

Table.xxx BRMS model outputs: propagation effects on maximum width analysis across species. Model structure per species: (log(max width) ~ log(cutting length)*Site.

	Estimate	Est. Error	Lower 95% CI (log)	Upper 95% CI (log)	Rhat	Bulk Effective Sample Size	Tail Effective Sample Size	Effect	Sample Size	Species
Intercept	3.00	1.97	-0.75	6.95	1	2623.96	3075.51	fixed	42	Salix richardsonii
log(Cutting length)	0.18	0.55	-0.91	1.22	1	2641.25	3073.42	fixed	42	Salix richardsonii
Site:Qikiqtaruk	-0.18	3.39	-6.90	6.42	1	2235.58	2614.26	fixed	42	Salix richardsonii
log(Cutting length) * Site	-0.20	0.94	-2.02	1.65	1	2237.53	2584.91	fixed	42	Salix richardsonii
Sigma	0.56	0.07	0.45	0.71	1	3211.76	3336.57	residual	42	Salix richardsonii
Intercept	2.14	2.79	-3.27	7.73	1	1701.10	1883.80	fixed	57	Salix pulchra
log(Cutting length)	0.38	0.78	-1.19	1.90	1	1708.46	1969.11	fixed	57	Salix pulchra
Site:Qikiqtaruk	0.24	2.86	-5.48	5.82	1	1683.40	2031.01	fixed	57	Salix pulchra
log(Cutting length) * Site	-0.35	0.79	-1.90	1.23	1	1684.58	1959.04	fixed	57	Salix pulchra
Sigma	0.60	0.06	0.50	0.74	1	2881.39	2942.44	residual	57	Salix pulchra
Intercept	2.28	1.12	0.19	4.49	1	2751.82	3297.91	fixed	23	Salix arctica
log(Cutting length)	0.27	0.37	-0.46	0.96	1	2759.30	3613.38	fixed	23	Salix arctica
Site:Qikiqtaruk	-0.08	2.11	-4.33	3.97	1	2013.91	2655.55	fixed	23	Salix arctica
log(Cutting length) * Site	-0.06	0.65	-1.31	1.26	1	1964.79	2695.76	fixed	23	Salix arctica
Sigma	0.53	0.10	0.39	0.75	1	3097.69	3297.94	residual	23	Salix arctica