

Ecography

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Do metacommunity mass effects predict changes in
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Supplementary material

Appendix 1

Table A1. Example to illustrate predictions of the incidence model. Matrix O represents the initial occurrence of four species across six sites at time A. Matrix E represents the expected probabilities that each species will occur at each site according to the incidence model at a subsequent time, B. Because matrix E maintains the same row and column totals as matrix O, no changes in overall incidence are predicted. Matrix N represents the expectations of a neutral 'random walk' model, where s represents an average (unidirectional) deviation from the initial incidence values (0 or 1). Note that this matrix N generates row and column totals that differ from matrix O with incidence values that initially increase when starting from a sparse matrix like this one.

Matrix O: Observed incidence matrix

	Sites						Row sums:
Species	1	1	1	0	0	0	3
	0	0	0	1	1	1	3
	1	1	0	0	0	0	2
	0	0	0	0	1	1	2
Col. sums:	2	2	1	1	2	2	10

Matrix E: Predicted incidence matrix

Row sums:

	.6	.6	.3	.3	.6	.6	3
	.6	.6	.3	.3	.6	.6	3
	.4	.4	.2	.2	.4	.4	2
	.4	.4	.2	.2	.4	.4	2
Col sums:	2	2	1	1	2	2	10

Matrix N: Neutral model matrix

Row sums:

	1-s	1-s	1-s	s	s	s	3
	s	s	s	1-s	1-s	1-s	3
	1-s	1-s	s	s	s	s	2 + 2s
	s	s	s	s	1-s	1-s	2 + 2s
Col sums:	2	2	1 + 2s	1 + 2s	2	2	10 + 4s

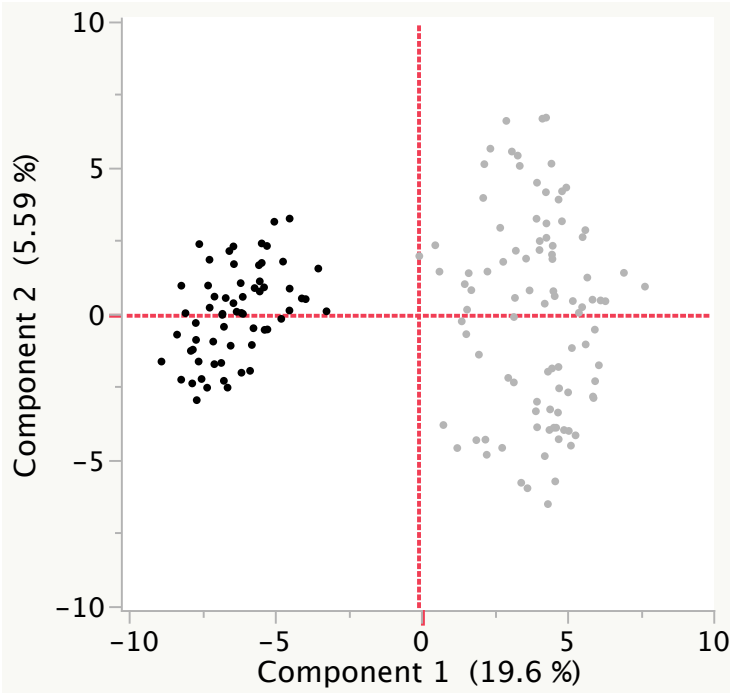


Figure A1. An ordination (principal component analysis) of all forest stands used in this study. Species abundances were estimated using frequency data. These values were log transformed using $\log(\text{frequency} + 1)$. The northern forest sites emerge together as the cluster on the left while all southern sites lie removed to the right. This demonstrates their highly contrasting species composition, supporting our division of these sites into two metacommunities.

