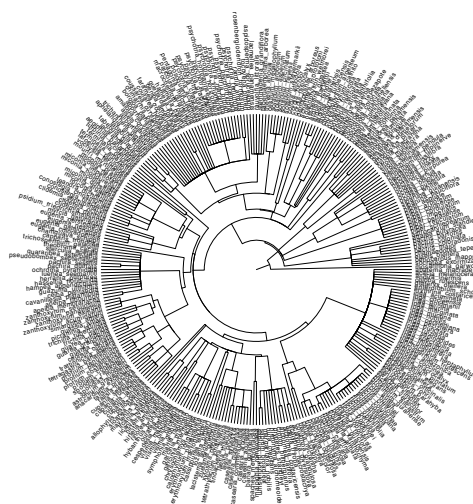


1 Supplementary analyses and results

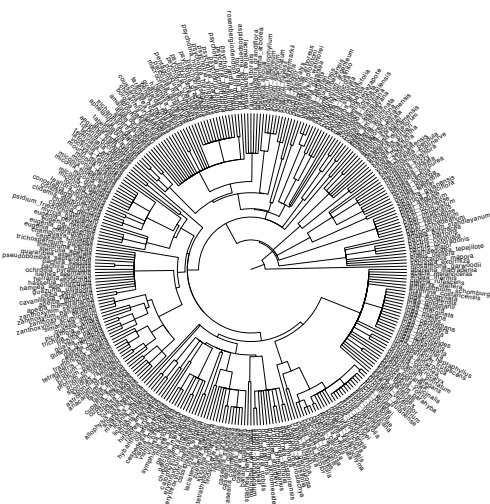
2 Phylogenies



(a) Kress phylogeny



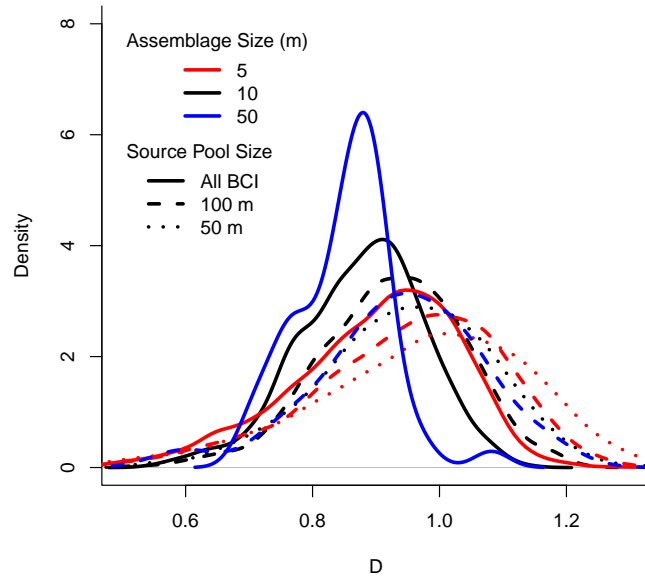
(b) Phylomatic phylogeny



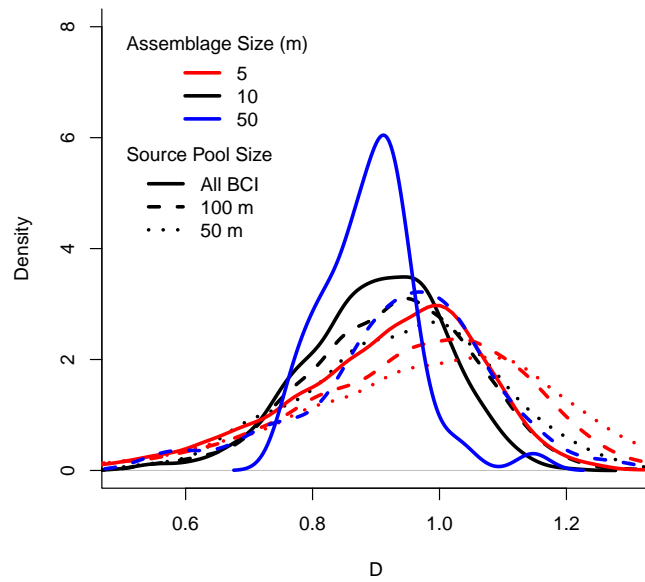
(c) Control Phylogeny

Fig. A1: The three phylogenies used in the study. Note the lack of resolution in the Phylomatic (b) and control (c) phylogenies, as compared to the Kress phylogeny (a). Newick files of the phylogenies are in a separate files in in the Supplementary Materials.

3 Density Plots

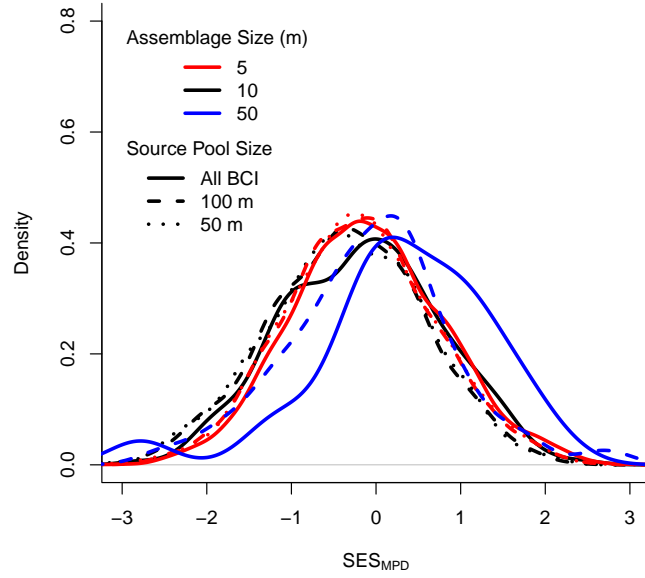


(a) Phylomatic Phylogeny

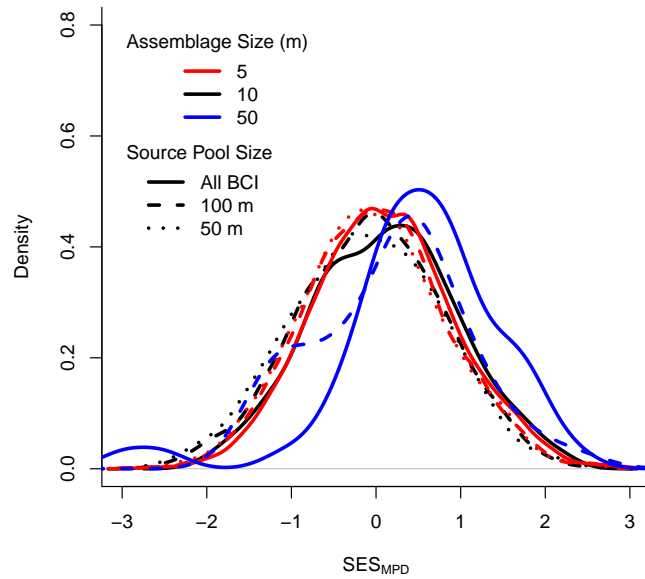


(b) Control Phylogeny

Fig. A2: Density plots of D with different assemblage and source pool sizes in the Phylomatic and Control phylogenies.

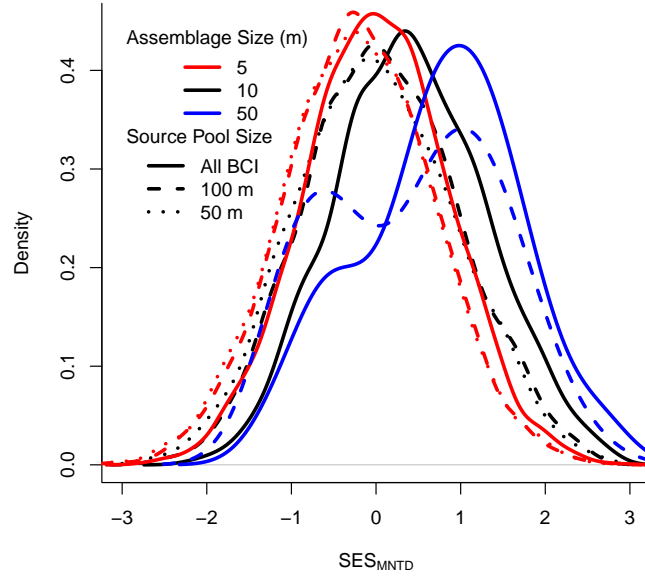


(a) Phylomatic Phylogeny

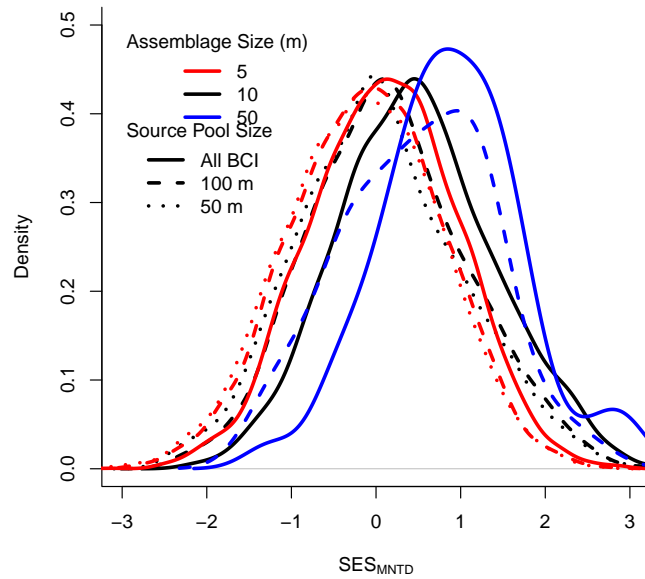


(b) Control Phylogeny

Fig. A3: Density plots of SES_{MPD} with different assemblage and source pool sizes in the Phylomatic and control phylogenies.

