

Ecography

ECOG-04117

Antão, L. H., McGill, B., Magurran, A. E., Soares, A. and Dornelas, M. 2019. β -diversity scaling patterns are consistent across metrics and taxa. – Ecography doi: 10.1111/ecog.04117

Supplementary material

Appendix 1

Items in the supplementary material

Supplementary Fig. A1 – Median β_{SOR} values across all the splitting trials vs β_{SOR} from a single trial.

Supplementary Fig. A2 – *Multiple-site* β -diversity values across all the splitting trials.

Supplementary Fig. A3 – *Multiple-site* β -diversity scaling curves with area as grain * number of samples.

Supplementary Fig. A4 – Comparison of power law and linear logit models fit to β_{SOR} scaling curves.

Supplementary Fig. A5 – Estimated *multiple-site* β -diversity power law scaling curves coefficients.

Table A1 – Estimated *multiple-site* β -diversity power law coefficients (plotted curves in Fig. 2).

Supplementary Fig. A6 – Relationship between pairwise dissimilarities and geographic distance.

Supplementary Fig. A7 – Species-Area Relationship plots for each dataset.

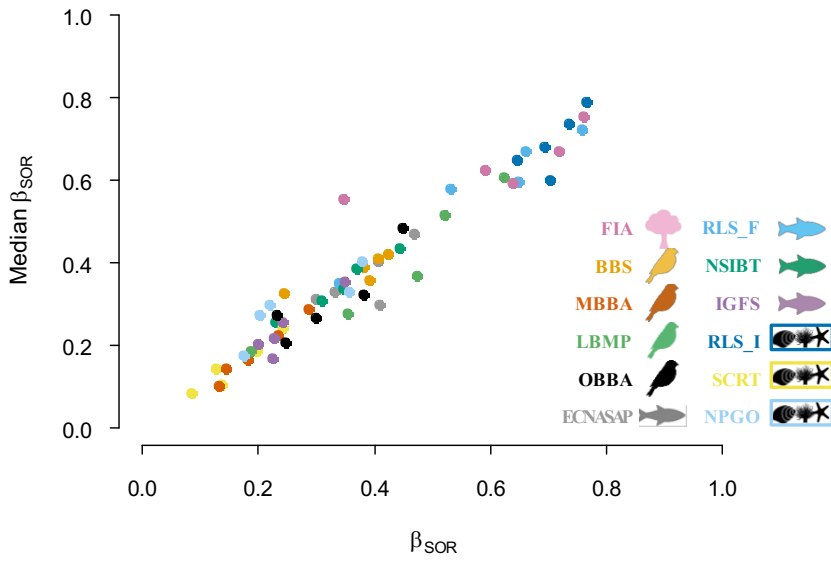


Figure A1 – Median β_{SOR} values across all the splitting trials (excluding the last one) vs β_{SOR} from a single trial used in the analysis.