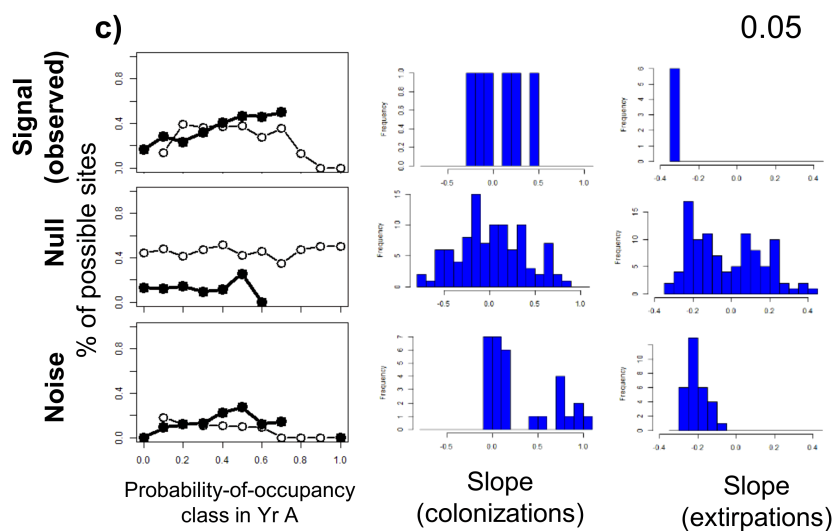
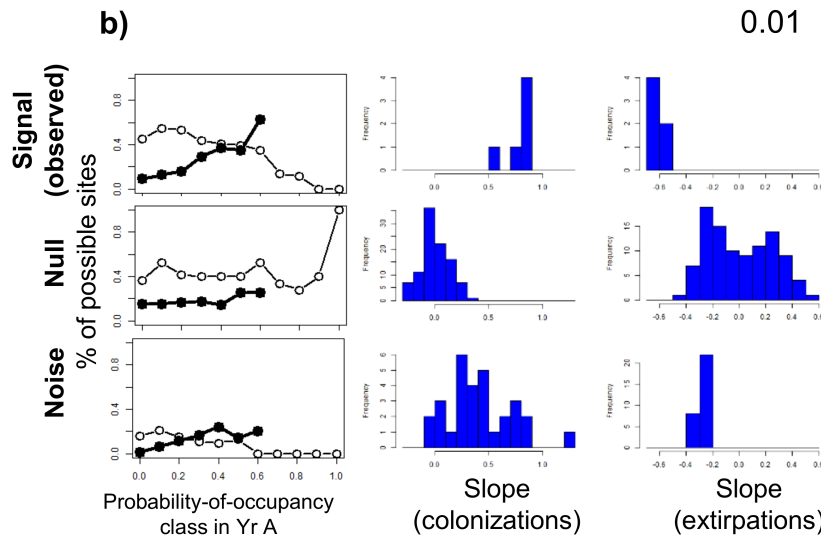
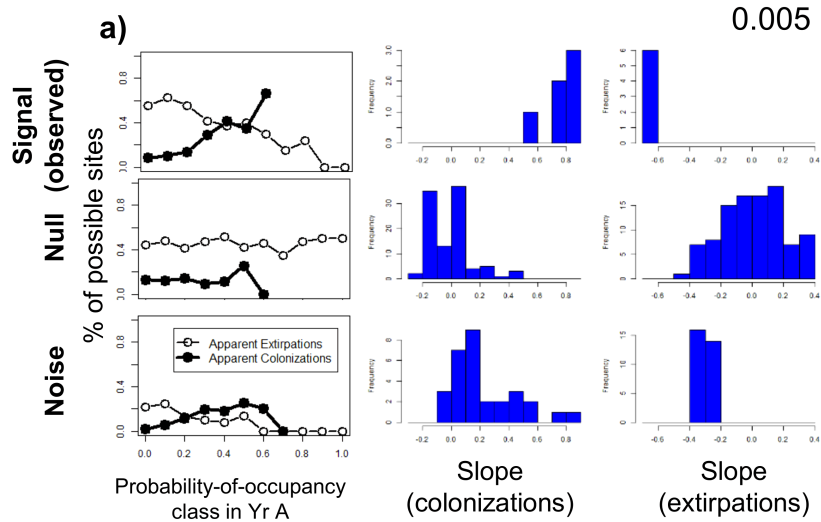


Figure A2. Null model results showing effects of species abundance on the incidence model. This figure is based on the northern sites oversampled in the 2000s. Models include or exclude species based on three abundance thresholds: 0.005 (a), 0.01 (b) or 0.05 (c). 'Signal' rows show empirical results comparing the 1950s and 6 replicate 2000s metacommunities (see Material and methods). 'Null' rows use 100 simulations of randomized matrices to calculate ΔO_{ij} . 'Noise' rows pair each of the six 2000s replicate samples to predict the other five replicates. The left column shows an example of the local extinction trends (empty circles) and colonization trends (filled circles) with increasing P_{ij} classes. The center column shows histograms of values for the slope of the best-fit line to the colonization trends for each data type. The right column compares histograms of values for the slope of the best-fit line to the local extinction trends for each data type.