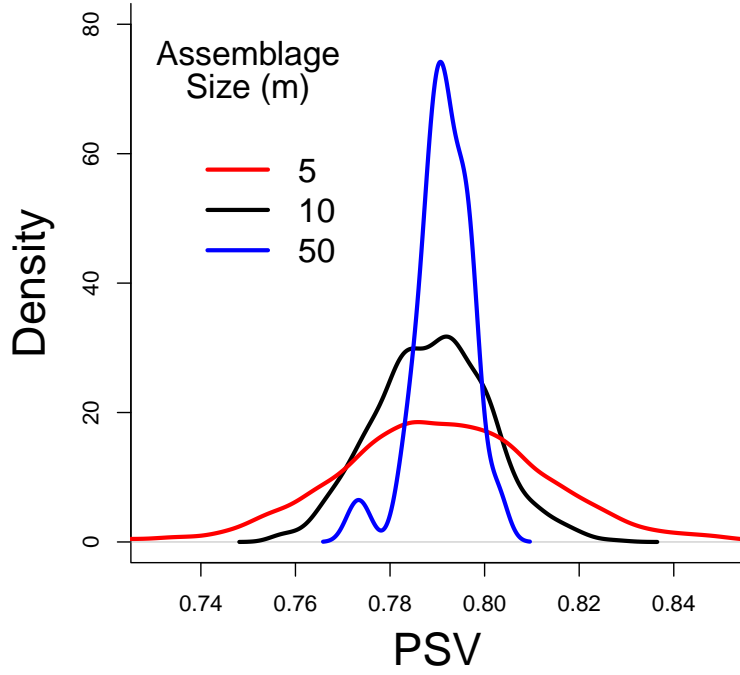


(a) Phylomatic Phylogeny

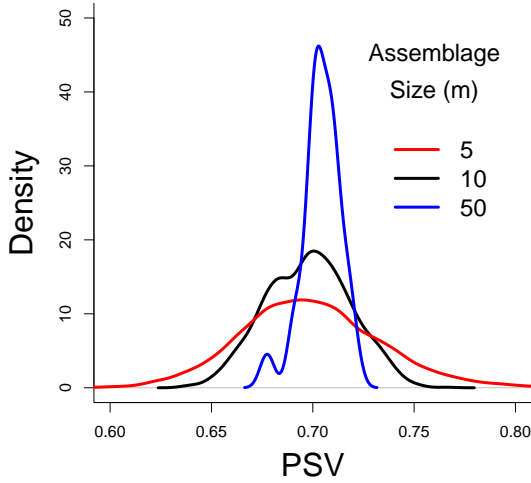


(b) Control Phylogeny

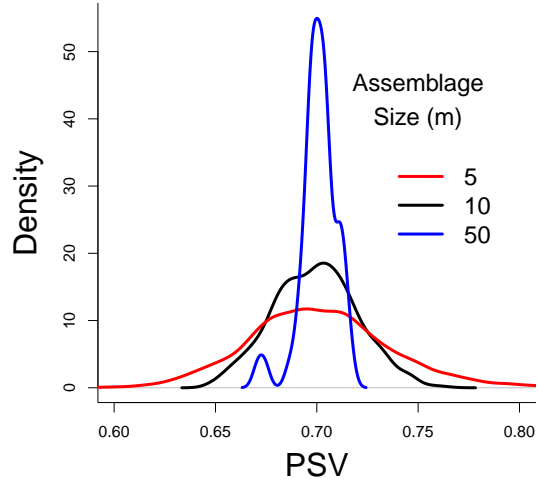
Fig. A4: Density plots of SES_{MNTD} with different assemblage and source pool sizes in the Phylomatic and control phylogenies.



(a) Kress Phylogeny

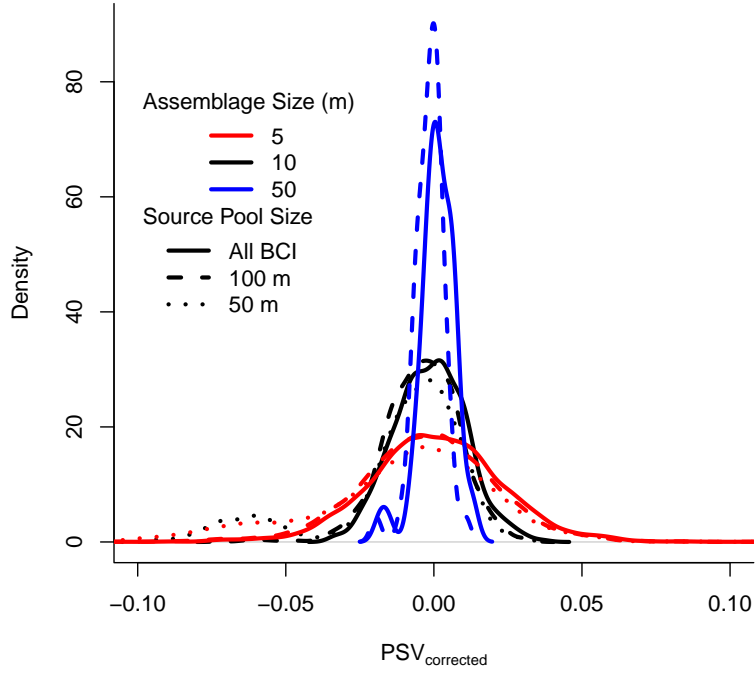


(b) Phylomatic Phylogeny

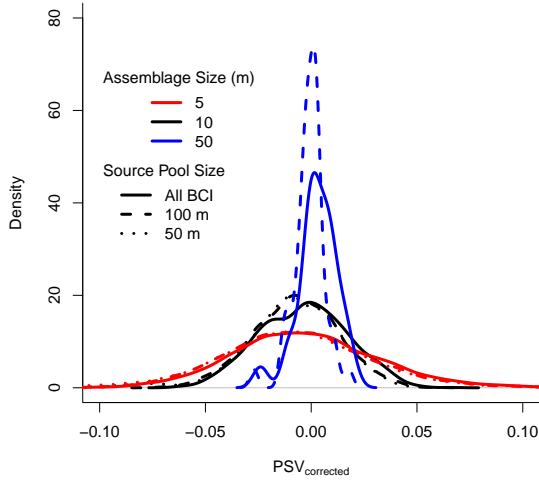


(c) Control Phylogeny

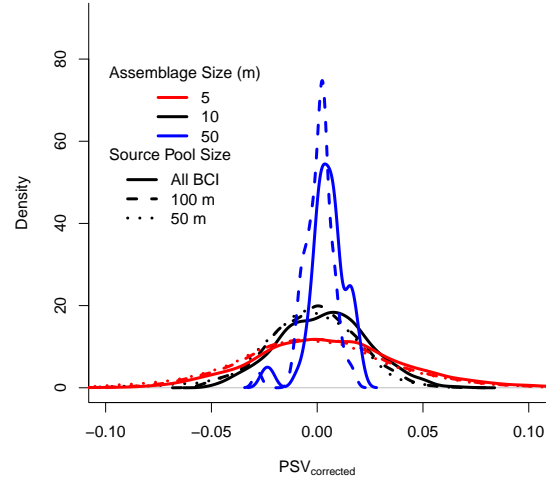
Fig. A5: Density plots of PSV with different assemblage sizes in all three phylogenies. PSV was calculated using the function `psv` in the R package `picante` (Kembel *et al.*, 2010), using the same community definitions as described in the main text. See the next figure for an explanation of how source pool size was assessed using PSV .



(a) Kress Phylogeny



(b) Phylomatic Phylogeny



(c) Control Phylogeny

Fig. A6: Density plots of corrected PSV with different assemblage sizes in all three phylogenies. Since PSV values are calculated across a phylogeny of present species, we subtracted the mean PSV of 1000 randomly-assembled assemblages with the same species richness from each assemblage's source pool to give 'corrected PSV '.

4 Mixed effects models

Assemblage	Source Pool	Phylomatic	Control
5	50	0.97 ± 0.0052	0.97 ± 0.0070
5	100	0.95 ± 0.0052	0.95 ± 0.0070
5	All BCI	0.90 ± 0.0052	0.90 ± 0.0070
10	50	0.95 ± 0.0074	0.93 ± 0.0074
10	100	0.92 ± 0.0074	0.91 ± 0.0074
10	All BCI	0.88 ± 0.0074	0.89 ± 0.0074
50	100	0.94 ± 0.0181	0.93 ± 0.0154
50	All BCI	0.86 ± 0.0181	0.88 ± 0.0154

(a) D Values

Assemblage	Source Pool	Phylomatic	Control
5	50	-0.13 ± 0.0215	0.03 ± 0.0290
5	100	-0.13 ± 0.0215	0.06 ± 0.0290
5	All BCI	-0.03 ± 0.0215	0.16 ± 0.0290
10	50	-0.30 ± 0.0394	-0.01 ± 0.0409
10	100	-0.30 ± 0.0394	0.05 ± 0.0409
10	All BCI	-0.11 ± 0.0394	0.23 ± 0.0409
50	100	-0.10 ± 0.1099	0.39 ± 0.1026
50	All BCI	0.40 ± 0.1089	0.73 ± 0.1017

(b) SES_{MPD} Values

Assemblage	Source Pool	Phylomatic	Control
5	50	-0.19 ± 0.0218	-0.11580 ± 0.0270
5	100	-0.17 ± 0.0218	-0.06508 ± 0.0270
5	All BCI	0.04 ± 0.0218	0.13488 ± 0.0270
10	50	0.04 ± 0.0388	0.08723 ± 0.0417
10	100	0.12 ± 0.0388	0.19955 ± 0.0417
10	All BCI	0.44 ± 0.0388	0.52777 ± 0.0417
50	100	0.51 ± 0.1072	0.64197 ± 0.1090
50	All BCI	0.84 ± 0.1071	1.04558 ± 0.1090

(c) SES_{MNTD} Values

Table A1: Mixed effects model estimates of mean values (\pm SE) of D , SES_{MPD} , and SES_{MNTD} values across BCI in the Phylomatic and control phylogenies. D Phylomatic (AIC — -22886 vs. -21496; p-value of likelihood ratio test < 0.0001) and control (AIC — -24604 vs. -22896; p-value of likelihood ratio test < 0.0001) models showed statistically significant effects of source pool and assemblage size when compared with a null model containing neither variable. SES_{MPD} Phylomatic (AIC — 44678 vs. 44848; p-value of likelihood ratio test < 0.0001) and control (AIC — 41518 vs. 41778; p-value of likelihood ratio test < 0.0001) models showed statistically significant effects of source pool and assemblage size when compared with a null model containing neither variable.