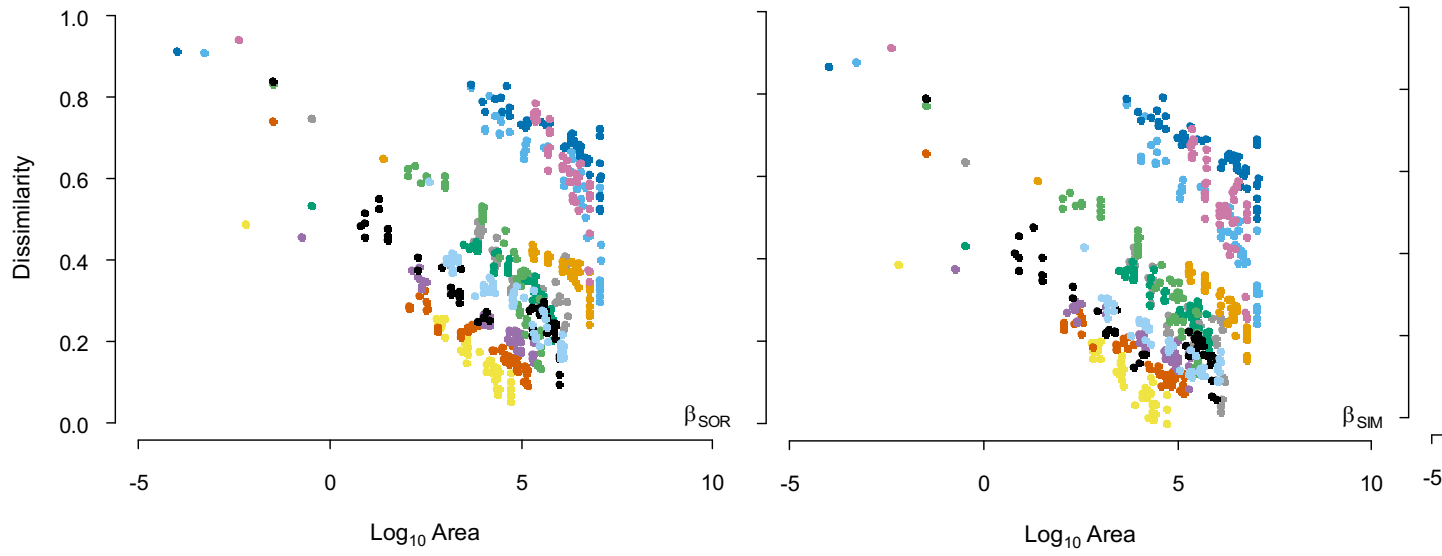


Figure A2 – *Multiple-site* dissimilarity values across all the splitting trials for each dataset.

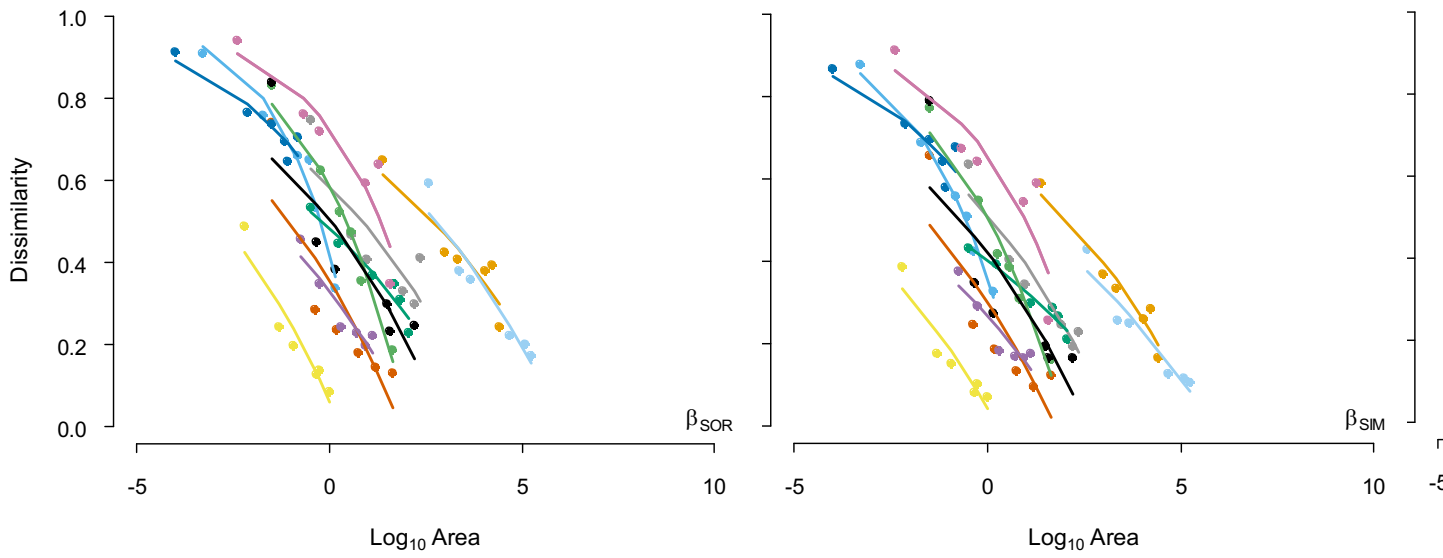


Figure A3 – *Multiple-site* β -diversity scaling curves with area calculated as grain * number of samples (on a semi-log plot); the patterns are similar to using the convex hull polygons of the sections presented in Fig. 2.

