

# Supplement B: Parameter estimates

## Pulsed-resource mast systems and the movement, demographic storage, and diet breadth of consumers

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These are estimates for the AR(4) model fitted to *Pinus*. The sample contains 27,406 tree-years and 6910 trap-years on 1325 individuals and 475 seed traps on 10 plots, over 27 years . The RMSPE is 7.44, and the DIC is 358,383. Random effects were fitted on 1325 individuals.

Table SB0.1: Posterior estimates for maturation coefficients  $\beta^v$ , main effect of species (intercepts) and species-diameter interaction.

	estimate	se	2.5%	97.5%
pinuEchi	-6.68	1.40	-9.51	-4.04
pinuRigi	-6.91	1.23	-9.11	-4.48
pinuStro	-8.32	0.35	-8.96	-7.59
pinuTaed	-7.14	0.23	-7.59	-6.67
pinuVirg	-4.45	0.90	-6.29	-2.74
pinuEchi:I(log(diam))	2.82	0.49	1.92	3.84
pinuRigi:I(log(diam))	3.25	0.52	2.27	4.18
pinuStro:I(log(diam))	3.24	0.13	2.96	3.50
pinuTaed:I(log(diam))	2.64	0.08	2.48	2.79
pinuVirg:I(log(diam))	2.09	0.35	1.44	2.82

lag-1 lag-2 lag-3 lag-4 pinuRigi-sApps -0.434+0.626i -0.434-0.626i 0.503+0.404i 0.503-0.404i pinuStro-sApps -0.013+0.414i 0.115-0.341i -0.113+0.085i 0.040-0.159i pinuTaed-piedmont 0.479+0.734i 0.479-0.734i -0.507+0.298i -0.159-0.298i pinuEchi-piedmont -0.502+0.738i -0.502-0.738i 0.562+0.367i 0.551-0.367i pinuVirg-piedmont 0.453+0.525i 0.453-0.525i -0.247+0.339i -0.247-0.339i pinuStro-NE -0.784+0.016i 0.212+0.466i 0.002-0.291i 0.482-0.191i ; xtable::xtable( xk, caption=tnames[k] ) Error in x ; 0 : invalid comparison with complex values [1] "eigenSe"

Table SB0.2: Posterior estimates for fecundity coefficients  $\beta^x$ , main effect of species (intercepts) and species-diameter interaction.

	estimate	se	2.5%	97.5%
pinuEchi	-4.91	1.92	-8.71	-1.15
pinuRigi	-0.84	1.92	-4.74	2.95
pinuStro	2.26	1.00	0.41	4.35
pinuTaed	0.06	0.70	-1.35	1.39
pinuVirg	4.76	2.02	0.91	8.77
pinuEchi:I(log(diam))	2.72	0.54	1.66	3.78
pinuRigi:I(log(diam))	1.39	0.58	0.24	2.58
pinuStro:I(log(diam))	-0.08	0.29	-0.68	0.47
pinuTaed:I(log(diam))	1.35	0.19	0.99	1.74
pinuVirg:I(log(diam))	0.61	0.72	-0.79	1.98
$\sigma^2$	2.78	0.06	2.69	2.92

lag-1 lag-2 lag-3 pinuRigi-sApps 0.01580-0.01480i 0.01580+0.01480i 0.0238+0.0215i  
pinuStro-sApps 0.37000+0.11600i 0.07100+0.20000i 0.2660-0.0340i pinuTaed-piedmont  
0.24800-0.05400i 0.24800+0.05400i 0.2410+0.1980i pinuEchi-piedmont 0.02430+0.02510i  
0.02430-0.02510i 0.0510+0.1030i pinuVirg-piedmont 0.00881+0.00027i 0.00881-0.00027i  
0.0050-0.0263i pinuStro-NE 0.11400+0.10300i 0.25900-0.34200i 0.0120-0.6060i lag-4 pinuRigi-  
sApps 0.0238-0.0215i pinuStro-sApps 0.3010+0.0390i pinuTaed-piedmont 0.3230+0.1730i  
pinuEchi-piedmont 0.0870-0.1070i pinuVirg-piedmont 0.0050+0.0263i pinuStro-NE 0.3080+0.2920i

