Supplemental figures and table

Figure S1. Principle component analysis (PCA) conducted on 17 environmental variables.

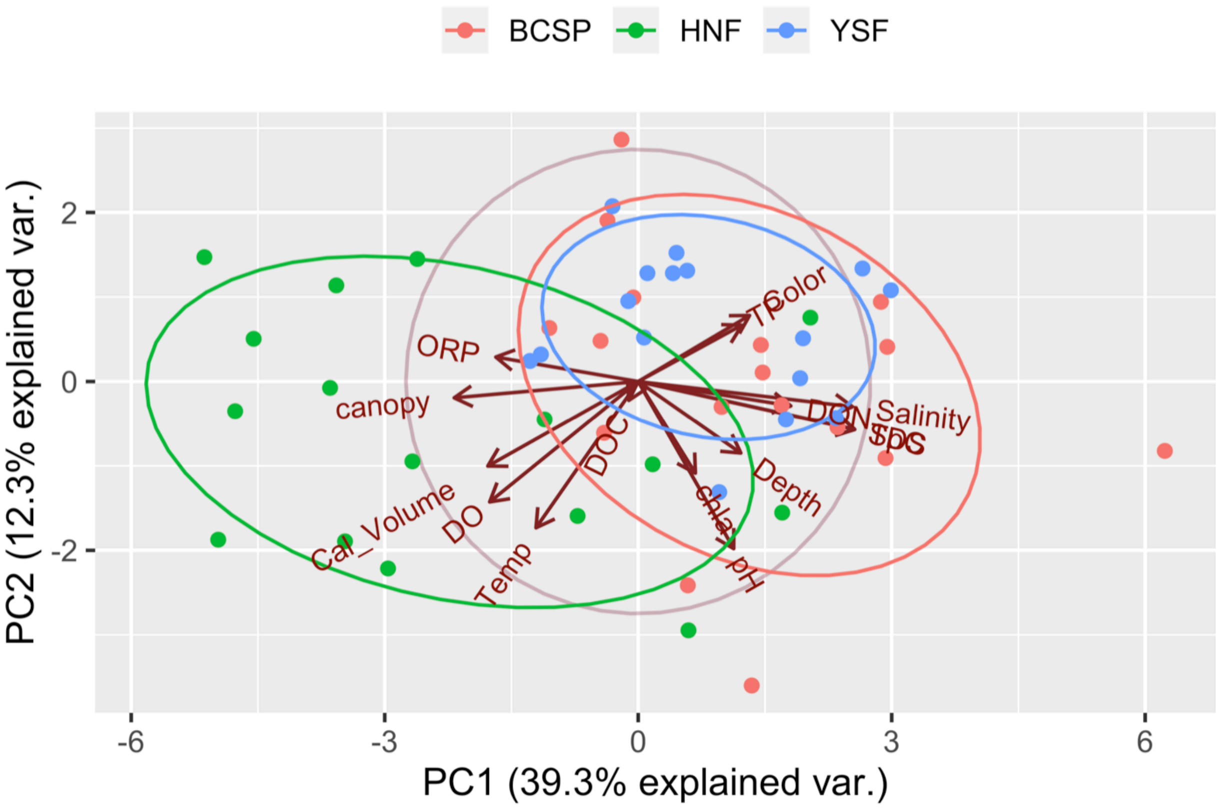
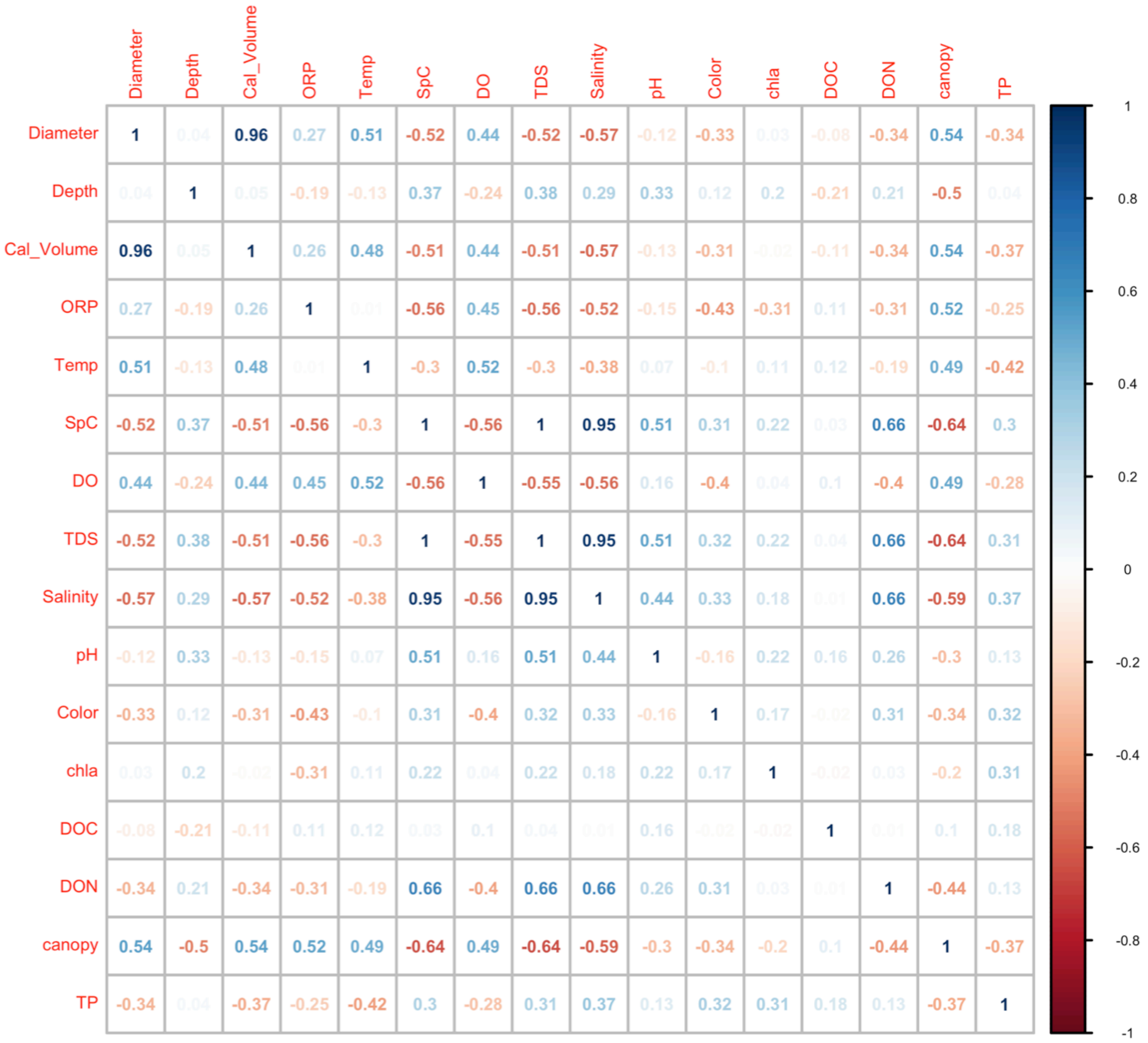