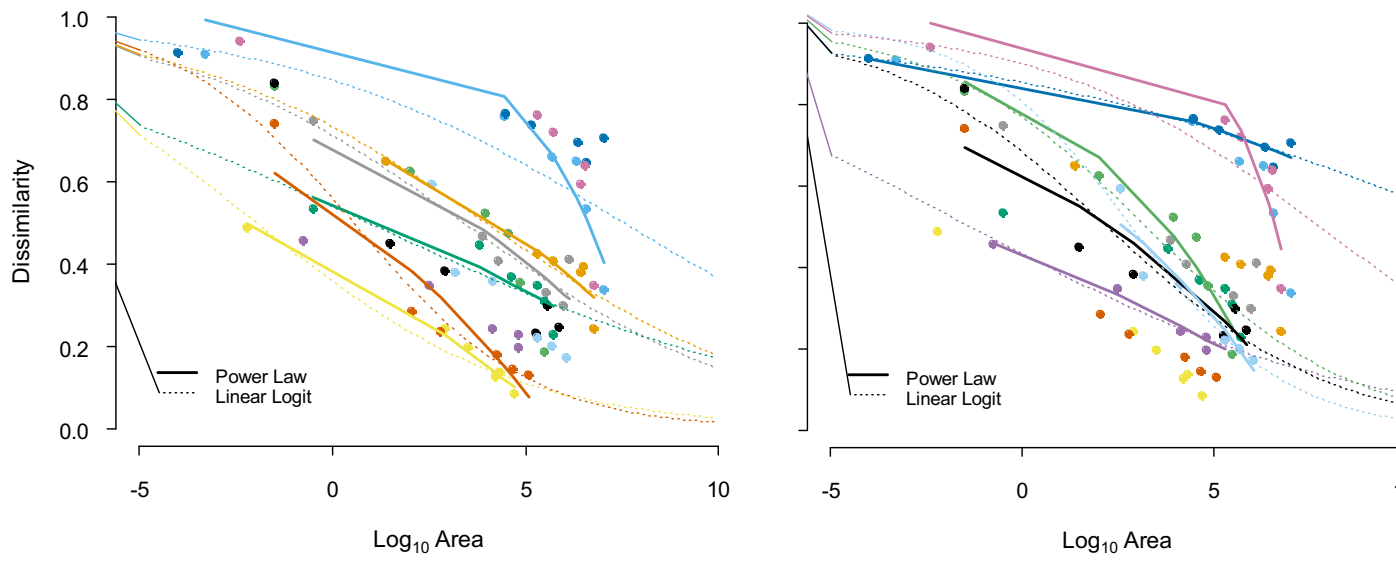


Figure A4 – Comparison of power law (full lines) and linear model of the logit transformations of dissimilarities (dashed lines) fit to the β_{SOR} scaling curves (to aid visualization two panels are shown, each with the fits for six datasets); in all cases, the power law provided a better fit according to AIC.

Table A1 – Estimated *multiple-site* β -diversity power law coefficients.