Table SB0.3: Group-level random fecundity coefficients  $\beta^w$ , with the main effects of species (intercepts) and species-diameter interaction. Below are AR(4) coefficients as fixed effects,  $\alpha_l, l = 1, \dots, p$ .

	estimate	std err
pinuEchi	0.69	0.08
pinuRigi	0.70	0.08
pinuStro	0.69	0.08
pinuTaed	0.69	0.08
pinuVirg	0.69	0.07
pinuEchi:I(log(diam))	0.61	0.06
pinuRigi:I(log(diam))	0.61	0.07
pinuStro:I(log(diam))	0.33	0.03
pinuTaed:I(log(diam))	0.41	0.03
pinuVirg:I(log(diam))	0.72	0.07
AR(4) coefficients:		
lag-1	0.38	0.24
lag-2	-0.13	0.25
lag-3	-0.25	0.15
lag-4	-0.09	0.27

Table SB0.4: AR(4) coefficients for random groups  $\alpha_{g,t}$ . Groups are defined by species-region. Between-group standard deviation (SD) is  $diag(\mathbf{A}_\alpha)^{1/2}$ .

	lag-1	lag-2	lag-3	lag-4
pinuRigi-sApps	-0.25	0.01	0.47	-0.15
pinuStro-sApps	-0.36	0.09	0.22	0.06
pinuTaed-piedmont	-0.12	-0.12	-0.00	-0.14
pinuEchi-piedmont	-0.27	-0.01	0.68	-0.28
pinuVirg-piedmont	0.03	-0.08	0.17	0.00
pinuStro-NE	-0.47	0.20	0.17	0.34
SD	0.24	0.25	0.15	0.27

Table SB0.5: Posterior mean estimates for the  $M \times H$  matrix  $\mathbf{M}$  in table SB0.5. Species-plot combinations not shown are unambiguous and thus do not have estimates.

	pinuRigi	pinuStro	pinuTaed	pinuUNKN
pinuRigi-CW118	0.54	0.00	0.00	0.46
pinuStro-MHF	0.00	0.01	0.00	0.99
pinuStro-MHP	0.00	0.06	0.00	0.94

Table SB0.6: Posterior standard errors for the  $M \times H$  matrix  $\mathbf{M}$  in table SB0.5.

	pinuRigi	pinuStro	pinuTaed	pinuUNKN
pinuRigi-CW118	0.02	0.00	0.00	0.02
pinuStro-MHF	0.00	0.00	0.00	0.00
pinuStro-MHP	0.00	0.02	0.00	0.02

Table SB0.7: Posterior estimates for dispersal parameters  $u_g$  for random species-region groups, overall mean and variance, and transformed to mean dispersal distance  $d$ .

	group	parameter	estimate	std.err	2.5%	97.5%
1	pinuRigi-sApps	$u$ (m <sup>2</sup> )	271	4.74	262	280
2	pinuStro-sApps		268	4.06	260	276
3	pinuTaed-piedmont		265	4.30	257	274
4	pinuEchi-piedmont		267	5.11	258	280
5	pinuVirg-piedmont		346	3.70	339	354
6	pinuStro-NE		274	3.75	266	281
7	mean		265	2.79	259	270
8	variance		10.30	0.06	10.1	10.4
9	pinuRigi-sApps	$d$ (m)	25.8	0.23	25.4	26.3
10	pinuStro-sApps		25.7	0.20	25.3	26.1
11	pinuTaed-piedmont		25.6	0.21	25.2	26.0
12	pinuEchi-piedmont		25.7	0.24	25.2	26.3
13	pinuVirg-piedmont		29.2	0.16	28.9	29.6
14	pinuStro-NE		26.0	0.18	25.6	26.3
15	mean		25.6	0.13	25.3	25.8
16	variance		5.03	0.02	5.00	5.06