Figure S2. Correlation plot for environmental variables from 49 forested ponds.



	Diameter	Depth	Cal_Volume	ORP	Temp	SpC	DO	TDS	Salinity	pH	Color	chla	DOC	DON	canopy	TP
Diameter	1	0.04	0.96	0.27	0.51	-0.52	0.44	-0.52	-0.57	-0.12	-0.33	0.03	-0.08	-0.34	0.54	-0.34
Depth	0.04	1	0.05	-0.19	-0.13	0.37	-0.24	0.38	0.29	0.33	0.12	0.2	-0.21	0.21	-0.5	0.04
Cal_Volume	0.96	0.05	1	0.26	0.48	-0.51	0.44	-0.51	-0.57	-0.13	-0.31	-0.02	-0.11	-0.34	0.54	-0.37
ORP	0.27	-0.19	0.26	1	0.01	-0.56	0.45	-0.56	-0.52	-0.15	-0.43	-0.31	0.11	-0.31	0.52	-0.25
Temp	0.51	-0.13	0.48	0.01	1	-0.3	0.52	-0.3	-0.38	0.07	-0.1	0.11	0.12	-0.19	0.49	-0.42
SpC	-0.52	0.37	-0.51	-0.56	-0.3	1	-0.56	1	0.95	0.51	0.31	0.22	0.03	0.66	-0.64	0.3
DO	0.44	-0.24	0.44	0.45	0.52	-0.56	1	-0.55	-0.56	0.16	-0.4	0.04	0.1	-0.4	0.49	-0.28
TDS	-0.52	0.38	-0.51	-0.56	-0.3	1	-0.55	1	0.95	0.51	0.32	0.22	0.04	0.66	-0.64	0.31
Salinity	-0.57	0.29	-0.57	-0.52	-0.38	0.95	-0.56	0.95	1	0.44	0.33	0.18	0.01	0.66	-0.59	0.37
pH	-0.12	0.33	-0.13	-0.15	0.07	0.51	0.16	0.51	0.44	1	-0.16	0.22	0.16	0.26	-0.3	0.13
Color	-0.33	0.12	-0.31	-0.43	-0.1	0.31	-0.4	0.32	0.33	-0.16	1	0.17	-0.02	0.31	-0.34	0.32
chla	0.03	0.2	-0.02	-0.31	0.11	0.22	0.04	0.22	0.18	0.22	0.17	1	-0.02	0.03	-0.2	0.31
DOC	-0.08	-0.21	-0.11	0.11	0.12	0.03	0.1	0.04	0.01	0.16	-0.02	-0.02	1	0.01	0.1	0.18
DON	-0.34	0.21	-0.34	-0.31	-0.19	0.66	-0.4	0.66	0.66	0.26	0.31	0.03	0.01	1	-0.44	0.13
canopy	0.54	-0.5	0.54	0.52	0.49	-0.64	0.49	-0.64	-0.59	-0.3	-0.34	-0.2	0.1	-0.44	1	-0.37
TP	-0.34	0.04	-0.37	-0.25	-0.42	0.3	-0.28	0.31	0.37	0.13	0.32	0.31	0.18	0.13	-0.37	1

Figure S3. Geographical and environmental distances (from PCA axis 1) among ponds were unrelated (*p* > 0.5) (Fig. S3). Geographical and environmental distances have been rescaled to values between 0 and 1, as described in the main text.

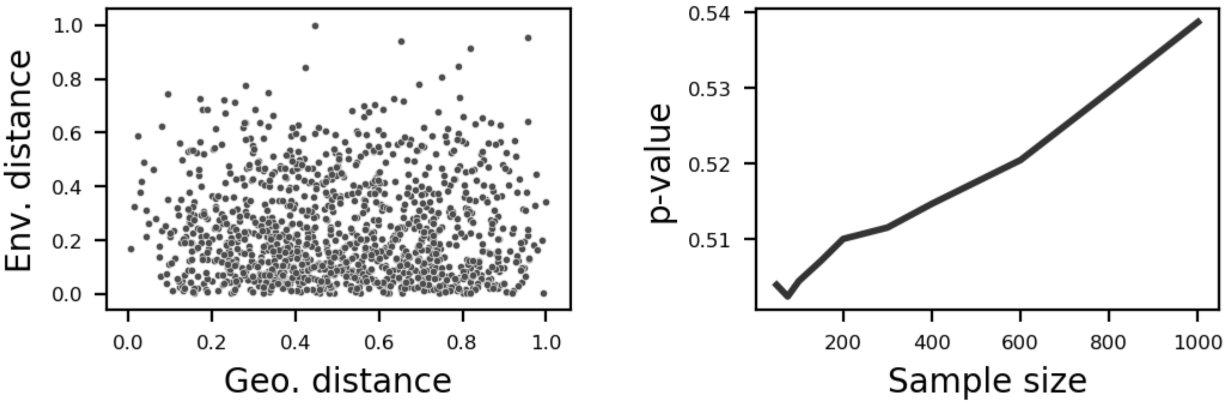


Figure S4. Results for distance decay relationships (DDR) for Bray-Curtis similarity. Environmental DDRs for the active community and for the total community differed by 25.2% (p = 0.002). Geographical DDRs for the active community and for the total community differed by 31.8 % (*P* = 0.016). The red line is the DDR resulting from a null model whereby communities were randomly assigned to different locations. Slopes of environmental and geographical DDRs differed from the null expectation.

