used this dispersal kernel for all species ( $f(x|\mu) = \mu \cdot e^{-\mu \cdot x}$ ). Species-specific estimates of parameters  $\beta$ ,  $\mu$  and  $k$  can be found in Appendix S4. The fitted fecundity parameter  $\beta$  was related to species-specific traits using generalized linear models, and the fitted fecundity function  $Q(p_i, b_i | \beta)$  was incorporated in the IPMs.

### S3.2 Seedling establishment

For every species, the mean seed to seedling transition probability,  $p_{\text{establishment}}$ , was estimated by dividing the total flux of seedlings arriving per area per year by the total flux of seeds arriving per area per year in the corresponding set of years. We used data for recruitment into the seedling plots during 1995-2010, combined with appropriately paired data from seed rain into the seed traps, accounting for species-specific delays in germination between seed arrival and seedling recruitment, where relevant. Species-specific estimates of  $p_{\text{establishment}}$  can be found in Appendix S5. The fitted seed-to-seedling transition probability,  $p_{\text{establishment}}$ , was related to seed mass, wood density and breeding system using generalized linear models, and incorporated in the IPMs.

### S3.3 Recruit size distribution

The height distribution of new recruits was first estimated per species, including species for which at least 40 new recruits were observed during 1995-2011, using a Weibull distribution. A maximum likelihood approach was used to estimate the shape ( $k$ ) and scale ( $\lambda$ ) parameter. These were separately related to species-specific traits using generalized linear models.

### S3.4 Reproduction probability

Individual reproductive status (either sterile or reproductive) was related to individual size and species-specific traits, using mixed effects logistic regression.

### S3.5 Seedling growth and survival

Annual seedling height growth was calculated using data from consecutive censuses in 2001, 2002, and 2003. We used two time intervals; between 2001 and 2002, and between 2002 and 2003. For each individual and each interval, the difference in height was divided by time interval to obtain the absolute growth rate (mm/yr). The absolute growth rate was then related to initial size and species-specific traits using mixed effects linear regression with individual and year as a random effect. Variation in growth around the expected value, which is incorporated in the IPM, was first estimated on a species-level, including all species that were used in the trait-based seedling growth models. To do so, we fitted generalized linear growth models for each species separately, with initial size (mm height) as explanatory variable and growth (in mm/yr) as response variable. The standard deviations of the residuals for each model are then related to species-specific traits using generalized linear models. Yearly survival (0 or 1) was related to initial size and species-specific traits, using mixed effects logistic regression and individual and year as random effects.

### S3.6 Relation between DBH and seedling height

For this analysis we used seedlings for which both DBH and height was measured. Individual seedling DBH (mm) was then related to individual height (mm) and species-specific traits, using mixed effects linear regression including individual and year as random effects.

### S3.7 Tree growth and survival

Tree growth and survival were calculated in the same way as for seedlings, using data collected between 1990 and 2005. We used each consecutive census to fit growth and survival models. The natural logarithm of DBH as initial size was used in case of the growth models. Yearly growth was calculated as the difference in DBH divided by the time interval (in years). Variation in growth, which is incorporated in the IPM, is first estimated on a species-level, by fitting generalized linear growth models for each species separately, including initial DBH as explanatory variable and growth (mm DBH/yr) as response variable. All species that were used in the trait-based tree growth models were included. The standard deviations of the residuals of each of these models were then related to species-specific traits using generalized linear models. Survival was related to individual size and species-specific traits, using mixed effects logistic regression. We took the fifth root of the estimated probabilities, since tree survival was censused on a 5 year basis.

## S4 Seed production and dispersal results

Table S4.1: Seed production (fecundity) and seed dispersal parameters (with standard errors) estimated using inverse modeling as described in Appendix S3.1. Annual potential fecundity for trees of different DBH was calculated from the fecundity parameter  $\beta$  as  $f_{seeds}(DBH|\beta) = [\exp(\beta) \cdot \pi \cdot (DBH/2)^2]$ , and used in the IPMs. The dispersal kernel has a single dispersal parameter,  $\mu$ , from which median dispersal distance (in m) is calculated. The parameter  $k$  is for the negative binomial distribution for clumping of seed rain around the expected value. Median dispersal distance is on average 43 ( $\pm 59$  SD) meters for dioecious species, and 36 ( $\pm 33$  SD) meters for hermaphroditic species. *Pouteria reticulata* was excluded from this calculation, because the estimated  $\mu$  value was equal to the lower limit of the constrained parameter range for  $\mu$ . The value of this lower limit did not influence the estimated fecundity parameter for *P. reticulata*.

Latin binomial	$\beta$	$\mu$	k	breeding	Median distance
<i>Cecropia insignis</i>	1.8782 ( $\pm 0.343$ )	-3.9902 ( $\pm 0.332$ )	0.0446 ( $\pm 0.006$ )	Dioecious	37
<i>Pouteria reticulata</i>	-3.0138 ( $\pm 0.422$ )	-6.9078 ( $\pm 1.97$ )	0.0489 ( $\pm 0.011$ )	Dioecious	NA
<i>Protium tenuifolium</i>	-2.2976 ( $\pm 0.326$ )	-2.5895 ( $\pm 0.188$ )	0.1109 ( $\pm 0.026$ )	Dioecious	9
<i>Simarouba amara</i>	-2.4964 ( $\pm 0.296$ )	-3.2703 ( $\pm 0.152$ )	0.1089 ( $\pm 0.024$ )	Dioecious	18
<i>Triplaris cumingiana</i>	0.0635 ( $\pm 0.333$ )	-1.965 ( $\pm 0.126$ )	0.331 ( $\pm 0.074$ )	Dioecious	5
<i>Virola sebifera</i>	-1.6499 ( $\pm 0.247$ )	-5.3545 ( $\pm 0.635$ )	0.0748 ( $\pm 0.013$ )	Dioecious	147
<i>Cordia alliodora</i>	0.7082 ( $\pm 0.375$ )	-3.5621 ( $\pm 0.175$ )	0.0873 ( $\pm 0.012$ )	Hermaphroditic	24
<i>Cordia bicolor</i>	-2.0668 ( $\pm 0.175$ )	-3.6712 ( $\pm 0.171$ )	0.1791 ( $\pm 0.024$ )	Hermaphroditic	27
<i>Coussarea curvigemma</i>	-1.9829 ( $\pm 0.223$ )	-4.0991 ( $\pm 0.257$ )	0.1392 ( $\pm 0.034$ )	Hermaphroditic	42
<i>Desmopsis panamensis</i>	-1.1773 ( $\pm 0.257$ )	-2.9028 ( $\pm 0.509$ )	0.1396 ( $\pm 0.023$ )	Hermaphroditic	13
<i>Dipteryx oleifera</i>	-4.5218 ( $\pm 0.312$ )	-3.8011 ( $\pm 0.193$ )	0.0748 ( $\pm 0.019$ )	Hermaphroditic	31
<i>Hirtella triandra</i>	-3.021 ( $\pm 0.207$ )	-2.8388 ( $\pm 0.191$ )	0.1509 ( $\pm 0.027$ )	Hermaphroditic	12
<i>Jacaranda copaia</i>	0.0856 ( $\pm 0.083$ )	-3.5901 ( $\pm 0.088$ )	1.1461 ( $\pm 0.101$ )	Hermaphroditic	25
<i>Luehea seemannii</i>	0.503 ( $\pm 0.109$ )	-3.6447 ( $\pm 0.068$ )	0.6246 ( $\pm 0.051$ )	Hermaphroditic	27
<i>Mouriri myrtilloides</i>	-0.6029 ( $\pm 0.194$ )	-1.4827 ( $\pm 0.189$ )	0.2275 ( $\pm 0.031$ )	Hermaphroditic	3
<i>Poulsenia armata</i>	-4.1841 ( $\pm 0.335$ )	-4.8917 ( $\pm 0.437$ )	0.0879 ( $\pm 0.025$ )	Hermaphroditic	92
<i>Quararibea asterolepis</i>	-2.0078 ( $\pm 0.158$ )	-5.0952 ( $\pm 0.347$ )	0.192 ( $\pm 0.019$ )	Hermaphroditic	113
<i>Terminalia oblonga</i>	-1.0385 ( $\pm 0.266$ )	-3.4388 ( $\pm 0.107$ )	0.2271 ( $\pm 0.041$ )	Hermaphroditic	22

## S5 Seedling establishment results

Table S5.1: Species-specific seedling establishment probabilities (with standard errors) estimated following methods described in Appendix S3.2.

Latin binomial	Probability	Breeding
<i>Alchornea costaricensi</i>	4.77e-04 ( $\pm 5.339e-05$ )	Dioecious
<i>Brosimum alicastrum</i>	2.08e-03 ( $\pm 1.992e-04$ )	Dioecious
<i>Cecropia insignis</i>	4.33e-04 ( $\pm 3.195e-05$ )	Dioecious
<i>Drypetes standleyi</i>	1.04e-02 ( $\pm 1.060e-03$ )	Dioecious
<i>Garcinia intermedia</i>	1.13e-02 ( $\pm 1.103e-03$ )	Dioecious
<i>Guapira standleyana</i>	5.22e-03 ( $\pm 3.956e-04$ )	Dioecious
<i>Guarea guidonia</i>	2.30e-02 ( $\pm 1.625e-03$ )	Dioecious
<i>Hampea appendiculata</i>	1.46e-01 ( $\pm 1.576e-02$ )	Dioecious
<i>Picramnia latifolia</i>	3.46e-02 ( $\pm 3.384e-03$ )	Dioecious
<i>Pouteria reticulata</i>	2.68e-02 ( $\pm 1.423e-03$ )	Dioecious
<i>Protium tenuifolium</i>	1.55e-02 ( $\pm 1.452e-03$ )	Dioecious
<i>Randia armata</i>	1.34e-01 ( $\pm 2.804e-03$ )	Dioecious
<i>Simarouba amara</i>	1.68e-03 ( $\pm 1.580e-04$ )	Dioecious
<i>Tetragastris panamensis</i>	1.98e-02 ( $\pm 8.050e-04$ )	Dioecious

Table S5.1: Species-specific seedling establishment probabilities (with standard errors) estimated following methods described in Appendix S3.2.