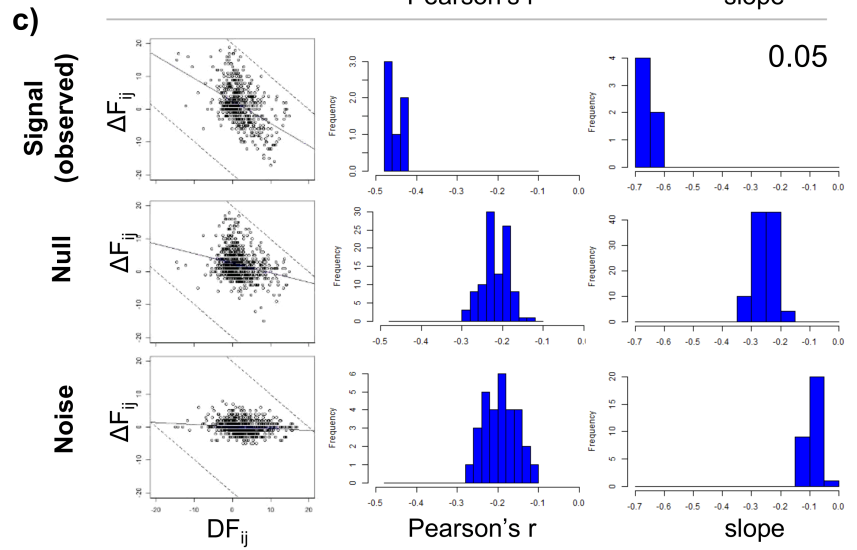
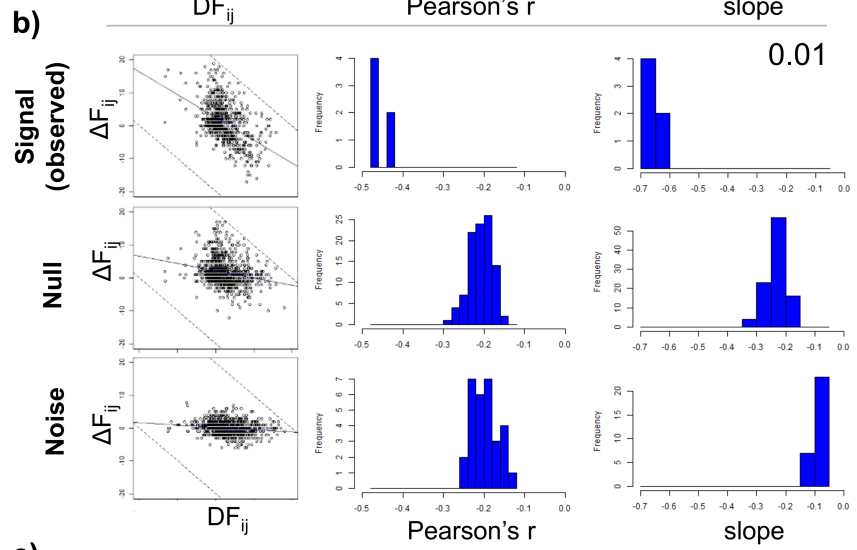
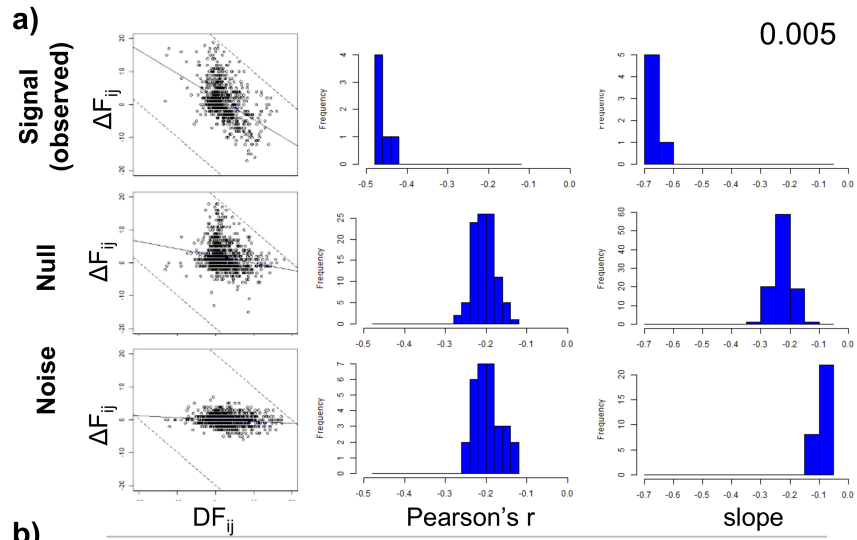


Figure A3. Null model results for the frequency model. These null frequency models again used data from the northern sites and include only species when they occurred at an overall frequency of at least 0.005 (a), 0.01 (b) or 0.05 (c) across all quadrats. 'Signal' rows use observed 1950s data to predict changes and the 6 replicates from the 2000s dataset to test those predictions (see text). 'Null' rows use 100 simulations of randomized matrices for ΔF_{ij} . 'Noise' rows compare differences between pairs of the six 2000s replicates to assess effects of spatial variation (with 30 replicates). The left-most column shows an example scatter plot of ΔF_{ij} vs. DF_{ij} . The center column shows histograms of values for the Pearson's correlation coefficient r between ΔF_{ij} and DF_{ij} . The right-most column shows histograms of values for the slope of the best-fit line of ΔF_{ij} modeled by DF_{ij} for each data type.