Assemblage	Source Pool	Phylomatic	Control	
10	0.79 ± 0.0008	0.70 ± 0.0011	0.70 ± 0.0014	
5	0.79 ± 0.0006	0.70 ± 0.0008	0.70 ± 0.0011	
50	0.79 ± 0.0030	0.71 ± 0.0046	0.70 ± 0.0047	
AIC _{model}		-30961	-25450	-25382
AIC _{null}		-30958	-25451	-25382
LRT p-value		0.028	0.275	0.101

(a) *PSV* Values

Assemblage	Source Pool	Kress	Phylomatic	Control
10	50	-0.01 \pm 0.0011	-0.01 \pm 0.0014	0.00 \pm 0.0016
10	All BCI	0.00 \pm 0.0011	0.00 \pm 0.0014	0.01 \pm 0.0016
10	100	0.00 \pm 0.0011	-0.01 \pm 0.0014	0.00 \pm 0.0016
5	50	-0.01 \pm 0.0007	-0.01 \pm 0.0008	0.00 \pm 0.0011
5	All BCI	0.00 \pm 0.0007	0.00 \pm 0.0008	0.01 \pm 0.0011
5	100	0.00 \pm 0.0007	0.00 \pm 0.0008	0.00 \pm 0.0011
50	All BCI	0.00 \pm 0.0031	0.01 \pm 0.0039	0.01 \pm 0.0040
50	100	0.00 \pm 0.0031	0.00 \pm 0.0039	0.01 \pm 0.0040
AIC_{model}		-89790	-80758	-79999
AIC_{null}		-88842	-80581	-79651
LRT p-value		<0.0001	<0.0001	<0.0001

(b) Corrected *PSV* Values

Table A2: Mixed effects model estimates of of mean values (\pm SE) of *PSV* and corrected *PSV* values across BCI in the three phylogenies. Mixed effect model AIC and LRT p-values are given in the final three rows for each dataset; each was calculated as described in the text for *D* and *SES_{MPD}*. The exception to this is *PSV* (but not corrected *PSV*); no random effect term was fitted for each 5m radius circle, since these uncorrected values do not allow for variation in source pool size, and so fitting such a model would fit a random effect term for each 5m radius assemblage and so cause fitting errors. Note that the estimates for *PSV* do not change appreciably with spatial scale; therefore there is no danger that a change in the way in which spatial variation was accounted for led to an artifactual increase in effect size.

5 Quantile Regressions

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	0.74	0.87	0.99	1.10	1.18
5	100	0.74	0.86	0.97	1.06	1.13
5	All BCI	0.71	0.82	0.92	1.00	1.05
10	50	0.78	0.87	0.95	1.04	1.11
10	100	0.78	0.85	0.93	1.01	1.06
10	All BCI	0.75	0.81	0.89	0.95	1.00
50	100	0.76	0.86	0.95	1.03	1.08
50	All BCI	0.75	0.80	0.86	0.89	0.92
Range		0.07	0.07	0.13	0.21	0.26

(a) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	0.71	0.85	1.00	1.12	1.22
5	100	0.72	0.85	0.98	1.08	1.17
5	All BCI	0.70	0.82	0.94	1.02	1.09
10	50	0.73	0.84	0.95	1.04	1.12
10	100	0.75	0.84	0.93	1.01	1.08
10	All BCI	0.75	0.83	0.91	0.98	1.03
50	100	0.74	0.87	0.96	1.03	1.12
50	All BCI	0.79	0.84	0.89	0.92	0.97
Range		0.09	0.05	0.11	0.20	0.25

(b) Control Phylogeny

Table A3: Quantile regression of D values across BCI in the Phylomatic and control phylogenies.

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
10	50	0.0080	0.0054	0.0042	0.0042	0.0053
10	All BCI	0.0091	0.0065	0.0054	0.0048	0.0064
10	100	0.0093	0.0066	0.0060	0.0055	0.0068
5	50	0.0090	0.0062	0.0050	0.0049	0.0062
5	All BCI	0.0088	0.0058	0.0046	0.0046	0.0057
5	100	0.0090	0.0062	0.0050	0.0047	0.0058
50	All BCI	0.0383	0.0124	0.0085	0.0119	0.0059
50	100	0.0279	0.0112	0.0134	0.0144	0.0087

(a) Kress Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	0.0105	0.0067	0.0059	0.0053	0.0064
5	100	0.0102	0.0064	0.0057	0.0051	0.0063
5	All BCI	0.0099	0.0063	0.0056	0.0050	0.0062
10	50	0.0088	0.0055	0.0051	0.0046	0.0057
10	100	0.0103	0.0074	0.0069	0.0063	0.0074
10	All BCI	0.0098	0.0071	0.0061	0.0056	0.0074
50	100	0.0533	0.0109	0.0149	0.0069	0.0329
50	All BCI	0.0248	0.0194	0.0122	0.0046	0.0074

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
10	50	0.0069	0.0062	0.0060	0.0052	0.0078
10	100	0.0094	0.0079	0.0073	0.0072	0.0090
10	All BCI	0.0086	0.0080	0.0071	0.0059	0.0089
5	50	0.0097	0.0080	0.0072	0.0060	0.0085
5	100	0.0090	0.0073	0.0068	0.0060	0.0083
5	All BCI	0.0086	0.0072	0.0065	0.0056	0.0081
50	100	0.0149	0.0077	0.0217	0.0089	0.0678
50	All BCI	0.0305	0.0158	0.0170	0.0054	0.0261

(c) Control Phylogeny

Table A4: Standard errors of quantile regression of D values across BCI in all three phylogenies.

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	-1.34	-0.80	-0.20	0.40	0.98
5	100	-1.34	-0.79	-0.21	0.39	0.96
5	All BCI	-1.24	-0.71	-0.12	0.51	1.10
10	50	-1.56	-0.96	-0.36	0.31	0.84
10	100	-1.54	-0.98	-0.34	0.28	0.85
10	All BCI	-1.36	-0.87	-0.14	0.49	1.08
50	100	-1.45	-0.62	-0.07	0.40	1.12
50	All BCI	-1.09	-0.18	0.32	1.03	1.66
Range		0.47	0.80	0.68	0.75	0.82

(a) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	-1.12	-0.62	-0.06	0.52	1.08
5	100	-1.07	-0.58	-0.01	0.55	1.10
5	All BCI	-0.96	-0.48	0.08	0.63	1.20
10	50	-1.29	-0.76	-0.13	0.50	1.02
10	100	-1.19	-0.66	-0.04	0.52	1.04
10	All BCI	-1.00	-0.51	0.12	0.70	1.24
50	100	-1.19	-0.51	0.27	0.65	1.23
50	All BCI	-0.44	0.08	0.56	1.04	1.73
Range		0.85	0.84	0.69	0.54	0.71

(b) Control Phylogeny

Table A5: Quantile regression of SES_{MPD} values across BCI in the Phylomatic and Control phylogenies.

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
10	50	0.0454	0.0373	0.0320	0.0339	0.0272
10	100	0.0588	0.0522	0.0465	0.0459	0.0455
10	All BCI	0.0565	0.0478	0.0429	0.0463	0.0409
5	50	0.0492	0.0405	0.0350	0.0372	0.0315
5	100	0.0500	0.0401	0.0347	0.0359	0.0317
5	All BCI	0.0491	0.0399	0.0351	0.0367	0.0317
50	100	0.0539	0.4235	0.1351	0.0462	0.1549
50	All BCI	0.3776	0.0726	0.0837	0.1402	0.1055

(a) Kress Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
10	50	0.0382	0.0370	0.0300	0.0333	0.0537
10	All BCI	0.0614	0.0571	0.0451	0.0450	0.0670
10	100	0.0652	0.0534	0.0421	0.0465	0.0772
5	All BCI	0.0430	0.0407	0.0343	0.0386	0.0583
5	50	0.0425	0.0408	0.0339	0.0373	0.0580
5	100	0.0428	0.0409	0.0339	0.0385	0.0567
50	100	0.1061	0.2361	0.1103	0.0396	0.2841
50	All BCI	0.2991	0.0693	0.1907	0.0512	0.4082

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
10	50	0.0440	0.0366	0.0352	0.0277	0.0402
10	100	0.0658	0.0542	0.0437	0.0466	0.0640
10	All BCI	0.0593	0.0513	0.0451	0.0457	0.0600
5	50	0.0472	0.0398	0.0383	0.0331	0.0466
5	100	0.0484	0.0392	0.0382	0.0314	0.0460
5	All BCI	0.0480	0.0394	0.0386	0.0326	0.0470
50	100	0.0697	0.1562	0.1165	0.0905	0.0908
50	All BCI	0.1424	0.0753	0.0732	0.0405	0.2588

(c) Control Phylogeny

Table A6: Standard errors of quantile regression of SES_{MPD} values across BCI in all three phylogenies.