Latin binomial	Probability	Breeding
<i>Trichilia pallida</i>	5.48e-03 ( $\pm 8.034\text{e-}04$ )	Dioecious
<i>Trichilia tuberculata</i>	1.52e-02 ( $\pm 2.441\text{e-}04$ )	Dioecious
<i>Triplaris cumingiana</i>	3.67e-03 ( $\pm 2.914\text{e-}04$ )	Dioecious
<i>Virola sebifera</i>	1.23e-02 ( $\pm 1.106\text{e-}03$ )	Dioecious
<i>Zanthoxylum panamense</i>	3.40e-03 ( $\pm 3.934\text{e-}04$ )	Dioecious
<i>Alseis blackiana</i>	5.39e-05 ( $\pm 4.678\text{e-}06$ )	Hermaphroditic
<i>Apeiba membranacea</i>	8.49e-04 ( $\pm 7.289\text{e-}05$ )	Hermaphroditic
<i>Aspidosperma spruceanum</i>	9.70e-02 ( $\pm 1.873\text{e-}02$ )	Hermaphroditic
<i>Beilschmiedia pendula</i>	3.27e-02 ( $\pm 7.561\text{e-}04$ )	Hermaphroditic
<i>Cassipourea elliptica</i>	3.81e-03 ( $\pm 3.684\text{e-}04$ )	Hermaphroditic
<i>Chrysophyllum argenteum</i>	2.30e-01 ( $\pm 3.245\text{e-}02$ )	Hermaphroditic
<i>Chrysophyllum cainito</i>	1.48e-02 ( $\pm 9.914\text{e-}04$ )	Hermaphroditic
<i>Cordia alliodora</i>	3.35e-03 ( $\pm 3.093\text{e-}04$ )	Hermaphroditic
<i>Cordia bicolor</i>	1.22e-03 ( $\pm 1.474\text{e-}04$ )	Hermaphroditic
<i>Dendropanax arboreus</i>	5.47e-03 ( $\pm 3.881\text{e-}04$ )	Hermaphroditic
<i>Eugenia coloradoensis</i>	6.89e-03 ( $\pm 1.156\text{e-}03$ )	Hermaphroditic
<i>Eugenia oerstediana</i>	8.94e-02 ( $\pm 3.072\text{e-}03$ )	Hermaphroditic
<i>Genipa americana</i>	1.85e-02 ( $\pm 1.888\text{e-}03$ )	Hermaphroditic
<i>Guatteria dumetorum</i>	3.44e-03 ( $\pm 4.618\text{e-}04$ )	Hermaphroditic
<i>Hasseltia floribunda</i>	4.34e-03 ( $\pm 5.001\text{e-}04$ )	Hermaphroditic
<i>Heisteria concinna</i>	5.16e-02 ( $\pm 2.462\text{e-}03$ )	Hermaphroditic
<i>Hirtella triandra</i>	1.02e-02 ( $\pm 6.739\text{e-}04$ )	Hermaphroditic
<i>Inga marginata</i>	1.47e-01 ( $\pm 6.304\text{e-}03$ )	Hermaphroditic
<i>Jacaranda copaia</i>	3.07e-04 ( $\pm 2.439\text{e-}05$ )	Hermaphroditic
<i>Lacmellea panamensis</i>	9.28e-02 ( $\pm 1.077\text{e-}02$ )	Hermaphroditic
<i>Lonchocarpus heptaphyllus</i>	6.83e-02 ( $\pm 8.045\text{e-}03$ )	Hermaphroditic
<i>Luehea seemannii</i>	1.98e-04 ( $\pm 1.463\text{e-}05$ )	Hermaphroditic
<i>Mouriri myrtilloides</i>	4.20e-02 ( $\pm 1.877\text{e-}03$ )	Hermaphroditic
<i>Cinnamomum triplinerve</i>	5.09e-01 ( $\pm 6.621\text{e-}02$ )	Hermaphroditic
<i>Quararibea asterolepis</i>	9.27e-03 ( $\pm 2.421\text{e-}04$ )	Hermaphroditic
<i>Tabebuia guayacan</i>	3.37e-03 ( $\pm 4.230\text{e-}04$ )	Hermaphroditic
<i>Tabebuia rosea</i>	7.34e-03 ( $\pm 6.565\text{e-}04$ )	Hermaphroditic
<i>Tabernaemont arborea</i>	5.41e-03 ( $\pm 7.400\text{e-}04$ )	Hermaphroditic
<i>Unonopsis pittieri</i>	6.34e-03 ( $\pm 7.912\text{e-}04$ )	Hermaphroditic
<i>Vochysia ferruginea</i>	3.04e-02 ( $\pm 4.140\text{e-}03$ )	Hermaphroditic



## S6 Comparisons of species-specific vs. averaged trait-based estimates for each vital rate

For each vital rate, we compared averaged trait-based model predictions (without random effects) with predictions from models fitted separately for each species. To do so, the relevant vital rate for all included species for which seed mass, wood density, maximum DBH and breeding system data was available, was estimated using generalized linear models. Growth and survival predictions are shown for seedlings with average height (400 mm) and for trees with a DBH 75 percent of the species-specific maximum DBH. For reproduction probability we show the DBH at which reproduction probability equals 0.5.

The grey dots show single species estimates (with dot size scaled to sample size) while the colored dots show the averaged model predictions (with red indicating dioecious and blue hermaphroditic). For each vital rate we calculated coefficients of determination ( $R^2$ ) between averaged model predictions and species-specific predictions across all included species.  $R^2$  ranged between 0.08 (seedling growth) and 0.53 (tree growth). Species are ordered by their predicted values. Full species names can be found in Appendix S1. Standard errors for species-specific rates are shown as error bars.

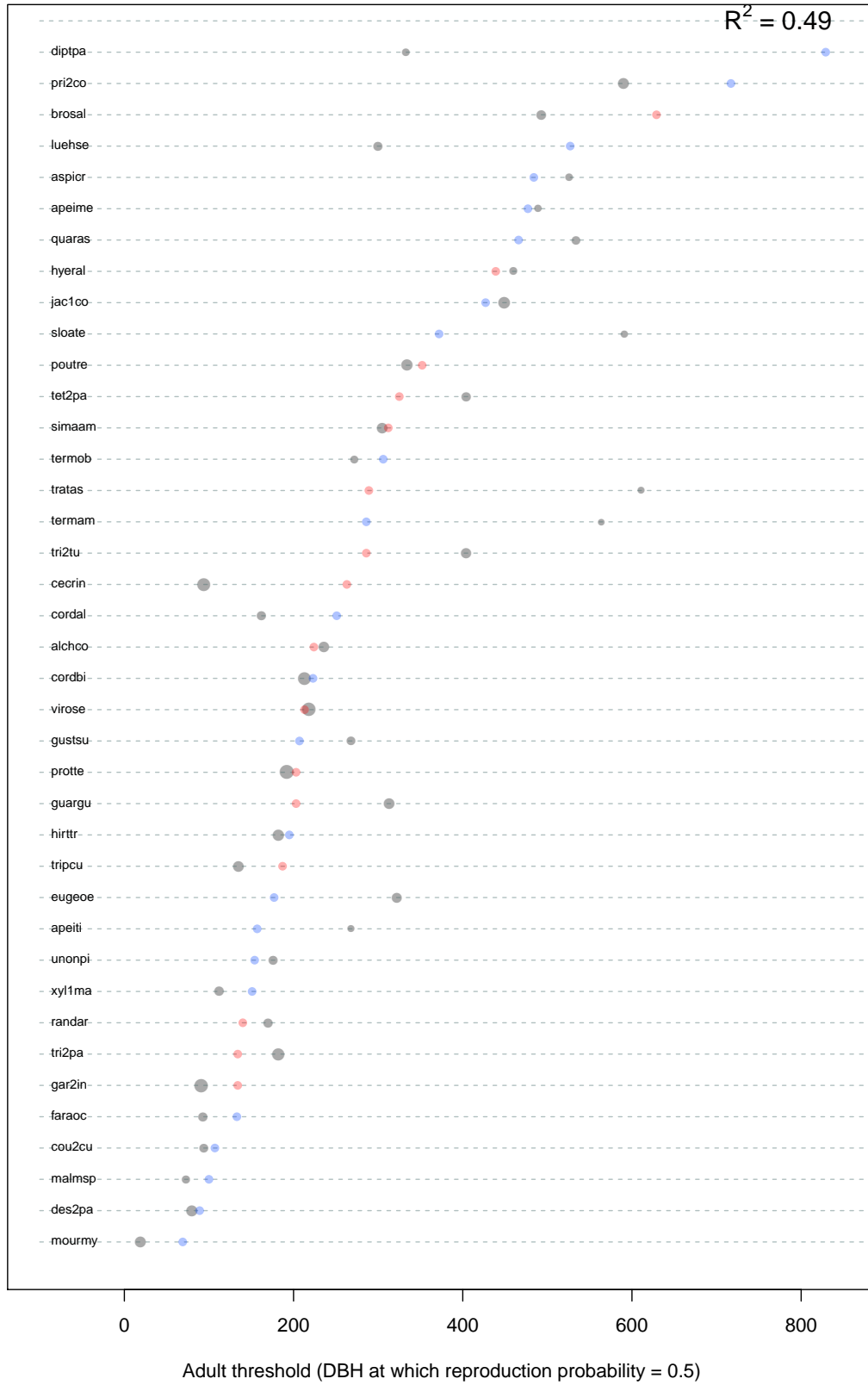


Figure S6.1: Comparison of species-specific predictions vs. estimates according to the averaged trait-based models for the DBH at which the reproduction probability is 0.5. Grey dots represent the species-specific predictions; the colored dots show the trait-based model predictions (red: dioecious; blue: hermaphroditic).