Dataset	β_{SOR}				β_{SIM}				β_{NES}		
	Value	Std.Error	t-value	p-value	Value	Std.Error	t-value	p-value	Value	Std.Error	t-value
FIA	0.0046	0.0056	0.8273	0.4122	0.0166	0.0145	1.1426	0.2589	0.9590	0.0193	49.5617
BBS	0.2870	0.0642	4.4735	0.0000	0.3168	0.0629	5.0402	0.0000	-0.0008	0.0395	-0.0193
MBBA	0.4616	0.0451	10.2293	0.0000	0.5144	0.0453	11.3469	0.0000	-0.0285	0.0265	-1.0730
LBMP	0.2013	0.0439	4.5844	0.0000	0.2768	0.0461	5.9979	0.0000	-0.0301	0.0268	-1.1232
OBBA	0.3674	0.0423	8.6788	0.0000	0.4310	0.0429	10.0582	0.0000	-0.0334	0.0261	-1.2794
ECNASAP	0.3111	0.0528	5.8886	0.0000	0.3697	0.0526	7.0229	0.0000	-0.0472	0.0303	-1.5554
RLS_F	0.0239	0.0212	1.1313	0.2635	0.0926	0.0474	1.9545	0.0565	-0.0124	0.0260	-0.4781
NSIBT	0.4507	0.0571	7.8968	0.0000	0.5407	0.0564	9.5915	0.0000	-0.0576	0.0307	-1.8783
IGFS	0.5625	0.0517	10.8852	0.0000	0.6260	0.0512	12.2183	0.0000	-0.0346	0.0288	-1.1985
RLS_I	0.1382	0.0536	2.5766	0.0131	0.1737	0.0511	3.3979	0.0014	-0.0042	0.0255	-0.1650
SCRT	0.6006	0.0481	12.4859	0.0000	0.6806	0.0464	14.6657	0.0000	-0.0433	0.0263	-1.6463
NPGO	0.3245	0.0555	5.8452	0.0000	0.4669	0.0646	7.2264	0.0000	-0.1637	0.0412	-3.9706
FIA	0.3076	0.0809	3.7994	0.0004	0.2313	0.0591	3.9131	0.0003	-0.0022	0.0015	-1.4146
BBS	-0.2531	0.0824	-3.0701	0.0035	-0.1771	0.0605	-2.9251	0.0052	-0.0013	0.0032	-0.4115
MBBA	-0.2492	0.0816	-3.0556	0.0037	-0.1816	0.0597	-3.0414	0.0038	0.0058	0.0028	2.1111
LBMP	-0.2056	0.0832	-2.4700	0.0171	-0.1531	0.0607	-2.5205	0.0151	0.0028	0.0027	1.0566
OBBA	-0.2521	0.0815	-3.0918	0.0033	-0.1815	0.0596	-3.0435	0.0038	0.0007	0.0025	0.2834
ECNASAP	-0.2528	0.0821	-3.0798	0.0034	-0.1798	0.0601	-2.9934	0.0043	0.0006	0.0028	0.2305
RLS_F	-0.1200	0.0938	-1.2789	0.2071	-0.1227	0.0654	-1.8750	0.0669	-0.0003	0.0021	-0.1500
NSIBT	-0.2745	0.0817	-3.3604	0.0015	-0.2099	0.0598	-3.5121	0.0010	0.0070	0.0029	2.4253
IGFS	-0.2793	0.0815	-3.4289	0.0013	-0.2089	0.0596	-3.5049	0.0010	0.0048	0.0029	1.6729
RLS_I	-0.2558	0.0851	-3.0056	0.0042	-0.1900	0.0619	-3.0708	0.0035	0.0023	0.0020	1.1337
SCRT	-0.2711	0.0814	-3.3299	0.0017	-0.2052	0.0595	-3.4483	0.0012	0.0074	0.0027	2.7402
NPGO	-0.2395	0.0822	-2.9134	0.0054	-0.1852	0.0602	-3.0776	0.0034	0.0133	0.0045	2.9931

comparisons. The different plotting symbols represent dissimilarity values for the different scaling levels (150 points were randomly sampled to plot the grain level). For this analysis we explored only three scaling levels (grain; 1/16; and 1/8) because the higher levels contain too few pairwise comparisons to confidently estimate DDR.