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	-1.37	-0.83	-0.23	0.39	0.92
5	100	-1.31	-0.80	-0.21	0.40	0.92
5	All BCI	-1.09	-0.57	0.00	0.58	1.11
10	50	-1.19	-0.66	-0.02	0.64	1.26
10	100	-1.10	-0.57	0.05	0.69	1.28
10	All BCI	-0.78	-0.22	0.37	1.01	1.59
50	100	-0.92	-0.55	0.63	1.30	1.79
50	All BCI	-0.62	0.14	0.81	1.38	1.81
Range		0.75	0.52	1.04	0.99	0.89

(a) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	-1.33	-0.78	-0.15	0.47	0.99
5	100	-1.26	-0.73	-0.09	0.50	1.04
5	All BCI	-1.05	-0.51	0.10	0.69	1.20
10	50	-1.18	-0.66	-0.01	0.67	1.35
10	100	-1.05	-0.52	0.10	0.75	1.41
10	All BCI	-0.71	-0.17	0.44	1.07	1.73
50	100	-0.79	-0.21	0.55	1.21	1.43
50	All BCI	-0.26	0.38	0.83	1.37	1.86
Range		1.07	1.16	0.98	0.90	0.87

(b) Control Phylogeny

Table A7: Quantile regression of SES_{MNTD} values across BCI in the Phylomatic and Control phylogenies.

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	0.0211	0.0179	0.0167	0.0165	0.0156
5	100	0.0230	0.0178	0.0163	0.0157	0.0166
5	All BCI	0.0204	0.0187	0.0160	0.0159	0.0190
10	50	0.0391	0.0363	0.0291	0.0374	0.0405
10	100	0.0380	0.0431	0.0276	0.0345	0.0294
10	All BCI	0.0512	0.0487	0.0272	0.0364	0.0460
50	100	0.0953	0.1292	0.1047	0.1041	0.0452
50	All BCI	0.0642	0.0753	0.0701	0.1853	0.6051

(a) Kress Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	0.0223	0.0155	0.0154	0.0168	0.0209
5	100	0.0212	0.0164	0.0152	0.0167	0.0204
5	All BCI	0.0198	0.0144	0.0154	0.0163	0.0206
10	50	0.0367	0.0300	0.0341	0.0410	0.0636
10	100	0.0382	0.0285	0.0347	0.0347	0.0573
10	All BCI	0.0357	0.0280	0.0297	0.0365	0.0497
50	100	0.0074	0.1468	0.0614	0.0969	0.2038
50	All BCI	0.0769	0.3560	0.0377	0.1310	0.0310

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	0.0204	0.0166	0.0163	0.0172	0.0223
5	100	0.0163	0.0179	0.0163	0.0177	0.0187
5	All BCI	0.0186	0.0173	0.0150	0.0173	0.0186
10	50	0.0339	0.0309	0.0271	0.0454	0.0506
10	100	0.0356	0.0346	0.0307	0.0387	0.0447
10	All BCI	0.0345	0.0302	0.0254	0.0465	0.0489
50	100	0.4747	0.0258	0.2407	0.0736	0.0762
50	All BCI	0.3204	0.0506	0.1084	0.0738	0.0547

(c) Control Phylogeny

Table A8: Standard errors of quantile regression of SES_{MNTD} values across BCI in all three phylogenies.

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$		
5	0.76	0.78	0.79	0.80	0.82
10	0.77	0.78	0.79	0.80	0.80
50	0.78	0.79	0.79	0.80	0.80
Range	0.02	0.01	0	0	0.02

(a) Kress Phylogeny

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$		
5	0.66	0.68	0.70	0.72	0.74
10	0.67	0.68	0.70	0.71	0.73
50	0.69	0.70	0.70	0.71	0.72
Range	0.03	0.02	0	0.01	0.02

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	
5	0.66	0.68	0.70	0.72	0.75
10	0.67	0.68	0.70	0.71	0.73
50	0.69	0.70	0.70	0.71	0.71
Range	0.03	0.02	0	0.01	0.04

(c) Control Phylogeny

Table A9: Quantile regression of PSV values across BCI in all three phylogenies.

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$		
5	0.0006	0.0004	0.0004	0.0004	0.0006
10	0.0006	0.0004	0.0005	0.0005	0.0006
50	0.0019	0.0005	0.0006	0.0008	0.0000

(a) Kress Phylogeny

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$		
5	0.0008	0.0006	0.0006	0.0008	0.0009
10	0.0011	0.0008	0.0007	0.0008	0.0011
50	0.0005	0.0018	0.0016	0.0008	0.0020

(b) Phylomatic Phylogeny

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$		
5	0.0009	0.0006	0.0006	0.0007	0.0010
10	0.0010	0.0008	0.0007	0.0008	0.0011
50	0.0008	0.0007	0.0007	0.0011	0.0008

(c) Control Phylogeny

Table A10: Standard errors of quantile regression of PSV values across BCI in all three phylogenies.

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	-0.06	-0.03	-0.01	0.01	0.02
5	100	-0.03	-0.02	0.00	0.01	0.03
5	All BCI	-0.03	-0.01	0.00	0.01	0.03
10	50	-0.06	-0.02	-0.01	0.00	0.01
10	100	-0.02	-0.01	0.00	0.00	0.01
10	All BCI	-0.02	-0.01	0.00	0.01	0.01
50	100	-0.01	0.00	0.00	0.00	0.00
50	All BCI	-0.01	0.00	0.00	0.01	0.01
Range		0.05	0.03	0.01	0.01	0.02

(a) Kress Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
10	50	-0.04	-0.02	-0.01	0.01	0.02
10	All BCI	-0.03	-0.02	0.00	0.01	0.02
10	200	-0.03	-0.02	-0.01	0.01	0.02
5	50	-0.05	-0.03	-0.01	0.01	0.04
5	All BCI	-0.04	-0.03	0.00	0.02	0.04
5	100	-0.05	-0.03	-0.01	0.01	0.04
50	All BCI	-0.01	0.00	0.00	0.01	0.01
50	100	-0.01	0.00	0.00	0.00	0.01
Range		0.04	0.03	0.01	0.02	0.03

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	-0.05	-0.03	0.00	0.02	0.04
5	100	-0.04	-0.02	0.00	0.02	0.05
5	All BCI	-0.04	-0.02	0.00	0.03	0.05
10	50	-0.03	-0.02	0.00	0.01	0.02
10	100	-0.03	-0.02	0.00	0.01	0.02
10	All BCI	-0.02	-0.01	0.00	0.02	0.03
50	100	-0.01	0.00	0.00	0.00	0.01
50	All BCI	0.00	0.00	0.01	0.01	0.02
Range		0.05	0.03	0.01	0.03	0.04

(c) Control Phylogeny

Table A11: Quantile regression of corrected *PSV* values across BCI in the Phylomatic and Control phylogenies.

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	0.0012	0.0007	0.0004	0.0004	0.0005
5	100	0.0006	0.0004	0.0004	0.0004	0.0006
5	All BCI	0.0006	0.0004	0.0004	0.0004	0.0006
10	50	0.0021	0.0007	0.0005	0.0004	0.0006
10	100	0.0007	0.0004	0.0004	0.0004	0.0005
10	All BCI	0.0006	0.0005	0.0005	0.0005	0.0006
50	100	0.0006	0.0004	0.0003	0.0007	0.0006
50	All BCI	0.0030	0.0003	0.0003	0.0005	0.0003

(a) Kress Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	0.0010	0.0007	0.0006	0.0007	0.0008
5	100	0.0008	0.0006	0.0006	0.0007	0.0008
5	All BCI	0.0009	0.0006	0.0006	0.0008	0.0009
10	50	0.0009	0.0010	0.0007	0.0007	0.0009
10	100	0.0015	0.0007	0.0006	0.0007	0.0012
10	All BCI	0.0010	0.0007	0.0007	0.0009	0.0013
50	100	0.0000	0.0012	0.0011	0.0011	0.0014
50	All BCI	0.0004	0.0010	0.0010	0.0004	0.0017

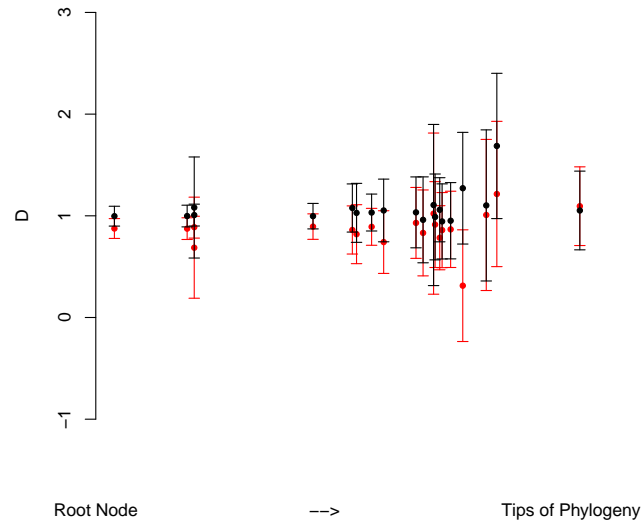
(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.10$	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	$\tau=0.90$
5	50	0.0009	0.0006	0.0006	0.0007	0.0011
5	100	0.0009	0.0006	0.0006	0.0006	0.0011
5	All BCI	0.0009	0.0005	0.0006	0.0007	0.0010
10	50	0.0012	0.0008	0.0007	0.0008	0.0009
10	100	0.0009	0.0008	0.0006	0.0009	0.0010
10	All BCI	0.0010	0.0008	0.0007	0.0007	0.0009
50	100	0.0008	0.0003	0.0008	0.0005	0.0010
50	All BCI	0.0009	0.0004	0.0003	0.0009	0.0006

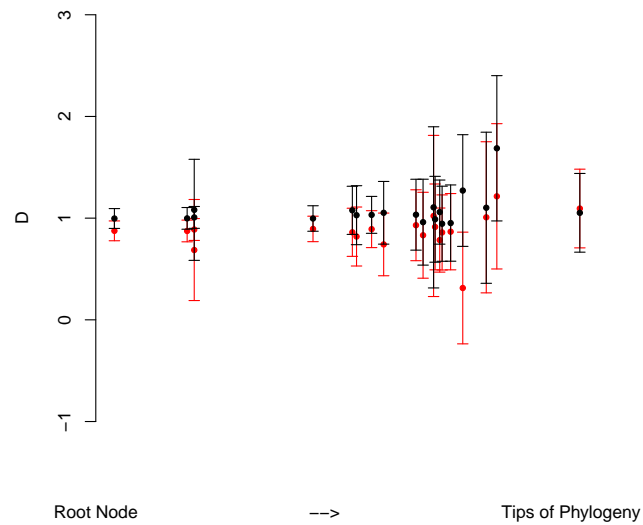
(c) Control Phylogeny

Table A12: Standard errors of quantile regression of corrected *PSV* values across BCI in all three phylogenies.