Figure S6.2: Comparison of species-specific predictions vs. estimates according to the averaged trait-based models for seedling survival. Grey dots represent the species-specific predictions ( $\pm 1$  SD); the colored dots show the trait-based model predictions (red: dioecious; blue: hermaphroditic).

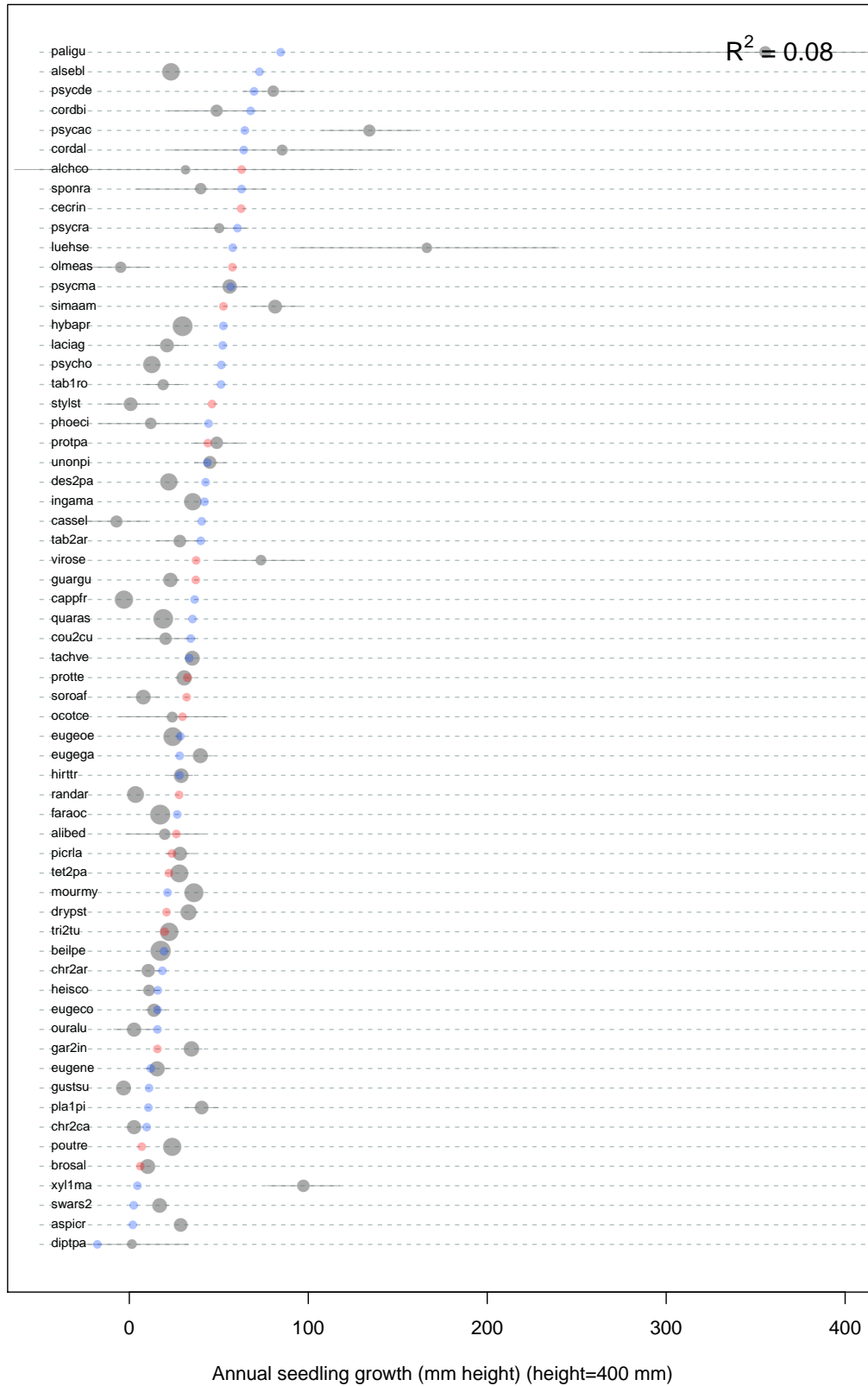


Figure S6.3: Comparison of species-specific predictions vs. estimates according to the averaged trait-based models for seedling growth. Grey dots represent the species-specific predictions ( $\pm 1$  SD); the colored dots show the trait-based model predictions (red: dioecious; blue: hermaphroditic).

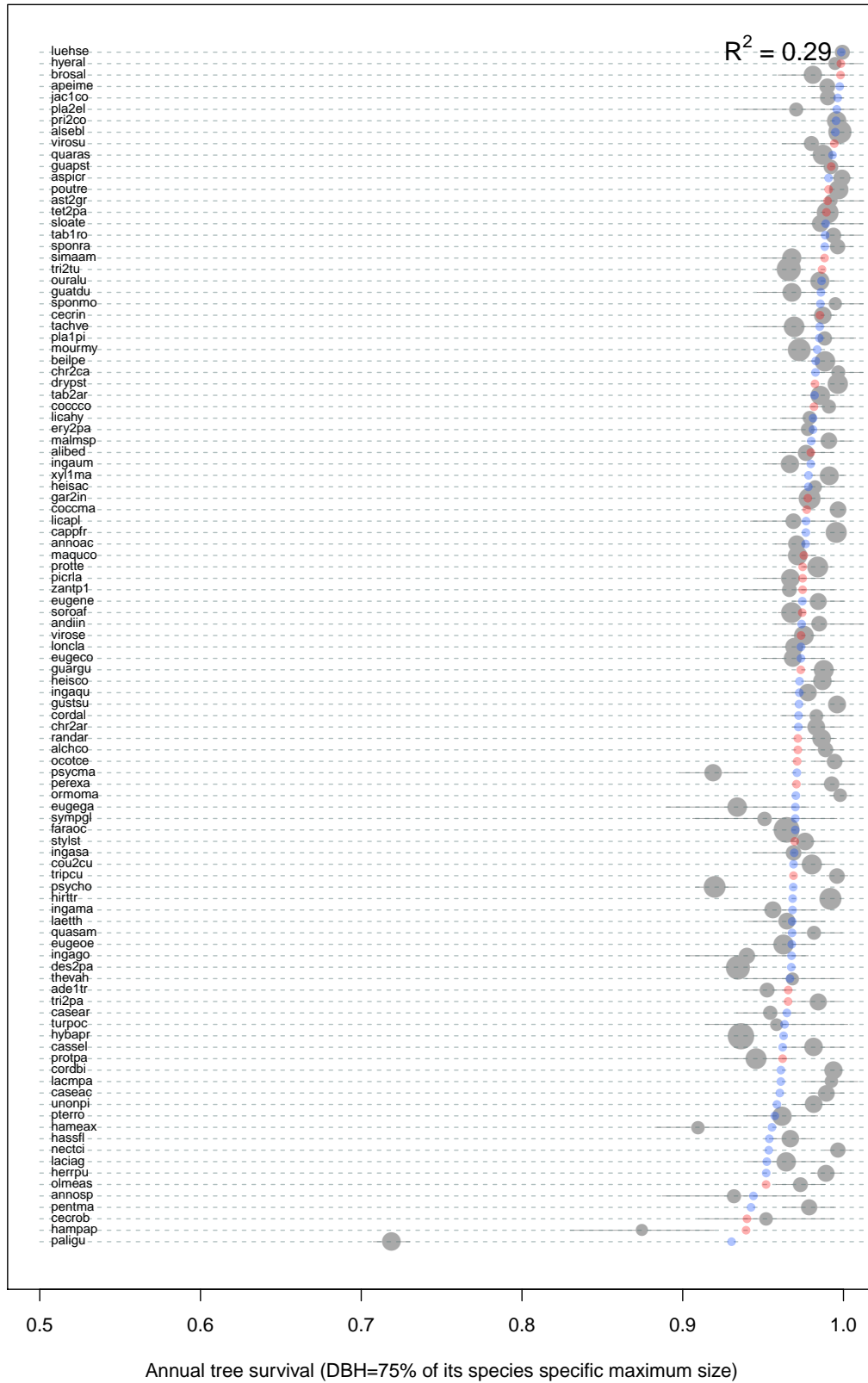


Figure S6.4: Comparison of species-specific predictions vs. estimates according to the averaged trait-based models for tree survival. Grey dots represent the species-specific predictions ( $\pm 1$  SD); the colored dots show the trait-based model predictions (red: dioecious; blue: hermaphroditic).