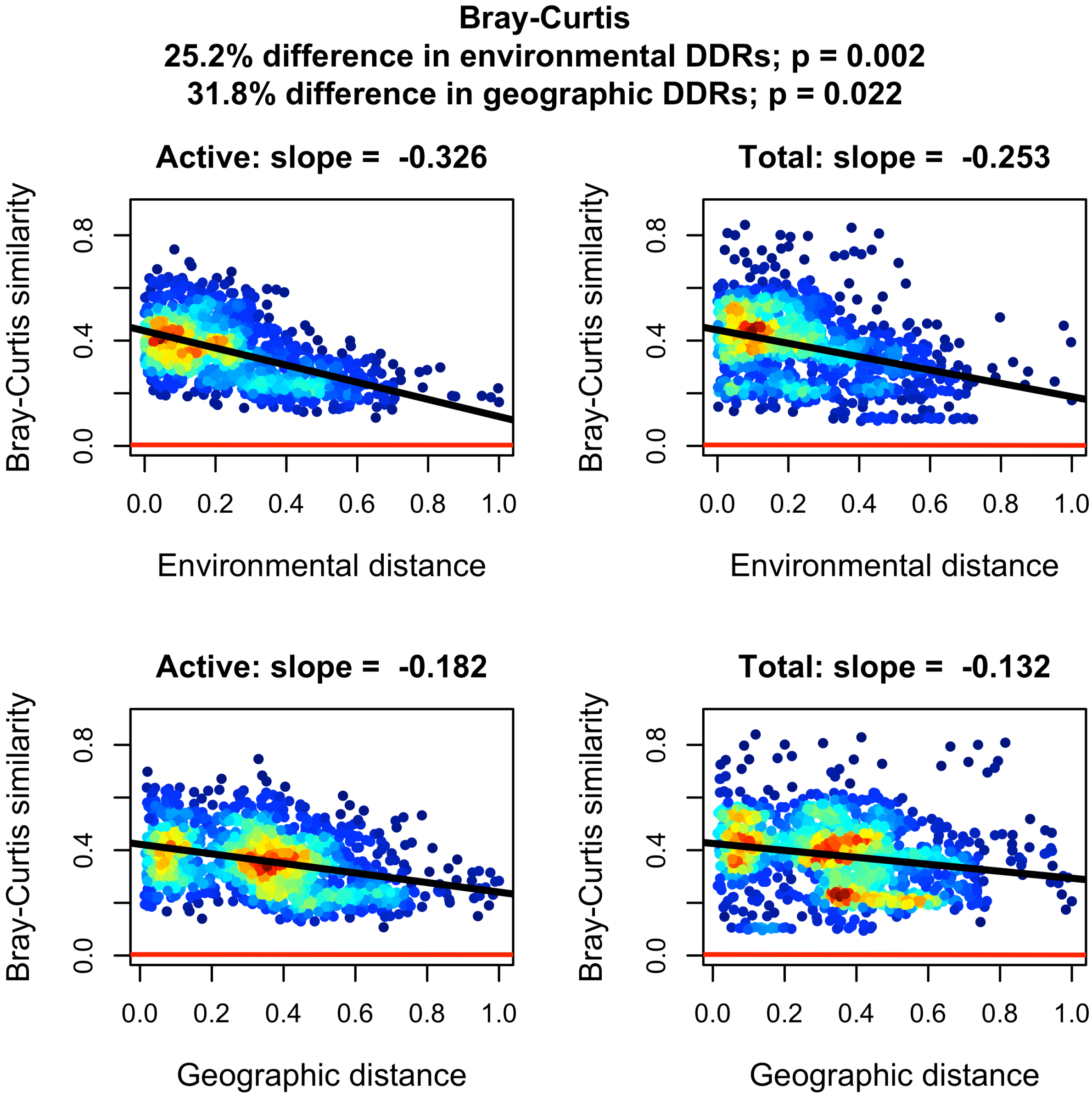


Figure S5. Results for distance decay relationships (DDR) for Sørensen’s similarity. Environmental DDRs for the active community and for the total community differed by 57.1 % (*P* = 0.001). Geographical DDRs for the active and total community differed by 47.6 % (*P* = 0.003). The red line is the DDR resulting from a null model whereby communities were randomly assigned to different locations. Except for the environmental DDR for the active community, slopes of DDRs did not differ from the null expectation.