6 Phylogenetic Depth Plots



(a) Phylomatic Phylogeny



(b) Control Phylogeny

Fig. A7: Phylogenetic depth plots of D for the observed and simulated assemblages in the Phylomatic and Control phylogenies. These plots seem much more discrete than those of the Kress phylogeny, reflecting the poor resolution of both these phylogenies.

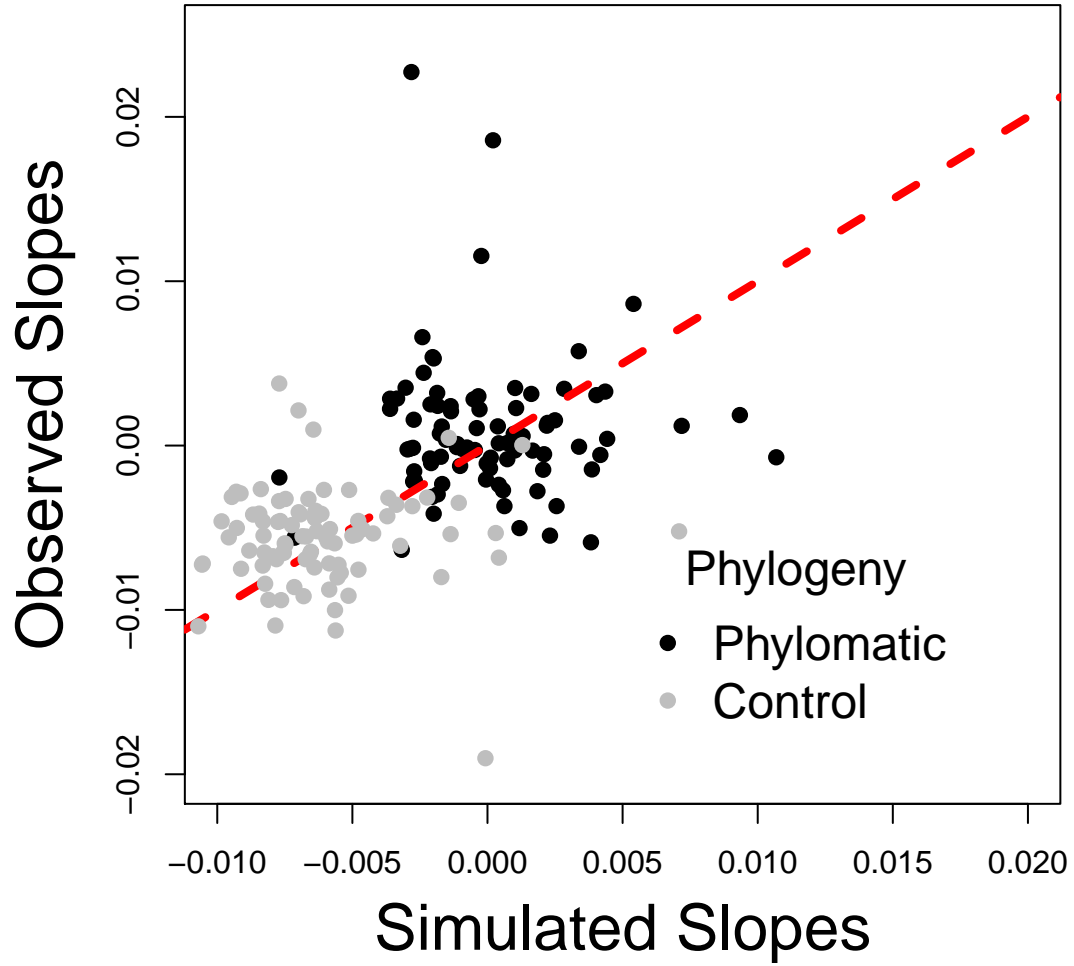
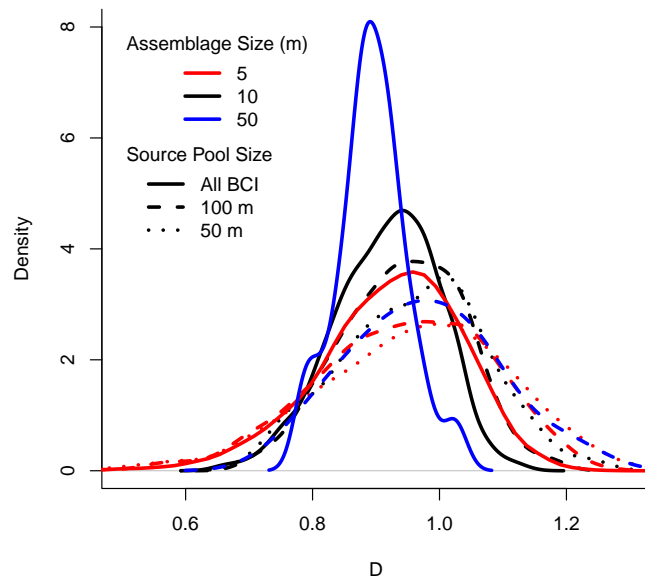


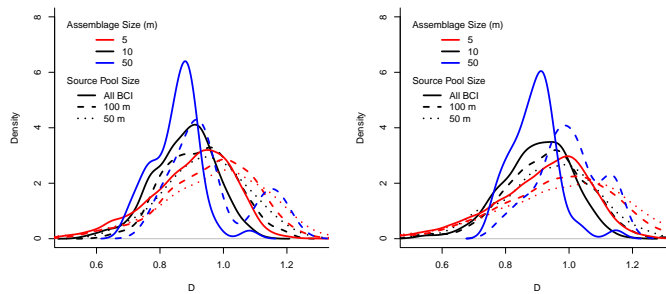
Fig. A8: Plot of observed and simulated slopes for regressions of D on clade age in the Phylomatic and control phylogenies. The red dashed line passes through the origin with a slope of 1 (the null expectation). Note the difference in scale of these figures in comparison with figure 5 in the main text; these slope estimates are extremely small.

7 Edge Results

7.1 Density plots



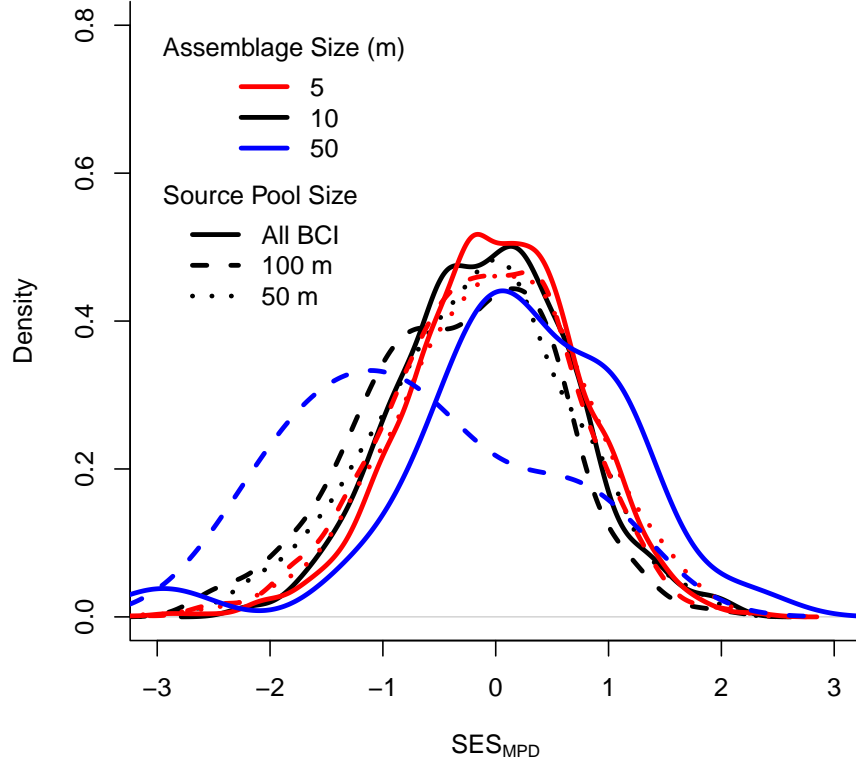
(a) Kress Phylogeny



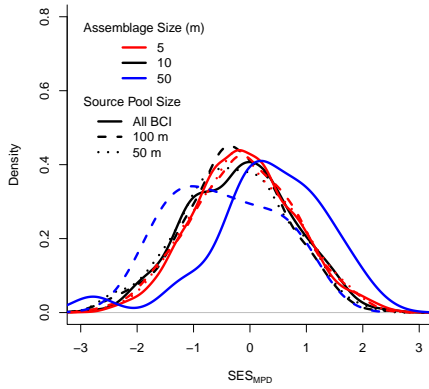
(b) Phylomatic Phylogeny

(c) Control Phylogeny

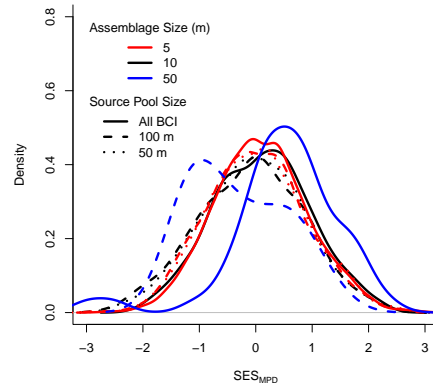
Fig. A9: Density plots of D with different assemblage and source pool sizes in all three phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.