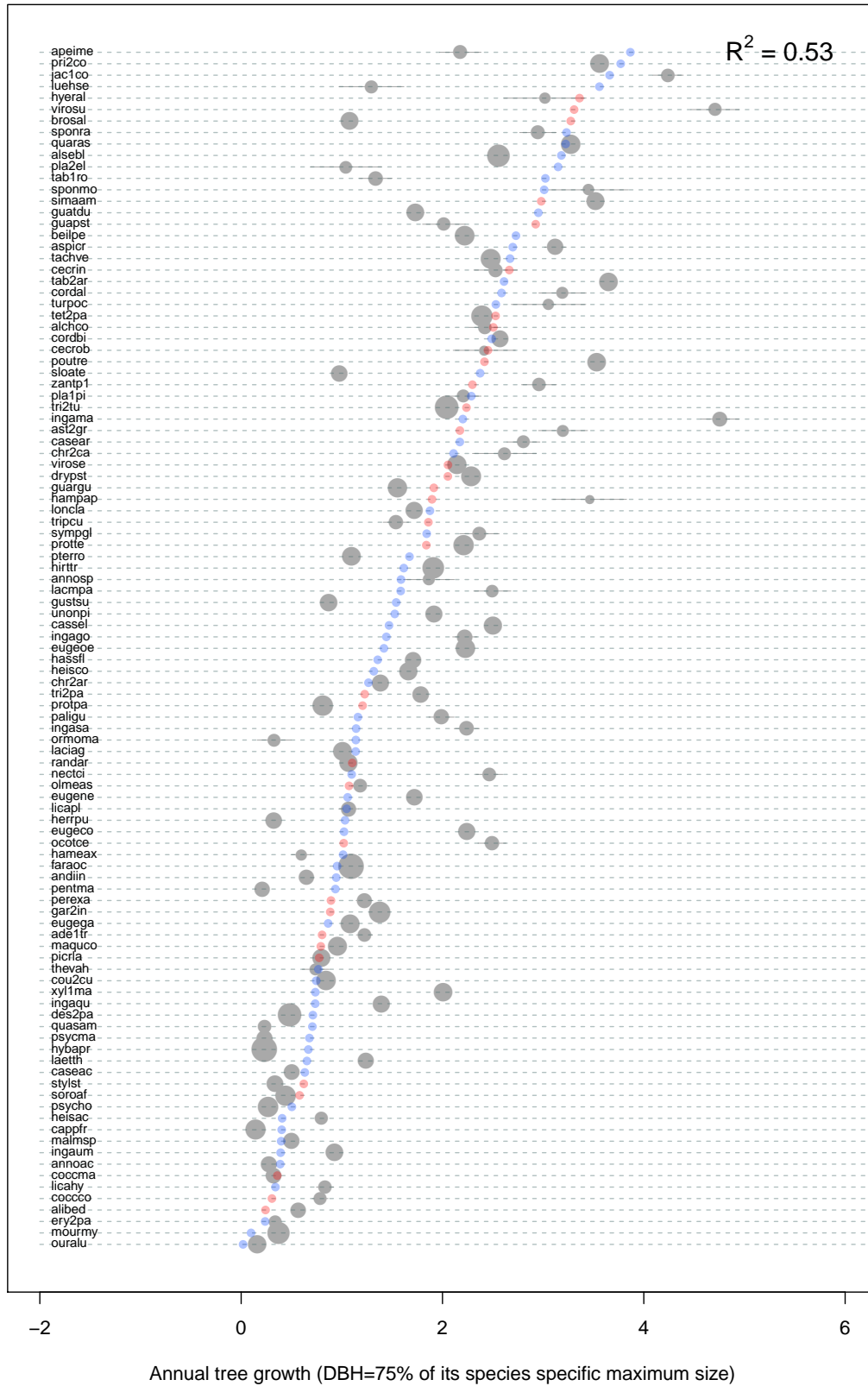


Figure S6.5: Comparison of species-specific predictions vs. estimates according to the averaged trait-based models for tree growth. Grey dots represent the species-specific predictions ( $\pm 1$  SD); the colored dots show the trait-based model predictions (red: dioecious; blue: hermaphroditic).

## S7 Correlations between vital rates

We tested whether our modeling averaging approach captures the well-documented interspecific tradeoff between growth and survival. To do so, we first fitted species-specific growth and survival models for each of our focal species, conducting a separate analyses for both seedlings and trees. We used these models to predict expected growth and survival probability for trees with 50 mm DBH and seedlings at 500 mm height, and examined the interspecific relationships between growth and survival. This analysis documents the well-known trade-off between growth and survival across species (Figs. S6.1, S6.2). We then checked whether our model averaging approach was also capable of capturing these patterns. We used averaged models of each vital rate combined with the trait values of each species to predict for each species expected growth and survival rates of trees at 50 mm DBH and seedlings of 500 mm height. We did this with and without including estimated species random effects in the predictions. Analyses of interspecific variation in these predictions show that the average models successfully recapture the growth-survival tradeoff (Figs. S6.1, S6.2). The model without species random effects shows this tradeoff even more strongly than the one with these random effects (Figs. S6.1, S6.2).

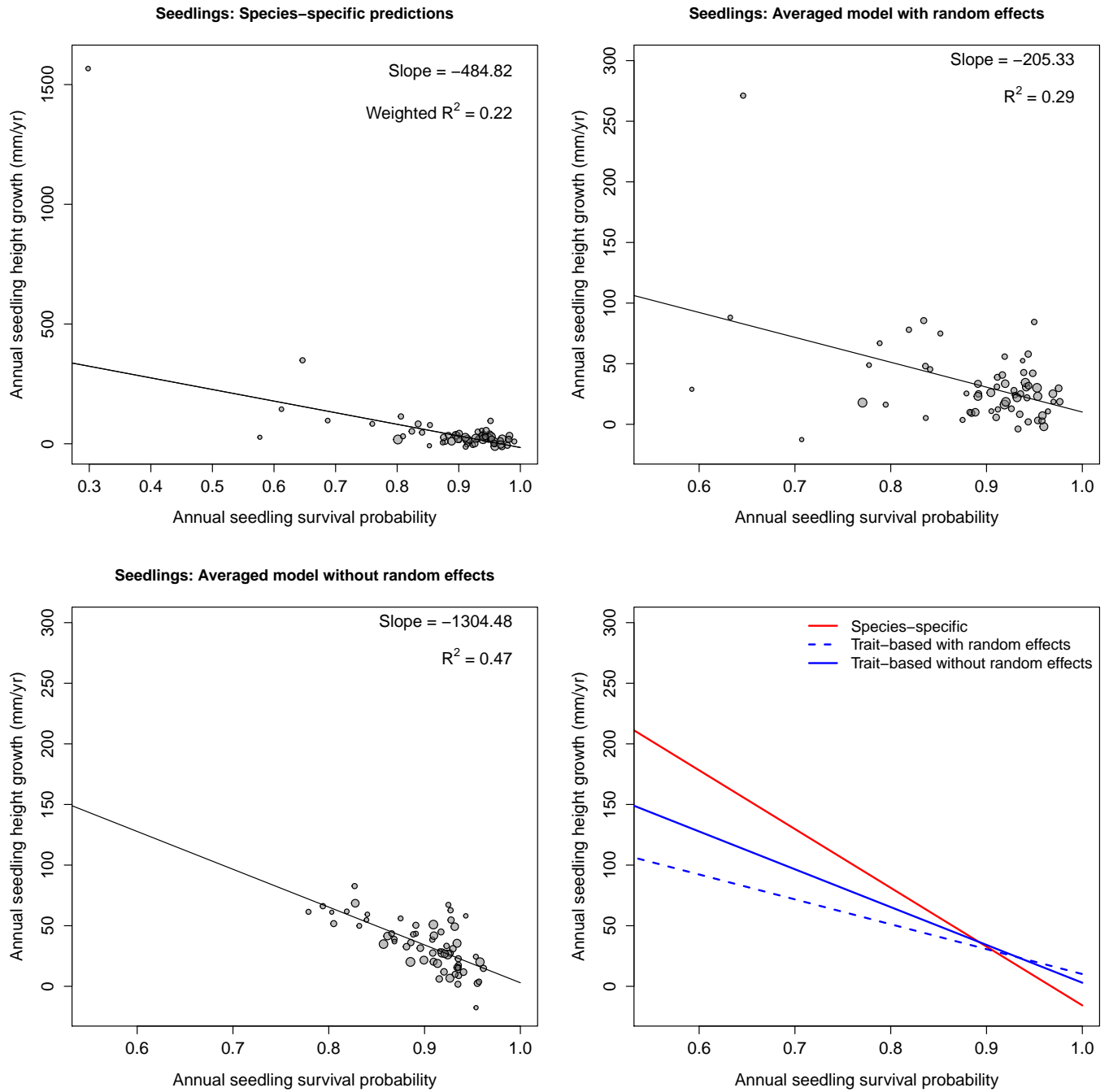


Figure S7.1: Interspecific trade-off between growth and survival in seedlings, based on linear regressions of independent estimates for each species (top-left), on estimates from the averaged trait-based models with random effects (top-right) and on estimates from the average trait-based model without random effects, as we included it in the composite IPM (bottom-left). In the top-left panel, the linear regression was performed by weighting by the number of data available for each species. Each point represents one species, and is scaled to the amount of data available. Note that the y-axis differs between panels a and b,c,d. In the bottom-right panel, we show the regression lines of the three approaches simultaneously in one graph.