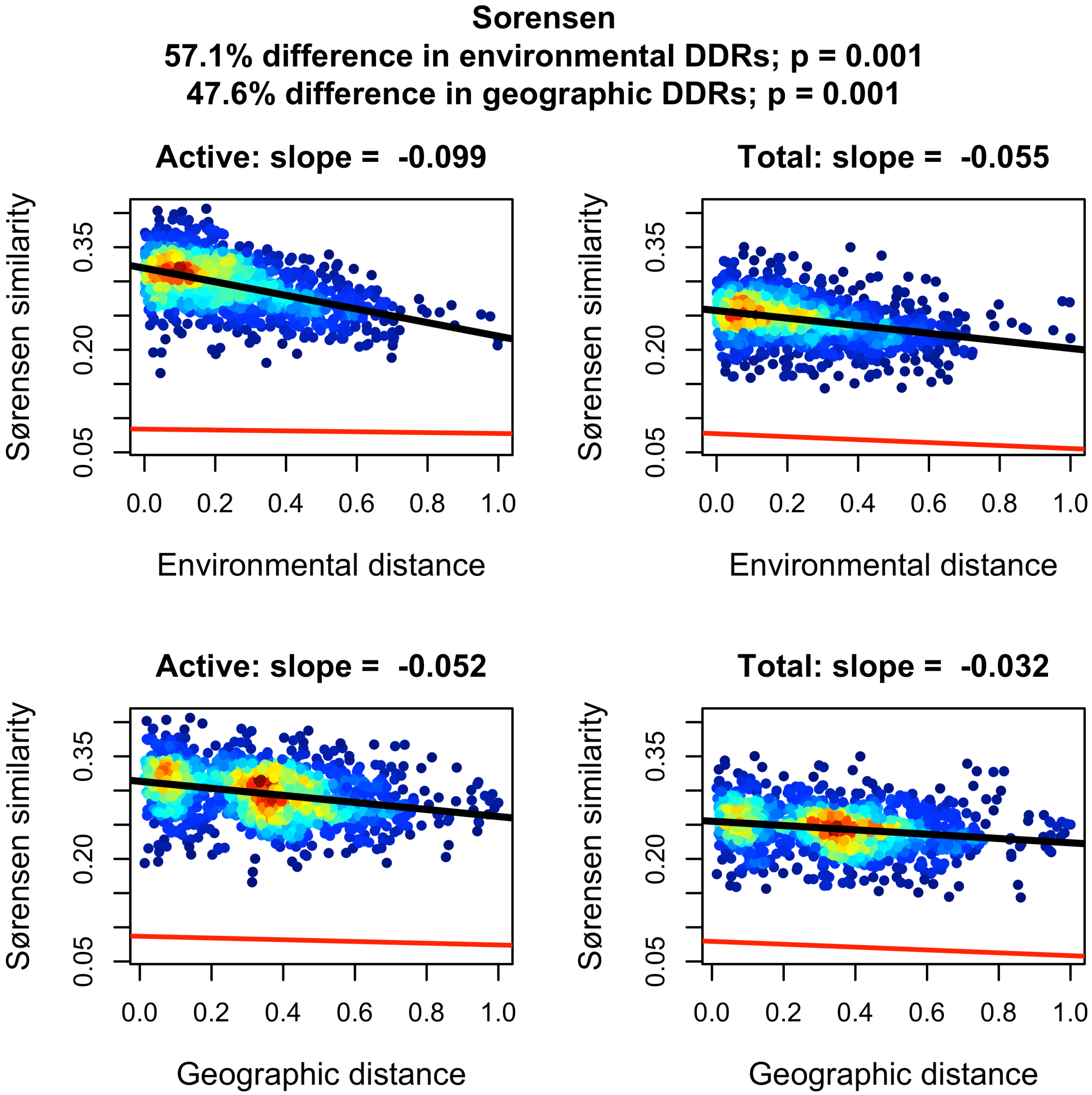


Figure S6. Slopes of environmental and geographical DDRs were steeper for the active community than for the total community regardless of the number of randomly chosen sample sites. Standard error bars and average values (points) were generated from 100 random resamplings.