(a) Kress Phylogeny

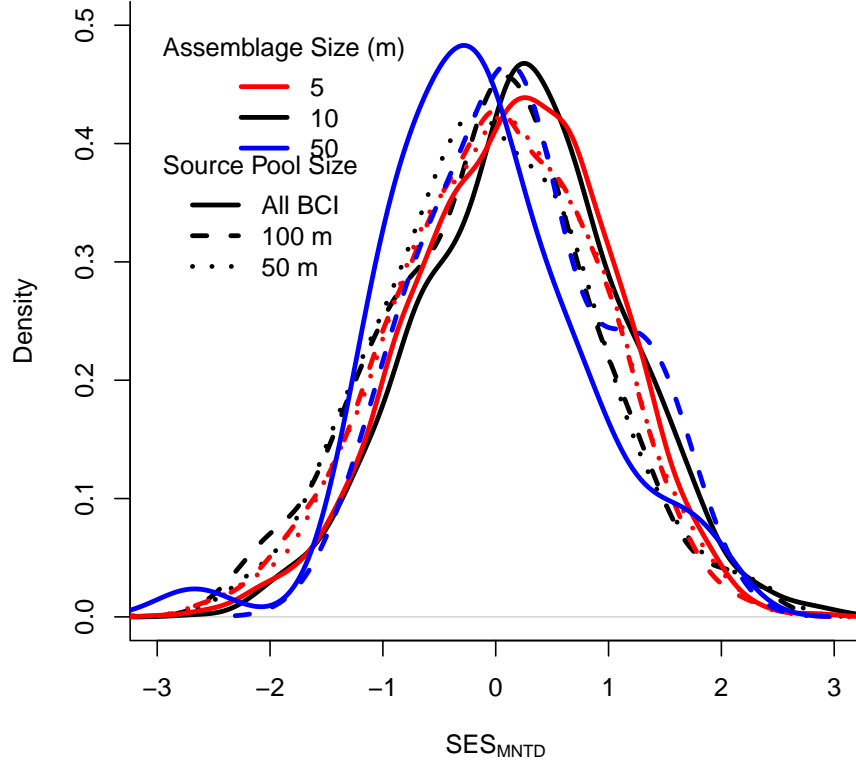


(b) Phylomatic Phylogeny

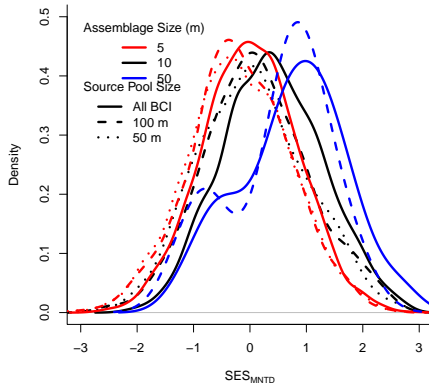


(c) Control Phylogeny

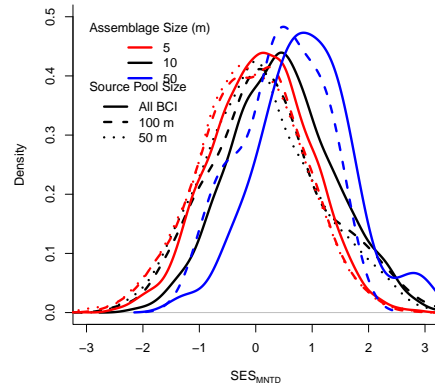
Fig. A10: Density plots of SES_{MPD} with different assemblage and source pool sizes in all three phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.



(a) Kress Phylogeny

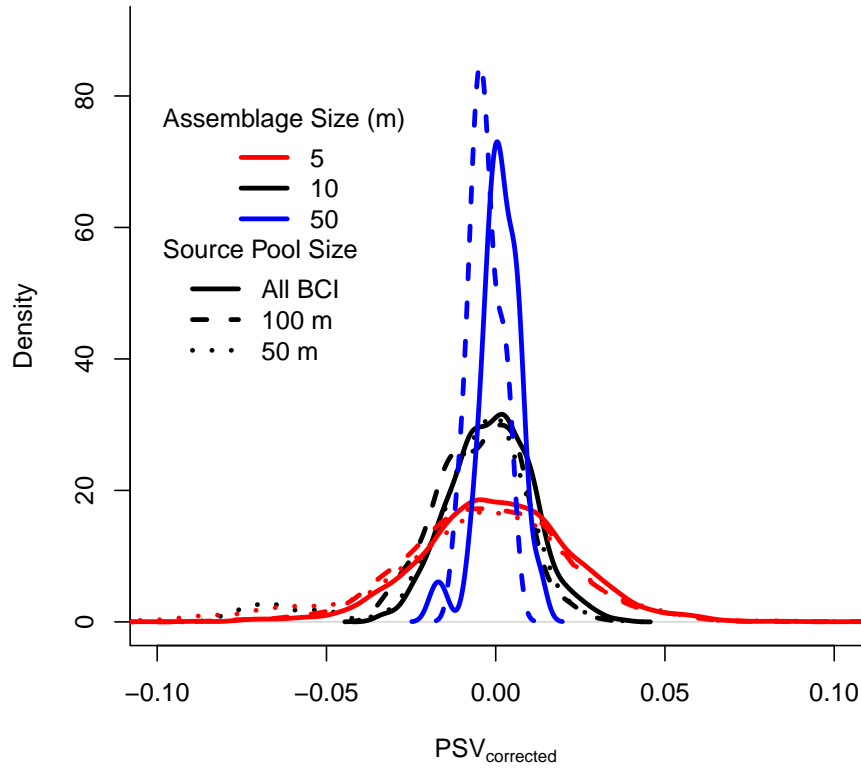


(b) Phylomatic Phylogeny

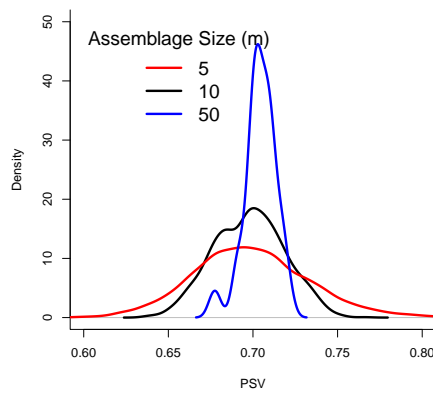


(c) Control Phylogeny

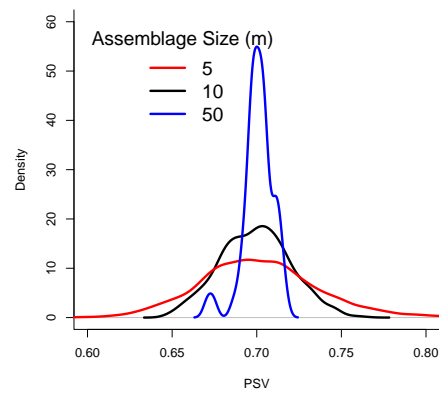
Fig. A11: Density plots of SES_{MNTD} with different assemblage and source pool sizes in all three phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.



(a) Kress Phylogeny



(b) Phylomatic Phylogeny



(c) Control Phylogeny

Fig. A12: Density plots of PSV with different assemblage and source pool sizes in all three phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.

7.2 Mixed Effects Models

Assemblage	Source Pool	Kress	Phylomatic	Control
5	50	0.96 ± 0.0059	0.96 ± 0.0055	0.97 ± 0.0073
5	100	0.94 ± 0.0060	0.95 ± 0.0058	0.95 ± 0.0075
5	All BCI	0.92 ± 0.0057	0.90 ± 0.0052	0.91 ± 0.0071
10	50	0.96 ± 0.0087	0.94 ± 0.0079	0.92 ± 0.0080
10	100	0.94 ± 0.0093	0.92 ± 0.0088	0.91 ± 0.0086
10	All BCI	0.92 ± 0.0084	0.89 ± 0.0073	0.89 ± 0.0077
50	100	0.95 ± 0.0247	0.94 ± 0.0302	1.02 ± 0.0254
50	All BCI	0.89 ± 0.0143	0.86 ± 0.0162	0.90 ± 0.0169
AIC_{model}		-15196	-13604	-13816
AIC_{null}		-14855	-13131	-13109

(a) D Values

Assemblage	Source Pool	Kress	Phylomatic	Control
5	50	0.02 ± 0.0227	-0.19 ± 0.0240	-0.10 ± 0.0283
5	100	0.00 ± 0.0255	-0.18 ± 0.0266	-0.07 ± 0.0306
5	All BCI	0.17 ± 0.0204	0.04 ± 0.0220	0.14 ± 0.0265
10	50	-0.03 ± 0.0420	0.05 ± 0.0425	0.12 ± 0.0450
10	100	-0.05 ± 0.0487	0.13 ± 0.0489	0.20 ± 0.0511
10	All BCI	0.23 ± 0.0379	0.44 ± 0.0387	0.52 ± 0.0413
50	100	0.26 ± 0.1909	0.38 ± 0.1863	0.70 ± 0.1886
50	All BCI	-0.13 ± 0.0987	0.80 ± 0.0968	1.03 ± 0.0987
AIC_{model}		20043	23656	21641
AIC_{null}		20175	23792	21819

(b) SES_{MPD} Values

Assemblage	Source Pool	Kress	Phylomatic	Control
5	50	0.02257 ± 0.02265	0.05 ± 0.0425	-0.10 ± 0.0283
5	100	-0.00222 ± 0.02545	0.13 ± 0.0489	-0.07 ± 0.0306
5	All BCI	0.16646 ± 0.02038	0.44 ± 0.0387	0.14 ± 0.0265
10	50	-0.03044 ± 0.04201	-0.19 ± 0.0240	0.12 ± 0.0450
10	100	-0.05332 ± 0.04867	-0.18 ± 0.0266	0.20 ± 0.0511
10	All BCI	0.22546 ± 0.03794	0.04 ± 0.0220	0.52 ± 0.0413
50	100	0.26091 ± 0.19088	0.38 ± 0.186	0.70 ± 0.1886
50	All BCI	-0.13081 ± 0.09868	0.80 ± 0.0968	1.03 ± 0.0987
AIC_{model}		20043	23656	21641
AIC_{null}		20175	23792	21819

(c) SES_{MNTD} Values

Table A13: Mixed effects models of D , SES_{MPD} , and SES_{MNTD} values across BCI, with assemblages whose source pools that cross the boundary of BCI removed from the analysis. Estimates of mean values (\pm SE) for each assemblage/source pool combination, with a different table for each dispersion measure, subdivided within each table according to the phylogeny used. AIC values for each model are given the last two rows of each table; all likelihood ratio tests had p-values < 0.0001 .