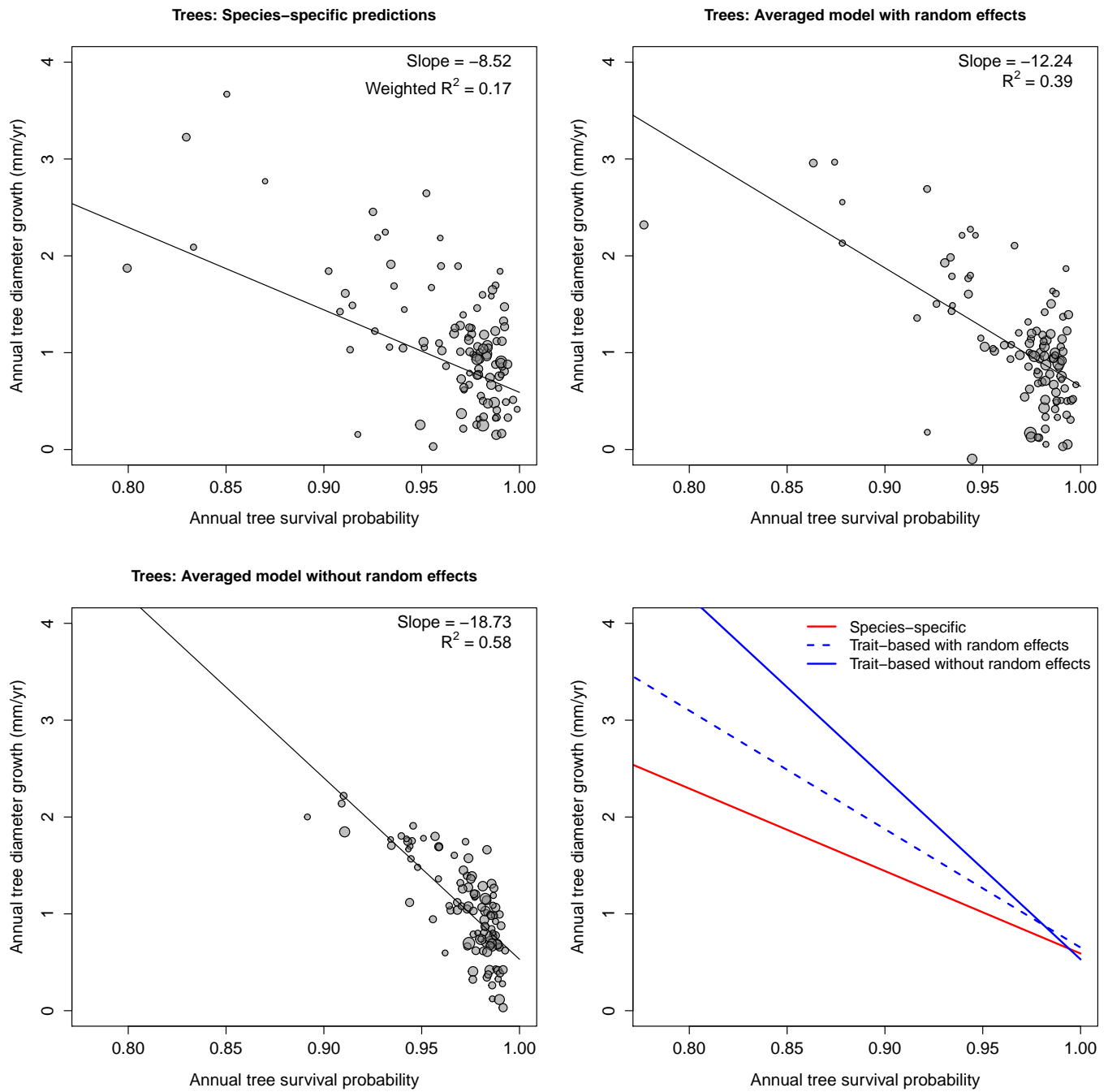


Figure S7.2: Interspecific trade-off between growth and survival in trees  $> 1$  cm DBH, based on linear regressions of independent estimates for each species (top-left), on estimates from the averaged trait-based models with random effects (top-right) and on estimates from the average trait-based model without random effects, as we included it in the composite IPM (bottom-left). In the top-left panel, the linear regression was performed by weighting by the number of data available for each species. Each point represents one species, and is scaled to the amount of data available. In the bottom-right panel, we show the regression lines of the three approaches simultaneously in one graph.

## S8 IPM Sensitivity analysis

The IPMs were used to project intrinsic growth rate  $r$  ( $\ln[\lambda]$ ) for hypothetical species with varying trait values and breeding system. To evaluate the relative effects of traits we quantified the sensitivity of  $r$  to changes in trait values via their effects on different vital rates by performing the following analysis: First, an IPM was constructed based on vital rate functions for which normalized seed mass, wood density and maximum size were set to 0 (the community average). Subsequently, one of the vital rate functions was replaced with a vital rate function containing a new trait value (either wood density, seed mass or maximum size, ranging between -1 and +1 SD from the mean, while the other trait was kept constant). The IPM was constructed again and a new  $r$  was calculated. Thus, all vital rates were altered one by one, for both breeding systems. The change in  $r$  caused by a change in trait value for a given vital rate, was used as a measure for the sensitivity.

The sensitivity of  $r$  to changes in trait values depends both on the sensitivity of  $r$  to a vital rate, and the influence of a trait on that vital rate. With respect to seed mass,  $r$  is most sensitive to effects on fecundity (i.e. higher seed mass is associated with lower fecundity, which has a large effect on  $r$ ), followed by an opposing effect of seed mass through tree survival (Fig. S7.1). On the other hand, seed mass had only a small influence on  $r$  through its effect on seedling establishment, seedling growth and survival, and tree growth. Changes in wood density affecting tree growth and tree survival resulted in the largest, but opposing, changes in  $r$ , followed by effects through seedling growth and survival. Changes in maximum DBH mainly affected seedling establishment.

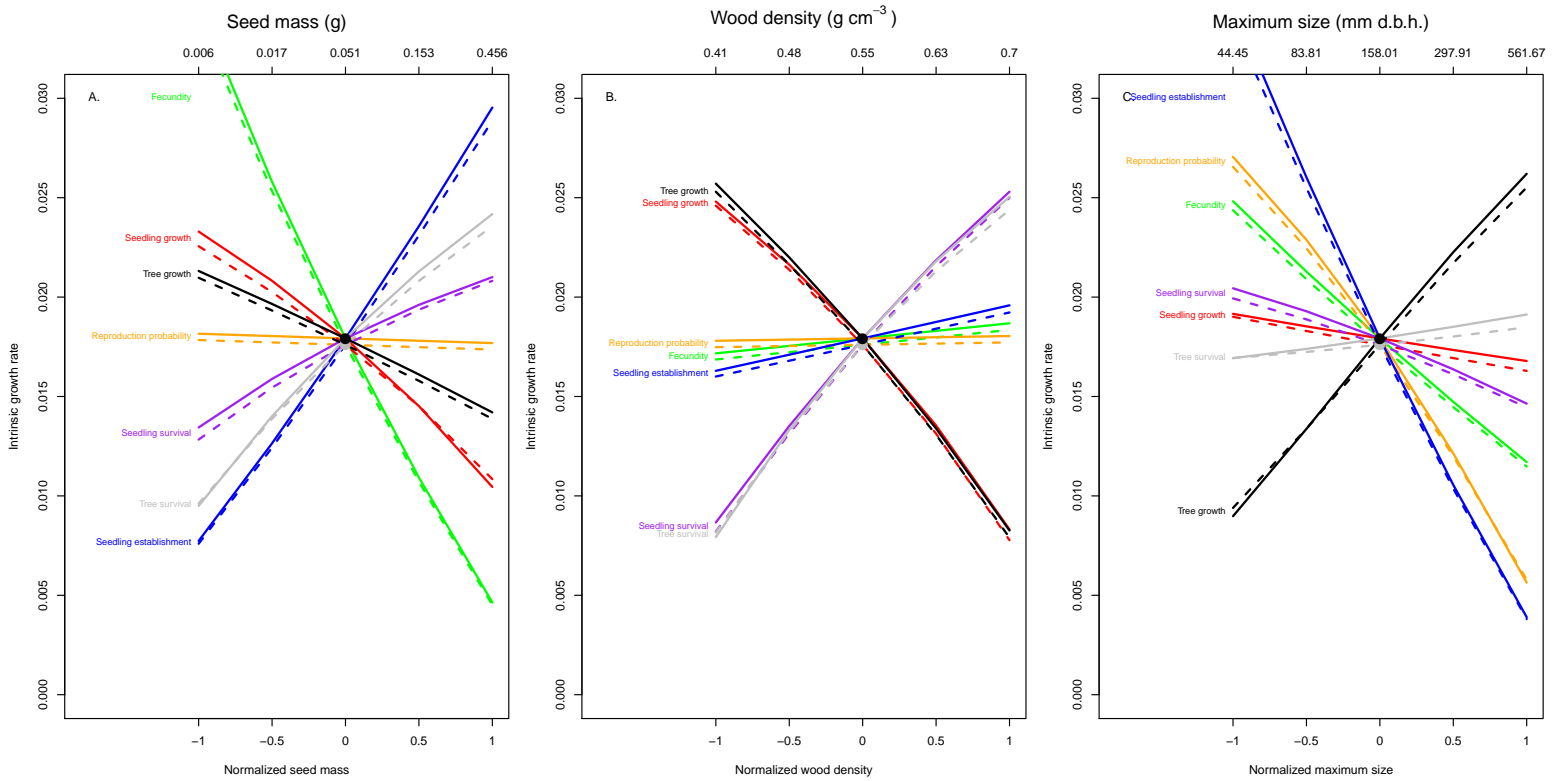


Figure S8.1: Effects on population growth rates ( $r=\ln(\lambda)$ ) of changes in individual vital rates corresponding to estimated mean effects of variation in individual functional traits of seed mass (a), wood density (b), or maximum size (c) combined with dioecy (solid lines) or hermaphroditism (dotted lines). Black and grey dots show where dashed lines and solid lines respectively intersect, showing the intrinsic growth rate at average trait values for hermaphroditic and dioecious species.

## S9 Best candidate models and their estimated coefficients for each vital rate

The following pages display two tables for each vital rate analysis: a first table listing the five best models with their AIC values and weights, and a second table giving the estimated parameters of each of these models and of the average model, where the average model was constructed from all models weighted by their Akaike weights. Recall that all possible models including each of the traits and interactions with size (when relevant), have been tested and used for averaging. For survival, reproduction and growth analyses, this resulted in a total of 82 models, the most complicated model being:  $\sim size * breeding + size * SM + size * WD + size * D_{max}$ .