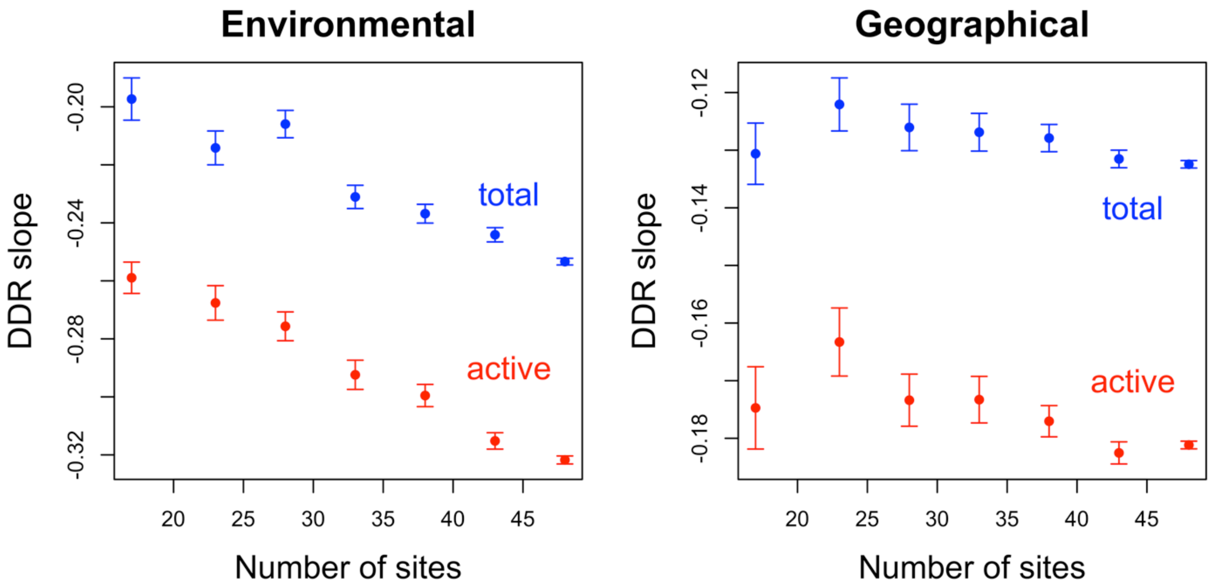


Figure S7. Slopes of environmental and geographical DDRs were steeper for the active community than for the total community regardless of the number of randomly chosen operational taxonomic units (OTUs). Columns (OTUs) were randomly chosen from site-by-taxa matrices. Abundances were then relativized. Standard error bars and average values (points) were generated from 100 random resamplings.