Assemblage	Kress	Phylomatic	Control	
10	0.79 ± 0.0008	0.70 ± 0.0011	0.70 ± 0.0014	
5	0.79 ± 0.0006375	0.70 ± 0.0008	0.70 ± 0.0011	
50	0.79 ± 0.0030	0.71 ± 0.0046	0.70 ± 0.0047	
AIC _{model}		-30961	-25450	-25382
AIC _{null}		-30958	-25451	-25382
LRT p-value		0.028	0.275	0.101

(a) *PSV* Values

Assemblage	Source Pool	Kress	Phylomatic	Control
10	50	-0.01 ± 0.0012	-0.01 ± 0.0016	0.00 ± 0.0018
10	All BCI	0.00 ± 0.0011	0.00 ± 0.0014	0.01 ± 0.0016
10	100	0.00 ± 0.0013	-0.01 ± 0.0018	0.00 ± 0.0020
5	50	-0.01 ± 0.0008	0.00 ± 0.0009	0.00 ± 0.0012
5	All BCI	0.00 ± 0.0008	0.00 ± 0.0008	0.01 ± 0.0012
5	100	0.00 ± 0.0009	0.00 ± 0.0010	0.00 ± 0.0013
50	All BCI	0.00 ± 0.0026	0.01 ± 0.0036	0.01 ± 0.0037
50	100	0.00 ± 0.0050	0.00 ± 0.0069	0.00 ± 0.0070
AIC_{model}		-50893	-43857	-43599
AIC_{null}		-50653	-43753	-43443
LRT p-value		<0.0001	<0.0001	<0.0001

(b) Corrected *PSV* Values

Table A14: Mixed effects models of *PSV* values across BCI, with assemblages whose source pools that cross the boundary of BCI removed from the analysis. Estimates of mean values (\pm SE) for each assemblage/source pool combination, with a different table for each dispersion measure, subdivided within each table according to the phylogeny used. AIC values for each model and likelihood ratio test p-values are given the last two rows of each table.

7.3 Quantile Regressions

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	0.86	0.97	1.07
5	100	0.85	0.95	1.04
5	All BCI	0.85	0.93	1.00
10	50	0.88	0.97	1.04
10	100	0.87	0.95	1.01
10	All BCI	0.86	0.92	0.98
50	100	0.89	0.96	1.05
50	All BCI	0.86	0.89	0.92
Range		0.04	0.08	0.15

(a) Kress Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	0.86	0.99	1.09
5	100	0.86	0.97	1.06
5	All BCI	0.82	0.92	1.00
10	50	0.85	0.94	1.03
10	100	0.85	0.93	1.01
10	All BCI	0.81	0.89	0.95
50	100	0.86	0.92	0.97
50	All BCI	0.80	0.86	0.89
Range		0.06	0.13	0.20

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	0.85	1.00	1.12
5	100	0.84	0.97	1.09
5	All BCI	0.82	0.94	1.02
10	50	0.84	0.94	1.04
10	100	0.85	0.94	1.01
10	All BCI	0.83	0.91	0.98
50	100	0.94	0.98	1.04
50	All BCI	0.84	0.89	0.92
Range		0.12	0.11	0.20

(c) Control Phylogeny

Table A15: Quantile regression of D values across BCI in all three phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	0.0060	0.0045	0.0047
5	100	0.0059	0.0055	0.0039
5	All BCI	0.0023	0.0020	0.0020
10	50	0.0082	0.0089	0.0059
10	100	0.0080	0.0075	0.0077
10	All BCI	0.0035	0.0036	0.0025
50	100	0.0055	0.0209	0.0272
50	All BCI	0.0144	0.0082	0.0135

(a) Kress Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	0.0057	0.0047	0.0056
5	100	0.0057	0.0052	0.0045
5	All BCI	0.0031	0.0022	0.0020
10	50	0.0071	0.0074	0.0068
10	100	0.0085	0.0108	0.0105
10	All BCI	0.0049	0.0033	0.0032
50	100	0.0704	0.0365	0.3063
50	All BCI	0.0340	0.0178	0.0103

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
10	50	0.0088	0.0075	0.0073
10	100	0.0074	0.0062	0.0077
10	All BCI	0.0052	0.0040	0.0028
5	50	0.0060	0.0050	0.0037
5	100	0.0077	0.0053	0.0053
5	All BCI	0.0038	0.0027	0.0020
50	100	0.0417	0.0331	0.1345
50	All BCI	0.0127	0.0250	0.0013

(c) Control Phylogeny

Table A16: Standard errors of quantile regression of D values across BCI in all three phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	-0.60	-0.02	0.53
5	100	-0.65	-0.09	0.43
5	All BCI	-0.50	0.00	0.51
10	50	-0.75	-0.15	0.36
10	100	-0.89	-0.27	0.30
10	All BCI	-0.59	-0.07	0.43
50	100	-1.41	-0.77	0.56
50	All BCI	-0.27	0.20	0.91
Range		1.14	0.97	0.61

(a) Kress Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	-0.77	-0.14	0.54
5	100	-0.75	-0.11	0.53
5	All BCI	-0.71	-0.12	0.51
10	50	-0.92	-0.30	0.37
10	100	-0.80	-0.26	0.35
10	All BCI	-0.87	-0.14	0.49
50	100	-1.15	-0.44	0.25
50	All BCI	-0.18	0.31	1.03
Range		0.97	0.73	0.78

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	-0.60	0.02	0.62
5	100	-0.60	-0.02	0.57
5	All BCI	-0.48	0.08	0.63
10	50	-0.68	-0.03	0.57
10	100	-0.74	-0.03	0.60
10	All BCI	-0.51	0.12	0.70
50	100	-1.03	-0.23	0.51
50	All BCI	0.08	0.54	1.04
Range		1.11	0.77	0.53

(c) Control Phylogeny

Table A17: Quantile regression of SES_{MPD} values across BCI in the Phylomatic and Control phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	0.0261	0.0252	0.0263
5	100	0.0352	0.0305	0.0179
5	All BCI	0.0149	0.0142	0.0140
10	50	0.0546	0.0489	0.0533
10	100	0.0650	0.0785	0.0577
10	All BCI	0.0325	0.0291	0.0318
50	100	0.3056	0.0328	1.6307
50	All BCI	0.0964	0.1107	0.1489

(a) Kress Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	0.0278	0.0252	0.0347
5	100	0.0341	0.0327	0.0367
5	All BCI	0.0164	0.0164	0.0199
10	50	0.0491	0.0542	0.0551
10	100	0.0771	0.0590	0.0782
10	All BCI	0.0432	0.0354	0.0326
50	100	0.4939	0.0984	0.3733
50	All BCI	0.2130	0.2350	0.1455

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	0.0281	0.0289	0.0290
5	100	0.0277	0.0333	0.0320
5	All BCI	0.0147	0.0153	0.0165
10	50	0.0760	0.0597	0.0479
10	100	0.0766	0.0450	0.1025
10	All BCI	0.0339	0.0300	0.0340
50	100	0.2534	0.4484	0.0257
50	All BCI	0.1436	0.0899	0.0787

(c) Control Phylogeny

Table A18: Standard errors of quantile regression of SES_{MPD} values across BCI in all three phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$		
5	50	-1.16	-0.61	0.04	0.66	1.14
5	100	-1.20	-0.61	0.01	0.64	1.10
5	All BCI	-0.99	-0.45	0.19	0.76	1.26
10	50	-1.24	-0.69	-0.09	0.55	1.06
10	100	-1.32	-0.72	-0.03	0.52	1.07
10	All BCI	-0.92	-0.39	0.24	0.82	1.39
50	100	-0.67	-0.48	0.19	0.92	1.28
50	All BCI	-1.07	-0.70	-0.19	0.41	1.19
Range						

(a) Kress Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$		
5	50	-1.34	-0.80	-0.22	0.44	1.00
5	100	-1.27	-0.74	-0.20	0.43	0.95
5	All BCI	-1.09	-0.57	0.00	0.58	1.11
10	50	-1.16	-0.65	0.02	0.72	1.42
10	All BCI	-0.78	-0.22	0.37	1.01	1.59
10	100	-1.04	-0.54	0.08	0.72	1.44
50	100	-0.77	-0.59	0.64	0.98	1.33
50	All BCI	-0.63	0.14	0.80	1.38	1.80
Range						