Table S9.1: Five best models of reproduction probability (out of 82 total), with their AIC values and weights.

model	formulas	weight	$\Delta AIC$
mod56	$repr \sim DBH * D_{max} + (1 species)$	0.352	0.000
mod59	$repr \sim DBH + SM + DBH * D_{max} + (1 species)$	0.135	1.915
mod58	$repr \sim DBH * breeding + DBH * D_{max} + (1 species)$	0.088	2.773
mod62	$repr \sim DBH * SM + DBH * D_{max} + (1 species)$	0.059	3.587
mod68	$repr \sim DBH + WD + SM + DBH * D_{max} + (1 species)$	0.054	3.735

Table S9.2: Estimated parameters of the five best models of reproduction probability, and of the average model, where the average model was constructed from all 82 models weighted by their weights.

	mod56	mod58	mod59	mod62	mod68	Weighted average
(Intercept)	-2.735e+00	-2.589e+00	-2.724e+00	-2.729e+00	-2.759e+00	-2.705e+00 ( $\pm 1.651e-01$ )
SM	0.000e+00	0.000e+00	-5.477e-02	-1.085e-01	-8.273e-02	-3.411e-02 ( $\pm 3.610e-02$ )
WD	0.000e+00	0.000e+00	0.000e+00	0.000e+00	9.485e-02	1.628e-02 ( $\pm 2.265e-02$ )
breedingDIO	0.000e+00	-2.908e-01	0.000e+00	0.000e+00	0.000e+00	-6.586e-02 ( $\pm 6.525e-02$ )
DBH	2.479e-02	2.388e-02	2.475e-02	2.490e-02	2.478e-02	2.461e-02 ( $\pm 5.108e-04$ )
$D_{max}$	-7.598e-01	-7.549e-01	-7.704e-01	-7.483e-01	-7.460e-01	-7.568e-01 ( $\pm 1.725e-01$ )
DBH:SM	0.000e+00	0.000e+00	0.000e+00	1.611e-04	0.000e+00	1.697e-05 ( $\pm 2.148e-05$ )
DBH:WD	0.000e+00	0.000e+00	0.000e+00	0.000e+00	0.000e+00	7.231e-06 ( $\pm 2.338e-05$ )
DBH:breedingDIO	0.000e+00	9.200e-04	0.000e+00	0.000e+00	0.000e+00	1.846e-04 ( $\pm 1.362e-04$ )
DBH: $D_{max}$	-1.189e-02	-1.148e-02	-1.185e-02	-1.203e-02	-1.188e-02	-1.182e-02 ( $\pm 3.947e-04$ )
var(species)	1.642e+00	1.652e+00	1.629e+00	1.598e+00	1.624e+00	1.634e+00

Table S9.3: Five best models of fecundity parameter  $\beta$  (out of 16 total), with their AIC values and weights.

model	formulas	weight	$\Delta AIC$
mod8	$fec \sim SM + D_{max} + breeding$	0.400	0.000
mod7	$fec \sim SM + D_{max} + WD + breeding$	0.235	1.066
mod5	$fec \sim SM + D_{max}$	0.127	2.302
mod3	$fec \sim SM + breeding$	0.063	3.691
mod6	$fec \sim SM + D_{max} + WD$	0.057	3.880

Table S9.4: Estimated parameters of the five best models of seed production (fecundity) parameter  $\beta$ , and of the average model, where the average model was constructed from all 16 models weighted by their weights.

	mod3	mod5	mod6	mod7	mod8	Weighted average
(Intercept)	-1.952e+00	-1.030e+00	-1.077e+00	-1.359e+00	-1.286e+00	-1.363e+00 ( $\pm 2.093e-01$ )
SM	-1.406e+00	-1.401e+00	-1.454e+00	-1.544e+00	-1.471e+00	-1.470e+00 ( $\pm 1.151e-01$ )
WD	0.000e+00	0.000e+00	1.514e-01	1.995e-01	0.000e+00	7.500e-02 ( $\pm 7.493e-02$ )
breedingDIO	8.047e-01	0.000e+00	0.000e+00	9.337e-01	8.946e-01	6.694e-01 ( $\pm 2.638e-01$ )
$D_{max}$	0.000e+00	-7.639e-01	-7.223e-01	-7.719e-01	-8.241e-01	-6.490e-01 ( $\pm 2.029e-01$ )

Table S9.5: Five best models of the scale parameter of the (Weibull) recruit size distribution ( $f_{dist}$ ) (out of 16 total), with their AIC values and weights.

model	formulas	weight	$\Delta AIC$
mod6	$scale \sim SM + D_{max}$	0.435	0.000
mod8	$scale \sim SM + breeding + D_{max}$	0.163	1.965
mod7	$scale \sim SM + WD + D_{max}$	0.160	1.994
mod2	$scale \sim SM$	0.096	3.022
mod9	$scale \sim SM + WD + breeding + D_{max}$	0.060	3.960

Table S9.6: Estimated parameters of the five best models of scale parameter of the (Weibull) recruit size distribution, and of the average model, where the average model was constructed from all 16 models weighted by their weights.

	mod2	mod6	mod7	mod8	mod9	Weighted average
(Intercept)	1.128e+02	1.084e+02	1.084e+02	1.089e+02	1.089e+02	1.093e+02 ( $\pm 2.439e+00$ )
SM	2.252e+01	2.023e+01	2.034e+01	2.037e+01	2.047e+01	2.072e+01 ( $\pm 2.372e+00$ )
WD	0.000e+00	0.000e+00	-3.853e-01	0.000e+00	-3.641e-01	-1.577e-01 ( $\pm 9.190e-01$ )
breedingDIO	0.000e+00	0.000e+00	0.000e+00	-1.645e+00	-1.630e+00	-3.184e-01 ( $\pm 1.642e+00$ )
$D_{max}$	0.000e+00	1.018e+01	1.015e+01	1.029e+01	1.025e+01	8.344e+00 ( $\pm 2.607e+00$ )

Table S9.7: Five best models of the shape parameter of the (Weibull) recruit size distribution ( $f_{dist}$ ) (out of 16 total), with their AIC values and weights.

model	formulas	weight	$\Delta AIC$
mod1	$shape \sim SM$	0.226	0.000
mod3	$shape \sim SM + breeding$	0.186	0.390
mod2	$shape \sim SM + WD$	0.138	0.988
mod5	$shape \sim SM + D_{max}$	0.122	1.225
mod4	$shape \sim SM + WD + breeding$	0.116	1.326

Table S9.8: Estimated parameters of the five best models of shape parameter of the (Weibull) recruit size distribution, and of the average model, where the average model was constructed from all 16 models weighted by their weights.

	mod1	mod2	mod3	mod4	mod5	Weighted average
(Intercept)	2.158e+00	2.165e+00	2.091e+00	2.097e+00	2.127e+00	2.122e+00 ( $\pm 3.508e-02$ )
SM	5.212e-01	5.456e-01	5.009e-01	5.255e-01	5.050e-01	5.166e-01 ( $\pm 3.289e-02$ )
WD	0.000e+00	-9.254e-02	0.000e+00	-9.375e-02	0.000e+00	-3.425e-02 ( $\pm 2.476e-02$ )
breedingDIO	0.000e+00	0.000e+00	2.034e-01	2.051e-01	0.000e+00	8.858e-02 ( $\pm 5.499e-02$ )
$D_{max}$	0.000e+00	0.000e+00	0.000e+00	0.000e+00	7.208e-02	2.141e-02 ( $\pm 1.819e-02$ )

Table S9.9: Five best models of seedling establishment (out of 16 total), with their AIC values and weights.

model	formulas	weight	$\Delta AIC$
mod6	$qlogis(p) \sim SM + D_{max} + WD$	0.347	0.000
mod5	$qlogis(p) \sim SM + D_{max}$	0.270	0.501
mod7	$qlogis(p) \sim SM + D_{max} + WD + breeding$	0.217	0.939
mod8	$qlogis(p) \sim SM + D_{max} + breeding$	0.167	1.463
mod12	$qlogis(p) \sim D_{max} + WD$	0.000	28.109

Table S9.10: Estimated parameters of the five best models of seedling establishment, and of the average model, where the average model was constructed from all 16 models weighted by their weights.

	mod5	mod6	mod7	mod8	mod12	Weighted average
(Intercept)	-3.237e+00	-3.334e+00	-3.237e+00	-3.139e+00	-3.537e+00	-3.254e+00 ( $\pm 1.093e-01$ )
SM	1.160e+00	1.079e+00	1.095e+00	1.176e+00	0.000e+00	1.120e+00 ( $\pm 9.444e-02$ )
WD	0.000e+00	3.002e-01	2.991e-01	0.000e+00	6.372e-01	1.689e-01 ( $\pm 1.097e-01$ )
breedingDIO	0.000e+00	0.000e+00	-3.418e-01	-3.448e-01	0.000e+00	-1.316e-01 ( $\pm 1.249e-01$ )
$D_{max}$	-1.633e+00	-1.574e+00	-1.545e+00	-1.603e+00	-1.356e+00	-1.588e+00 ( $\pm 1.070e-01$ )

Table S9.11: Five best models of seedling growth (out of 82 total), with their AIC values and weights.

model	formulas	weight	$\Delta AIC$
mod45	$growth \sim height + WD + height * SM + breeding + D_{max} + (1 species) + (1 tag)$	0.754	0.000
mod18	$growth \sim height + WD + height * SM + breeding + (1 species) + (1 tag)$	0.092	4.195
mod44	$growth \sim height + WD + height * SM + D_{max} + (1 species) + (1 tag)$	0.074	4.633
mod46	$growth \sim height + WD + height * SM + height * breeding + D_{max} + (1 species) + (1 tag)$	0.053	5.303
mod17	$growth \sim height + WD + height * SM + (1 species) + (1 tag)$	0.009	8.849

Table S9.12: Estimated parameters of the five best models of seedling growth, and of the average model, where the average model was constructed from all 82 models weighted by their weights.

	mod17	mod18	mod44	mod45	mod46	Weighted average
(Intercept)	4.775e+01	4.867e+01	4.970e+01	5.039e+01	4.925e+01	5.002e+01 ( $\pm 5.340e+00$ )
SM	-1.700e+01	-1.684e+01	-1.512e+01	-1.506e+01	-1.620e+01	-1.536e+01 ( $\pm 4.748e+00$ )
WD	-1.635e+01	-1.645e+01	-1.692e+01	-1.699e+01	-1.711e+01	-1.683e+01 ( $\pm 4.903e+00$ )
breedingDIO	0.000e+00	-2.793e+00	0.000e+00	-2.165e+00	3.050e+00	-1.719e+00 ( $\pm 8.264e+00$ )
height	-1.161e-02	-1.162e-02	-1.162e-02	-1.162e-02	-9.639e-03	-1.150e-02 ( $\pm 1.054e-03$ )
$D_{max}$	0.000e+00	0.000e+00	-5.291e+00	-5.189e+00	-4.754e+00	-4.593e+00 ( $\pm 4.811e+00$ )
height:SM	9.530e-03	9.529e-03	9.500e-03	9.503e-03	1.061e-02	9.574e-03 ( $\pm 1.068e-03$ )
height:WD	0.000e+00	0.000e+00	0.000e+00	0.000e+00	0.000e+00	-8.782e-07 ( $\pm 3.509e-06$ )
height:breedingDIO	0.000e+00	0.000e+00	0.000e+00	0.000e+00	-8.481e-03	-5.146e-04 ( $\pm 6.080e-04$ )
height: $D_{max}$	0.000e+00	0.000e+00	0.000e+00	0.000e+00	0.000e+00	-4.644e-06 ( $\pm 6.801e-06$ )
var(tag)	4.540e+03	4.539e+03	4.545e+03	4.542e+03	4.586e+03	4.545e+03
var(species)	1.382e+03	1.410e+03	1.386e+03	1.414e+03	1.447e+03	1.415e+03