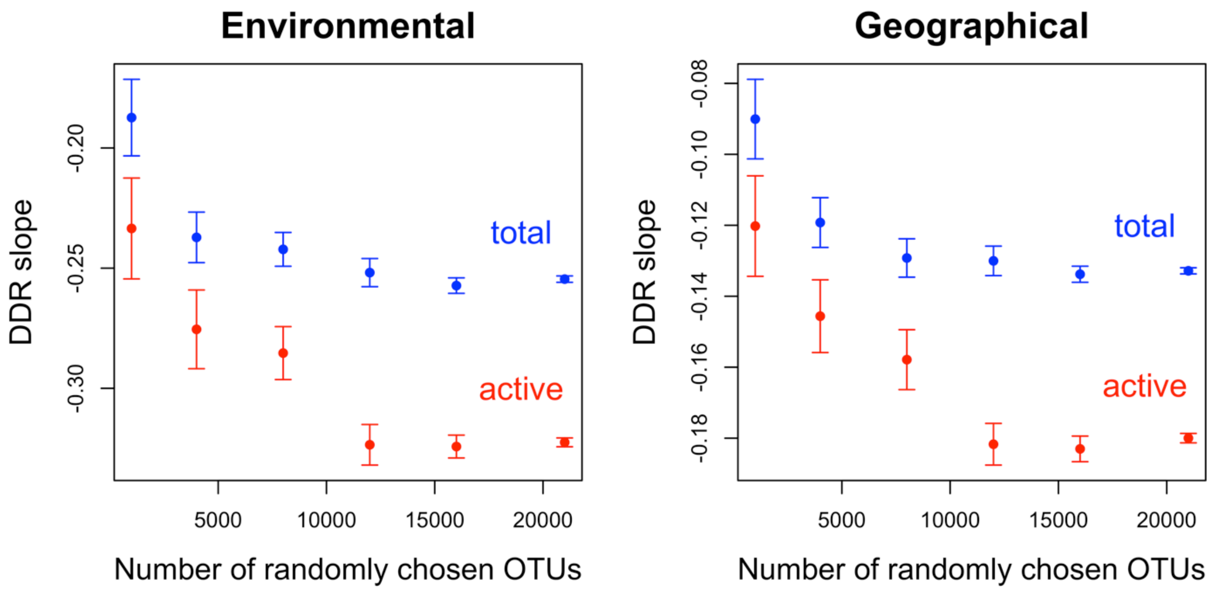


Figure S8. All 10^6 simulations reproduced at least 44 out of 50 aspects of our empirical results (Table S1). **Left:** Nearly 30% of models that included dispersal reproduced 50 out of 50 aspects of our empirical results; nearly 50% produced 49 out of 50. **Right:** Nearly 50% of models that excluded dispersal satisfied 50 out of 50 aspects of our empirical results; nearly 96% reproduce at least 49 out of 50 aspects.

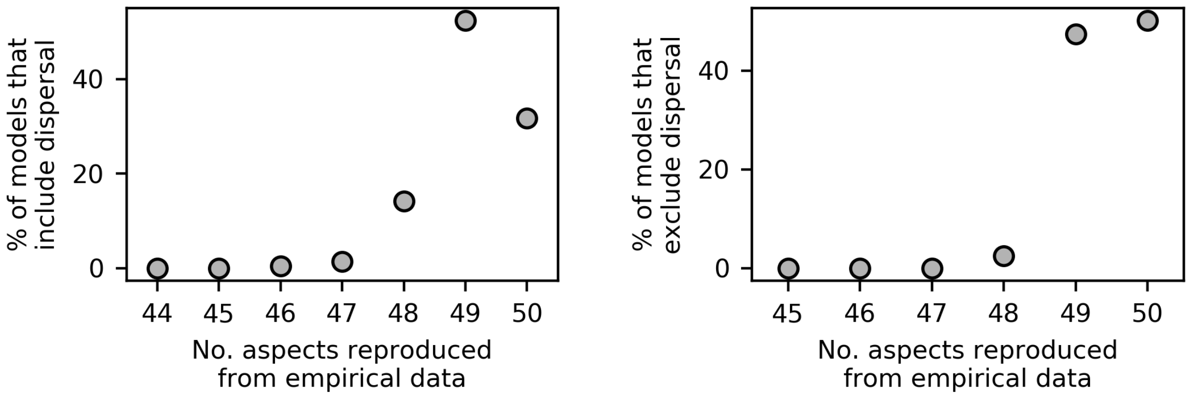


Table S1. To be counted as an appropriate simulation for the purpose of comparison to empirical results, individual simulations had to reproduce 50 aspects of our empirical DDR analyses for the active (RNA) community and the total (DNA) community. Simulations that met 50 or less of these criteria were not counted as appropriate simulations against which empirical results should be compared. Additional analyses revealed that each criterion could be met or fail to be met independent of all others. Numbers in parentheses indicate the number of times a given qualifier had to be satisfied, i.e., for each of three metrics and for multiple DDR types (e.g., environmental, geographical, RNA, DNA).

Qualifier	Number
49 communities with active and dormant populations	1
Mean total species richness among sites = 2082 ± 733	1
Distance-decay relationships are significant	8
Distance-decay slopes are less than 0.0	12
DDR intercepts are greater than 0.0	12
DDRs are steeper for RNA than corresponding DDRs for DNA	6
Environmental DDRs are steeper than corresponding geographical DDRs	6
For Canberra and Sørensen's similarity: DDR intercepts are greater for RNA than corresponding intercepts for DNA	4