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$		
5	50	-1.28	-0.72	-0.11	0.53	1.09
5	100	-1.24	-0.69	-0.05	0.56	1.09
5	All BCI	-1.05	-0.51	0.10	0.69	1.20
10	50-1.18	-0.62	0.03	0.73	1.51	
10	All BCI	-0.71	-0.17	0.44	1.07	1.73
10	100	-1.10	-0.48	0.15	0.79	1.70
50	100	-0.50	-0.20	0.36	1.04	1.39
50	All BCI	-0.27	0.38	0.83	1.37	1.86
Range						

(c) Control Phylogeny

Table A19: Quantile regression of SES_{MNTD} values across BCI in the Phylomatic and Control phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	0.0318	0.0270	0.0279
5	100	0.0352	0.0309	0.0340
5	All BCI	0.0183	0.0156	0.0160
10	50	0.0588	0.0420	0.0583
10	100	0.0844	0.0554	0.0571
10	All BCI	0.0441	0.0279	0.0352
50	100	0.3776	0.0500	1.4701
50	All BCI	0.2412	0.1633	0.2777

(a) Kress Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	0.0269	0.0271	0.0246
5	100	0.0270	0.0308	0.0308
5	All BCI	0.0151	0.0153	0.0153
10	50	0.0555	0.0481	0.0804
10	100	0.0699	0.0581	0.1092
10	All BCI	0.0277	0.0295	0.0359
50	100	1.6673	0.1506	0.5413
50	All BCI	0.4964	0.2027	0.2189

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	0.0243	0.0290	0.0331
5	100	0.0298	0.0381	0.0365
5	All BCI	0.0170	0.0155	0.0171
10	50	0.0539	0.0454	0.0804
10	100	0.0867	0.0628	0.0780
10	All BCI	0.0293	0.0261	0.0433
50	100	1.3553	0.0055	0.0929
50	All BCI	0.1631	0.2032	0.1518

(c) Control Phylogeny

Table A20: Standard errors of quantile regression of SES_{MNTD} values across BCI in all three phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	0.78	0.79	0.80
10	0.78	0.79	0.80
50	0.79	0.79	0.80
Range	0.01	0	0

(a) Kress Phylogeny

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	0.68	0.70	0.72
10	0.68	0.70	0.71
50	0.70	0.70	0.71
Range	0.02	0	0.01

(b) Phylomatic Phylogeny

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	0.68	0.70	0.72
10	0.68	0.70	0.71
50	0.70	0.70	0.71
Range	0.02	0	0.01

(c) Control Phylogeny

Table A21: Quantile regression of PSV values across BCI in the Phylomatic and Control phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	0.0004	0.0004	0.0004
10	0.0004	0.0005	0.0005
50	0.0005	0.0006	0.0008

(a) Kress Phylogeny

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	0.0006	0.0006	0.0008
10	0.0008	0.0007	0.0008
50	0.0018	0.0016	0.0008

(b) Phylomatic Phylogeny

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	0.0006	0.0006	0.0007
10	0.0008	0.0007	0.0008
50	0.0007	0.0007	0.0011

(c) Control Phylogeny

Table A22: Standard errors of quantile regression of PSV values across BCI in all three phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	-0.02	0.00	0.01
5	100	-0.02	0.00	0.01
5	All BCI	-0.01	0.00	0.01
10	50	-0.01	0.00	0.00
10	100	-0.01	0.00	0.00
10	All BCI	-0.01	0.00	0.01
50	100	-0.01	0.00	0.00
50	All BCI	0.00	0.00	0.01
Range		0.01	0	0.01

(a) Kress Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	-0.03	-0.01	0.02
5	100	-0.03	0.00	0.02
5	All BCI	-0.03	0.00	0.02
10	50	-0.02	-0.01	0.01
10	100	-0.02	-0.01	0.01
10	All BCI	-0.02	0.00	0.01
50	100	-0.01	0.00	0.00
50	All BCI	0.00	0.00	0.01
Range		0.03	0.01	0.01

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	-0.02	0.00	0.02
5	100	-0.02	0.00	0.02
5	All BCI	-0.02	0.00	0.03
10	50	-0.02	0.00	0.01
10	100	-0.02	0.00	0.01
10	All BCI	-0.01	0.00	0.02
50	100	-0.01	0.00	0.00
50	All BCI	0.00	0.01	0.01
Range		0.02	0.01	0.03

(c) Control Phylogeny

Table A23: Quantile regression of corrected PSV values across BCI in all three phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	
5	50	0.0010	0.0007	0.0007
5	100	0.0008	0.0009	0.0007
5	All BCI	0.0004	0.0004	0.0004
10	50	0.0012	0.0006	0.0007
10	100	0.0010	0.0012	0.0008
10	All BCI	0.0005	0.0005	0.0005
50	100	0.0011	0.0006	0.0066
50	All BCI	0.0006	0.0005	0.0011

(a) Kress Phylogeny

Assemblage	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$	
5	50	0.0011	0.0009	0.0013
5	100	0.0014	0.0013	0.0014
5	All BCI	0.0006	0.0006	0.0008
10	50	0.0011	0.0011	0.0012
10	100	0.0014	0.0010	0.0012
10	All BCI	0.0008	0.0007	0.0008
50	100	0.0061	0.0012	0.0003
50	All BCI	0.0014	0.0016	0.0009

(b) Phylomatic Phylogeny

Assemblage	Source Pool	$\tau=0.25$	$\tau=0.50$	$\tau=0.75$
5	50	0.0010	0.0012	0.0013
5	100	0.0011	0.0013	0.0014
5	All BCI	0.0005	0.0006	0.0007
10	50	0.0017	0.0012	0.0010
10	100	0.0014	0.0009	0.0028
10	All BCI	0.0008	0.0008	0.0007
50	100	0.0010	0.0023	0.0003
50	All BCI	0.0007	0.0008	0.0014

(c) Control Phylogeny

Table A24: Standard errors of quantile regressions of corrected *PSV* values across BCI in the all three phylogenies, with assemblages whose source pools that cross the boundary of BCI removed from the analysis.

8 Small assemblage simulations

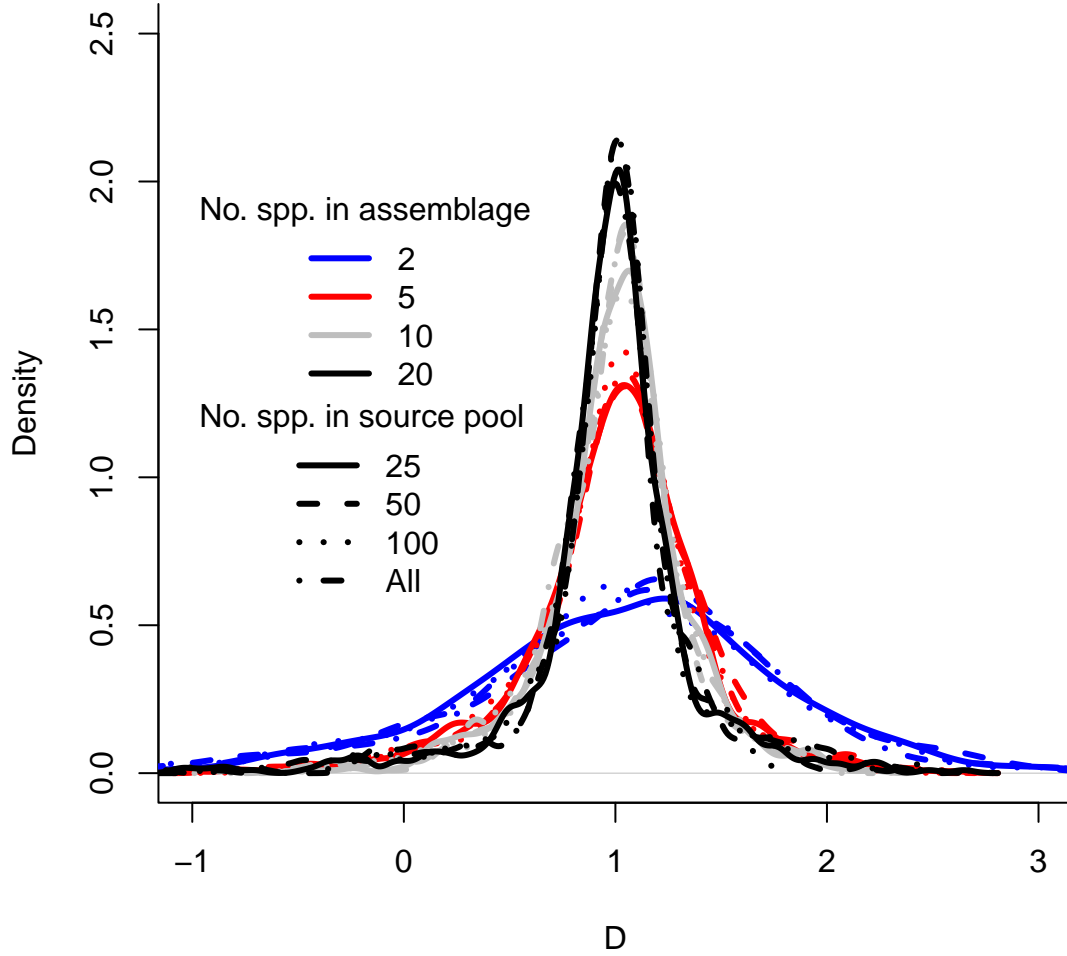


Fig. A13: Simulated small assemblages' D values. 30 randomly selected source pools containing 25, 50, 100, and all species in BCI, within with 30 different assemblages containing 2, 5, 10, and 20 species were created. D values were calculated for all 14400 assemblages, and are plotted above. A two-way ANOVA of D against assemblage and source pool size was significant ($F_{15,14384} = 1.739$), but only had an r^2 of 0.18%. This likely reflects the poorer resolution of D in assemblages containing only two species.

References

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