Table S9.13: Five best models of seedling survival (out of 82 total), with their AIC values and weights.

model	formulas	weight	$\Delta AIC$
mod71	$survive \sim height + WD + height * SM + height * D_{max} + (1 species) + (1 tag)$	0.340	0.000
mod80	$survive \sim height * WD + height * SM + height * D_{max} + (1 species) + (1 tag)$	0.277	0.407
mod72	$survive \sim height + WD + height * SM + breeding + height * D_{max} + (1 species) + (1 tag)$	0.127	1.974
mod81	$survive \sim height * WD + height * SM + height * D_{max} + breeding + (1 species) + (1 tag)$	0.103	2.381
mod73	$survive \sim height + WD + height * SM + height * breeding + height * D_{max} + (1 species) + (1 tag)$	0.081	2.858

Table S9.14: Estimated parameters of the five best models of seedling survival, and of the average model, where the average model was constructed from all 82 models weighted by their weights.

	mod71	mod72	mod73	mod80	mod81	Weighted average
(Intercept)	1.495e+00	1.505e+00	1.495e+00	1.511e+00	1.521e+00	1.505e+00 ( $\pm 5.538\text{e-}02$ )
SM	-9.274e-02	-9.135e-02	-9.169e-02	-8.903e-02	-8.766e-02	-9.044e-02 ( $\pm 5.348\text{e-}02$ )
WD	4.699e-01	4.684e-01	4.679e-01	4.325e-01	4.310e-01	4.518e-01 ( $\pm 5.643\text{e-}02$ )
breedingDIO	0.000e+00	-3.152e-02	2.481e-02	0.000e+00	-3.180e-02	-3.279e-03 ( $\pm 3.930\text{e-}02$ )
height	1.391e-03	1.391e-03	1.421e-03	1.356e-03	1.356e-03	1.380e-03 ( $\pm 2.870\text{e-}05$ )
$D_{max}$	-4.775e-01	-4.761e-01	-4.874e-01	-4.826e-01	-4.811e-01	-4.811e-01 ( $\pm 5.590\text{e-}02$ )
height:SM	4.355e-04	4.354e-04	4.338e-04	4.258e-04	4.258e-04	4.308e-04 ( $\pm 2.414\text{e-}05$ )
height:WD	0.000e+00	0.000e+00	0.000e+00	9.128e-05	9.130e-05	4.154e-05 ( $\pm 3.081\text{e-}05$ )
height:breedingDIO	0.000e+00	0.000e+00	-1.490e-04	0.000e+00	0.000e+00	-2.348e-05 ( $\pm 2.341\text{e-}05$ )
height: $D_{max}$	4.334e-04	4.337e-04	4.651e-04	4.426e-04	4.428e-04	4.427e-04 ( $\pm 2.926\text{e-}05$ )
var(tag)	1.492e-13	0.000e+00	2.108e-10	8.444e-11	5.843e-15	4.073e-11
var(species)	4.794e-01	4.792e-01	4.742e-01	4.753e-01	4.750e-01	4.768e-01



Table S9.15: Five best models of seedling growth residuals (out of 16 total), with their AIC values and weights.

model	formulas	weight	$\Delta AIC$
mod7	$par \sim SM + WD + D_{max}$	0.247	0.000
mod3	$par \sim SM + WD$	0.229	0.151
mod5	$par \sim SM + WD + breeding$	0.154	0.951
mod9	$par \sim SM + WD + breeding + D_{max}$	0.150	0.992
mod6	$par \sim SM + D_{max}$	0.073	2.442

Table S9.16: Estimated parameters of the five best models of seedling growth residuals, and of the average model, where the average model was constructed from all 16 models weighted by their Akaike weights.

	mod3	mod5	mod6	mod7	mod9	Weighted average
(Intercept)	1.756e+02	1.670e+02	1.567e+02	1.682e+02	1.609e+02	1.660e+02 ( $\pm 6.145e+00$ )
SM	-5.929e+01	-6.067e+01	-7.385e+01	-6.574e+01	-6.666e+01	-6.484e+01 ( $\pm 5.572e+00$ )
WD	-3.029e+01	-2.899e+01	0.000e+00	-2.839e+01	-2.731e+01	-2.251e+01 ( $\pm 6.574e+00$ )
breedingDIO	0.000e+00	2.522e+01	0.000e+00	0.000e+00	2.280e+01	9.925e+00 ( $\pm 7.148e+00$ )
$D_{max}$	0.000e+00	0.000e+00	2.193e+01	1.922e+01	1.823e+01	1.014e+01 ( $\pm 5.697e+00$ )

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Table S9.17: Five best models of relation between seedling height and DBH (out of 82 total), with their AIC values and weights.

model	formulas	weight	$\Delta AIC$
mod55	$DBH \sim height * WD + height * SM + height * breeding + D_{max} + (1 species) + (1 tag)$	0.780	0.000
mod28	$DBH \sim height * WD + height * SM + height * breeding + (1 species) + (1 tag)$	0.185	2.878
mod54	$DBH \sim height * WD + height * SM + breeding + D_{max} + (1 species) + (1 tag)$	0.014	8.038
mod81	$DBH \sim height * WD + height * SM + breeding + height * D_{max} + (1 species) + (1 tag)$	0.007	9.343
mod53	$DBH \sim height * WD + height * SM + D_{max} + (1 species) + (1 tag)$	0.006	9.760

Table S9.18: Estimated parameters of the five best models of the relation between seedling height and DBH, and of the average model, where the average model was constructed from all 82 models weighted by their Akaike weights.

	mod28	mod53	mod54	mod55	mod81	Weighted average
(Intercept)	-4.071e+00	-3.695e+00	-3.950e+00	-4.287e+00	-4.079e+00	-4.233e+00 ( $\pm 2.640e-01$ )
SM	-1.415e+00	-1.467e+00	-1.484e+00	-1.624e+00	-1.536e+00	-1.580e+00 ( $\pm 2.160e-01$ )
WD	1.344e-01	1.633e-01	1.505e-01	2.316e-01	2.690e-01	2.117e-01 ( $\pm 2.520e-01$ )
breedingDIO	2.198e+00	0.000e+00	8.623e-01	2.097e+00	8.713e-01	2.065e+00 ( $\pm 4.215e-01$ )
height	5.889e-03	5.705e-03	5.702e-03	5.887e-03	5.780e-03	5.882e-03 ( $\pm 6.031e-05$ )
$D_{max}$	0.000e+00	6.934e-01	6.439e-01	6.520e-01	1.178e+00	5.344e-01 ( $\pm 2.500e-01$ )
height:SM	4.953e-04	4.300e-04	4.296e-04	4.964e-04	4.488e-04	4.941e-04 ( $\pm 4.299e-05$ )
height:WD	-7.206e-04	-6.727e-04	-6.713e-04	-7.192e-04	-7.370e-04	-7.185e-04 ( $\pm 6.039e-05$ )
height:breedingDIO	-6.396e-04	0.000e+00	0.000e+00	-6.397e-04	0.000e+00	-6.175e-04 ( $\pm 1.018e-04$ )
height: $D_{max}$	0.000e+00	0.000e+00	0.000e+00	0.000e+00	-2.950e-04	-3.101e-06 ( $\pm 3.435e-06$ )
var(tag)	1.738e+00	1.711e+00	1.712e+00	1.738e+00	1.708e+00	1.737e+00
var(species)	2.835e+00	2.695e+00	2.530e+00	2.602e+00	2.557e+00	2.646e+00

Table S9.19: Five best models of tree growth (out of 82 total), with their AIC values and weights.

model	formulas	weight	$\Delta AIC$
mod71	$growth \sim \log(DBH) + WD + \log(DBH) * SM + \log(DBH) * D_{max} + (1 species) + (1 tag)$	0.471	0.000
mod73	$growth \sim \log(DBH) + WD + \log(DBH) * SM + \log(DBH) * breeding + \log(DBH) * D_{max} + (1 species) + (1 tag)$	0.206	1.652
mod70	$growth \sim \log(DBH) + WD + SM + \log(DBH) * breeding + \log(DBH) * D_{max} + (1 species) + (1 tag)$	0.146	2.340
mod72	$growth \sim \log(DBH) + WD + \log(DBH) * SM + breeding + \log(DBH) * D_{max} + (1 species) + (1 tag)$	0.086	3.397
mod67	$growth \sim \log(DBH) + WD + \log(DBH) * breeding + \log(DBH) * D_{max} + (1 species) + (1 tag)$	0.055	4.303

Table S9.20: Estimated parameters of the five best models of tree growth, and of the average model, where the average model was constructed from all 82 models weighted by their Akaike weights.