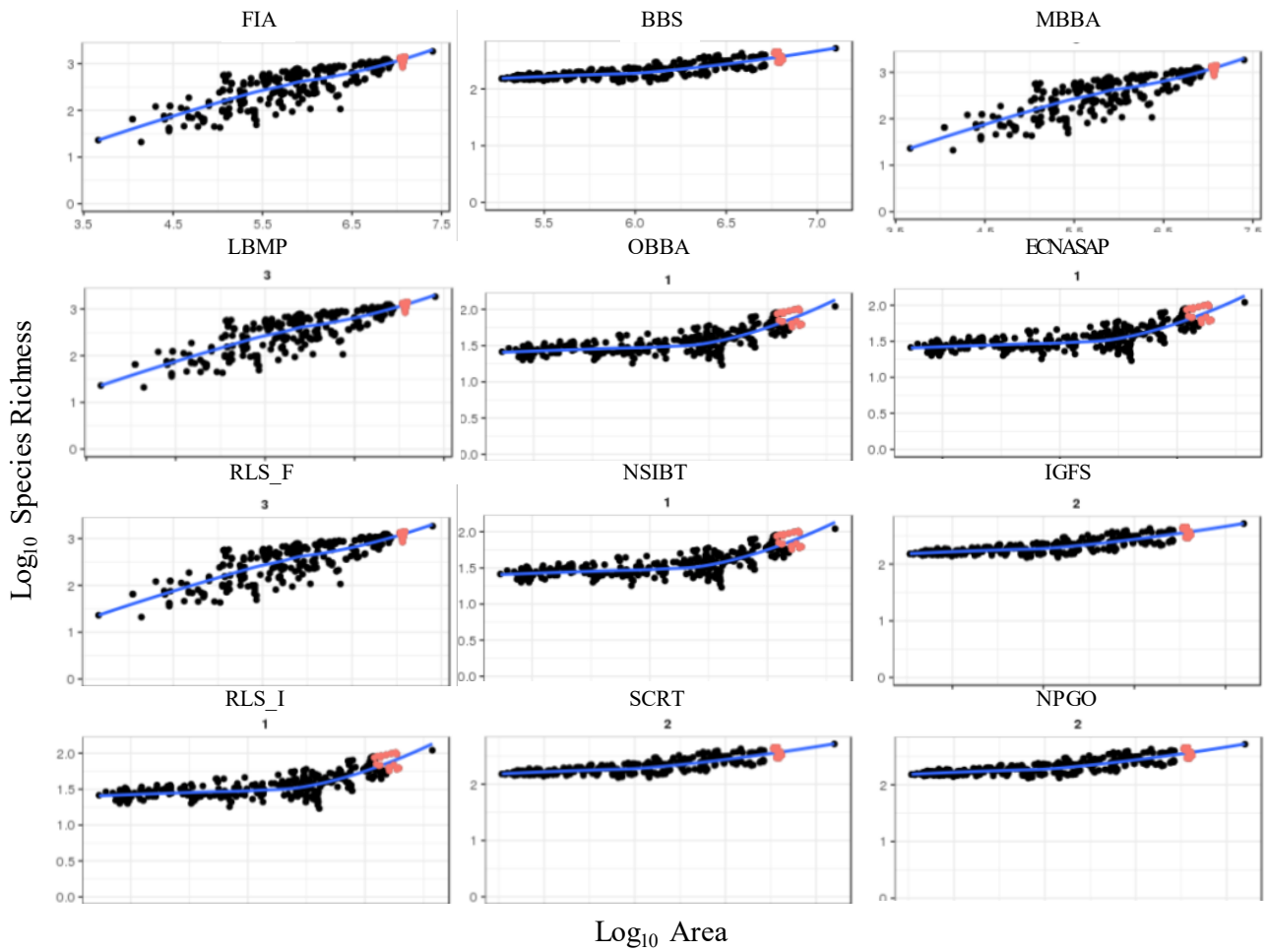


Figure A7 – Species Area Relationships for each dataset, plotted using the species richness and convex hull polygon area values across all the trials and the total extent; a smoothed line was fitted to aid identify the location of inflection points, and the bisection areas are plotted in red.