	mod67	mod70	mod71	mod72	mod73	Weighted average
(Intercept)	6.828e-01	6.790e-01	7.008e-01	6.667e-01	6.810e-01	6.893e-01 ( $\pm 3.070e-02$ )
SM	0.000e+00	-1.330e-01	-1.719e-01	-1.687e-01	-1.632e-01	-1.526e-01 ( $\pm 2.825e-02$ )
WD	-3.365e-01	-3.111e-01	-3.104e-01	-3.114e-01	-3.116e-01	-3.125e-01 ( $\pm 2.652e-02$ )
breedingDIO	5.098e-02	3.547e-02	0.000e+00	1.139e-01	4.848e-02	2.852e-02 ( $\pm 3.000e-02$ )
log(DBH)	5.507e-02	5.510e-02	5.822e-02	5.820e-02	5.439e-02	5.683e-02 ( $\pm 1.911e-03$ )
$D_{max}$	-1.117e+00	-1.089e+00	-1.096e+00	-1.102e+00	-1.089e+00	-1.096e+00 ( $\pm 3.425e-02$ )
log(DBH):SM	0.000e+00	0.000e+00	9.313e-03	9.317e-03	7.891e-03	6.862e-03 ( $\pm 1.961e-03$ )
log(DBH):WD	0.000e+00	0.000e+00	0.000e+00	0.000e+00	0.000e+00	2.216e-05 ( $\pm 2.299e-05$ )
log(DBH):breedingDIO	2.119e-02	2.119e-02	0.000e+00	0.000e+00	1.782e-02	7.971e-03 ( $\pm 4.968e-03$ )
log(DBH): $D_{max}$	3.991e-01	3.990e-01	4.035e-01	4.036e-01	3.997e-01	4.018e-01 ( $\pm 2.299e-03$ )
var(tag)	2.566e-01	2.566e-01	2.567e-01	2.567e-01	2.567e-01	2.567e-01
var(species)	2.015e-01	1.873e-01	1.903e-01	1.893e-01	1.888e-01	1.901e-01

Table S9.21: Five best models of tree survival (out of 82 total), with their AIC values and weights.

model	formulas	weight	$\Delta AIC$
mod82	$surv \sim DBH * WD + DBH * SM + DBH * breeding + DBH * D_{max} + (1 species) + (1 tag)$	1.000	0.000
mod80	$surv \sim DBH * WD + DBH * SM + DBH * D_{max} + (1 species) + (1 tag)$	0.000	65.249
mod81	$surv \sim DBH * WD + DBH * SM + breeding + DBH * D_{max} + (1 species) + (1 tag)$	0.000	67.220
mod73	$surv \sim DBH + WD + DBH * SM + DBH * breeding + DBH * D_{max} + (1 species) + (1 tag)$	0.000	109.681
mod64	$surv \sim DBH * SM + DBH * breeding + DBH * D_{max} + (1 species) + (1 tag)$	0.000	135.109

Table S9.22: Estimated parameters of the five best models of tree survival, and of the average model, where the average model was constructed from all 82 models weighted by their Akaike weights.

	mod64	mod73	mod80	mod81	mod82	Weighted average
(Intercept)	2.229e+00	2.088e+00	2.048e+00	2.041e+00	2.067e+00	2.067e+00 ( $\pm 9.179e-02$ )
SM	5.190e-01	4.461e-01	4.442e-01	4.450e-01	4.420e-01	4.420e-01 ( $\pm 7.058e-02$ )
WD	0.000e+00	4.235e-01	4.830e-01	4.830e-01	4.925e-01	4.925e-01 ( $\pm 7.528e-02$ )
breedingDIO	-2.782e-02	-3.683e-02	0.000e+00	2.417e-02	-5.958e-02	-5.958e-02 ( $\pm 1.418e-01$ )
DBH	-5.143e-03	-5.138e-03	-4.386e-03	-4.387e-03	-4.830e-03	-4.830e-03 ( $\pm 1.817e-04$ )
$D_{max}$	-3.182e-01	-2.270e-01	-2.247e-01	-2.258e-01	-2.146e-01	-2.146e-01 ( $\pm 9.527e-02$ )
DBH:SM	-1.262e-03	-1.262e-03	-1.223e-03	-1.223e-03	-1.179e-03	-1.179e-03 ( $\pm 6.525e-05$ )
DBH:WD	0.000e+00	0.000e+00	-8.341e-04	-8.340e-04	-9.437e-04	-9.437e-04 ( $\pm 8.852e-05$ )
DBH:breedingDIO	9.315e-04	9.305e-04	0.000e+00	0.000e+00	1.160e-03	1.160e-03 ( $\pm 1.397e-04$ )
DBH: $D_{max}$	5.655e-03	5.654e-03	5.377e-03	5.377e-03	5.302e-03	5.302e-03 ( $\pm 1.677e-04$ )
var(tag)	9.167e-12	1.618e-11	0.000e+00	0.000e+00	0.000e+00	2.467e-35
var(species)	5.960e-01	4.539e-01	4.455e-01	4.453e-01	4.471e-01	4.471e-01

Table S9.23: Five best models of tree growth residuals (out of 16 total), with their AIC values and weights.

model	formulas	weight	$\Delta AIC$
mod7	$par \sim WD + SM + D_{max}$	0.507	0.000
mod9	$par \sim WD + SM + breeding + D_{max}$	0.488	0.079
mod8	$par \sim WD + breeding + D_{max}$	0.003	10.401
mod6	$par \sim WD + D_{max}$	0.002	10.675
mod5	$par \sim WD + SM + breeding$	0.000	50.091

Table S9.24: Estimated parameters of the five best models of tree growth residuals, and of the average model, where the average model was constructed from all 16 models weighted by their Akaike weights.

	mod5	mod6	mod7	mod8	mod9	Weighted average
(Intercept)	1.271e+00	1.160e+00	1.153e+00	1.129e+00	1.126e+00	1.140e+00 ( $\pm 2.954\text{e-}02$ )
SM	-7.500e-02	0.000e+00	-1.173e-01	0.000e+00	-1.147e-01	-1.154e-01 ( $\pm 2.292\text{e-}02$ )
WD	-2.852e-01	-2.606e-01	-2.382e-01	-2.608e-01	-2.389e-01	-2.387e-01 ( $\pm 2.433\text{e-}02$ )
breedingDIO	1.307e-01	0.000e+00	0.000e+00	1.023e-01	8.874e-02	4.356e-02 ( $\pm 4.458\text{e-}02$ )
$D_{max}$	0.000e+00	3.324e-01	3.558e-01	3.275e-01	3.511e-01	3.534e-01 ( $\pm 3.091\text{e-}02$ )

## S10 Size dependency in sex ratios

In the inverse modelling analysis (Appendix S3.1), a female probability for each tree is implemented for the dioecious species. This probability is multiplied with the reproduction probability, to obtain a seed-producing probability. To obtain these female probabilities, we performed logistic regressions relating gender (male=0, female=1) to DBH, for each species separately. Only reproductive trees, with an identified gender, were included in this analysis. The results are shown below.

Table S10.1: Estimated coefficients ( $\pm 1$  SE) for the logistic regression between DBH and gender (0=male, 1=female) in reproducing trees with identified gender.

Species	Intercept	DBH
alchco	1.4276 ( $\pm 0.6782$ )	-0.0035 ( $\pm 0.0019$ )
cecrin	-0.9211 ( $\pm 0.3498$ )	0.003 ( $\pm 0.0012$ )
cecrob	-0.0281 ( $\pm 0.4876$ )	-0.0019 ( $\pm 0.0031$ )
simaam	-1.3312 ( $\pm 0.8475$ )	0.0034 ( $\pm 0.0021$ )
poutre	1.1718 ( $\pm 0.6646$ )	-0.004 ( $\pm 0.0017$ )
protte	0.8469 ( $\pm 0.4262$ )	-0.0046 ( $\pm 0.0018$ )
tripcu	-1.3055 ( $\pm 0.6883$ )	0.0082 ( $\pm 0.0034$ )
virose	-0.3995 ( $\pm 0.5975$ )	-0.0012 ( $\pm 0.0024$ )

## S11 Gender effects on growth

To test for growth differences in growth between males and females, a linear regression was performed to explain growth as a function of  $\log(\text{DBH})$  and gender (including only identified males and females). The results are shown below. These coefficients are not used in the IPM, because in the IPM, we used trait-based tree growth models (Appendix S1.7 for details).

Table S11.1: Estimated coefficients ( $\pm 1$  SE) for the linear relation between  $\log(\text{DBH})$  and annual diameter growth in adult trees with identified gender. Gender was included as factor influencing both the intercept and slope. No general patterns across species were found.

Species	Intercept	Log(DBH)	Effect males	$\log(\text{DBH})$ :Males
cecrin	3.6989 ( $\pm 3.527$ )	0.1137 ( $\pm 0.6798$ )	4.8552 ( $\pm 4.3379$ )	-1.0807 ( $\pm 0.85$ )
poutre	8.3732 ( $\pm 2.9073$ )	-0.8053 ( $\pm 0.5527$ )	-10.6762 ( $\pm 4.814$ )	1.9749 ( $\pm 0.8949$ )
protte	6.5804 ( $\pm 1.122$ )	-0.8061 ( $\pm 0.2226$ )	-0.696 ( $\pm 1.5026$ )	0.1614 ( $\pm 0.295$ )
simaam	3.124 ( $\pm 2.4929$ )	0.3843 ( $\pm 0.4459$ )	-1.7582 ( $\pm 3.2124$ )	0.1193 ( $\pm 0.5911$ )
tripcu	0.6158 ( $\pm 2.2492$ )	0.3191 ( $\pm 0.4503$ )	6.5067 ( $\pm 3.4999$ )	-1.3564 ( $\pm 0.709$ )
alchco	11.3638 ( $\pm 2.4232$ )	-1.5167 ( $\pm 0.4509$ )	8.1896 ( $\pm 4.1956$ )	-1.5146 ( $\pm 0.7678$ )
cecrob	0.1179 ( $\pm 10.5251$ )	0.6596 ( $\pm 2.1281$ )	4.8345 ( $\pm 12.0959$ )	-0.8225 ( $\pm 2.4823$ )
virose	6.3472 ( $\pm 1.3399$ )	-0.7313 ( $\pm 0.257$ )	2.7989 ( $\pm 1.729$ )	-0.4993 ( $\pm 0.3309$ )

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