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Supplementary material

Appendix 1

Supplemental information for

Regional and global elevational patterns of microbial species richness and evenness

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Running title: Elevational patterns in microbial diversity

Table A1. Brief description of the mountains studied. Lowest-Highest elevations indicate the lowest and highest elevations of the stream samples. Sample numbers for bacteria and diatoms of each mountain may differ due to the failing in sample pretreatments. Geographic distance indicates the longest geographic distance between samples for each mountain.

Mountain	Mountain Latitude & Longitude (°)	Lowest-Highest elevations (m)	Treeline (m)	Visiting year	Samples (bacteria/diatoms)	Geographic distance (km)
Balgesvarri	69.3809N; 20.3483E	0 - 770	550	Jul, 2012	19 / 17	8.9
Pyrenees	42.5457N; 0.8907E	850 - 2500	2100	Oct, 2012	19 / 19	27.3
Laojun	26.6959N; 99.7759E	1800 - 4200	4200	Oct, 2009	22 / 26	33.5
Haba	27.3758N; 100.1259E	1810 - 3940	3900	Oct, 2013	20 / 20	9.8
Meili	28.3705N; 98.8057E	2210 - 3650	3700	Oct, 2013	16 / 17	8.8
Yulong	27.1508N; 100.2931E	1490 - 3320	3900	Oct, 2013	24 / 24	18.8

Table A2. Summary of Elevational patterns in literature. Citations are shown below the table.

First author	Year	Habitat	Microorganisms	Patterns
Ormerod	1994	Stream biofilm	Diatoms	Decreasing
Bryant	2008	Soil	Acidobacteria	Decreasing
Fierer	2011	Soil	Bacteria	Hump-shaped
Fierer	2011	soil	Bacteria	U-shaped
Bahram	2011	Soil	Ectomycorrhizal fungi	Decreasing
Bahram	2011	Soil	Ectomycorrhizal fungi	Decreasing
Bahram	2011	Soil	Ectomycorrhizal fungi	No pattern
Singh	2011	Soil	Bacteria	Hump-shaped
Wang	2011	Stream biofilm	Diatoms	Decreasing
Wang	2011	Stream biofilm	Bacteria	Increasing
Shen	2012	Soil	Bacteria	No pattern
Singh	2012	Soil	Archaea	Hump-shaped
Wang	2012	Stream biofilm	Proteobacteria	Increasing
Singh	2013	Soil	Bacteria	No pattern
Yuan	2013	Soil	Bacteria	No pattern
Wilhelm	2013	Stream water	Bacteria	Decreasing
Wilhelm	2013	Stream biofilm	Bacteria	Decreasing
Lear	2013	Stream biofilm	Bacteria	Decreasing
Lujan	2013	Stream biofilm	Algae	Increasing
Miyamoto	2014	Soil	Ectomycorrhizal fungi	Hump-shaped
Shen	2014	Soil	Eukaryotes	No pattern
Singh	2014	Soil	Bacteria	U-shaped
Singh	2014	Soil	Bacteria	Decreasing
Zhang	2014	Soil	Acidobacteria	U-shaped
Wang	2014	Soil	Bacteria	Decreasing
Wang	2014	Soil	Archaea	No pattern
Pellissier	2014	Soil	Fungi	Increasing
Zhang	2015	Soil	Bacteria	Decreasing
Wilhelm	2015	Stream biofilm	Bacteria	Decreasing
Jarvis	2015	Soil	Ectomycorrhizal fungi	No pattern

Citations: (Ormerod, et al. 1994); (Bryant, et al. 2012); (Fierer, et al. 2011); (Bahram, et al. 2011); (Dharmesh Singh, et al. 2012, D. Singh, et al. 2012, Singh, et al. 2013, Singh, et al. 2014); (Wang, et al. 2011); (Wang, et al. 2012); (Wilhelm, et al. 2013, Wilhelm, et al. 2015); (Lear, et al. 2013); (Lujan, et al. 2013); (Miyamoto, et al. 2014); (Shen, et al. 2013); (Zhang, et al. 2015); (Zhang, et al. 2014); (Wang, et al. 2014); (Pellissier, et al. 2014); (Jarvis, et al. 2015);

Table A3. The relationships between elevations, richness and evenness. The trends of richness or evenness along elevations, and the relationships between richness and evenness were modeled with both linear (L) and quadratic (Q) models. The better model was selected with the lower value of Akaike's Information Criterion.

Relations	Taxa	Locations	Linear model		Quadratic model		Better Model
			R ²	P	R ²	P	
Richness	Bacteria	Balggesarri	0.301	0.015	0.438	0.010	Q
		Pyrenees	0.277	0.021	0.283	0.070	L
		Laojun	0.378	0.003	0.544	0.001	Q
		Haba	0.353	0.006	0.434	0.008	L
		Meili	0.712	0.000	0.729	0.000	L
		Yulong	0.020	0.508	0.319	0.018	Q
Elevation	Diatom	Balggesarri	0.071	0.300	0.097	0.488	L
		Pyrenees	0.036	0.435	0.118	0.366	L
		Laojun	0.478	0.000	0.482	0.001	L
		Haba	0.365	0.005	0.568	0.001	Q
		Meili	0.022	0.574	0.051	0.695	L
		Yulong	0.012	0.613	0.012	0.882	L
Evenness	Bacteria	Balggesarri	0.000	0.930	0.071	0.555	L
		Pyrenees	0.130	0.129	0.190	0.186	L
		Laojun	0.070	0.246	0.141	0.254	L
		Haba	0.253	0.024	0.381	0.017	L
		Meili	0.704	0.000	0.719	0.000	L
		Yulong	0.252	0.012	0.255	0.045	L
Elevation	Diatom	Balggesarri	0.389	0.007	0.567	0.003	Q
		Pyrenees	0.424	0.003	0.567	0.001	Q
		Laojun	0.405	0.000	0.613	0.000	Q
		Haba	0.230	0.032	0.321	0.037	L
		Meili	0.233	0.049	0.234	0.155	L
		Yulong	0.184	0.036	0.190	0.110	L
Evenness	Bacteria	Balggesarri	0.264	0.025	0.301	0.057	L
		Pyrenees	0.624	0.000	0.652	0.000	L
		Laojun	0.575	0.000	0.600	0.000	L
		Haba	0.902	0.000	0.939	0.000	Q
		Meili	0.798	0.000	0.914	0.000	Q
		Yulong	0.389	0.001	0.463	0.001	L
Richness	Diatom	Balggesarri	0.511	0.001	0.748	0.000	Q
		Pyrenees	0.104	0.179	0.305	0.054	Q
		Laojun	0.343	0.002	0.372	0.005	L
		Haba	0.002	0.848	0.012	0.900	L
		Meili	0.310	0.020	0.362	0.043	L
		Yulong	0.383	0.001	0.388	0.006	L

Figure A1. The relationships of richness-evenness for bacteria (A-B) and diatoms (C-D) with two evenness metrics for the whole data set. These two metrics are Evar (A, C) and Pielou's evenness (B, D). All relationships were significantly ($P < 0.01$) fitted by a linear model.

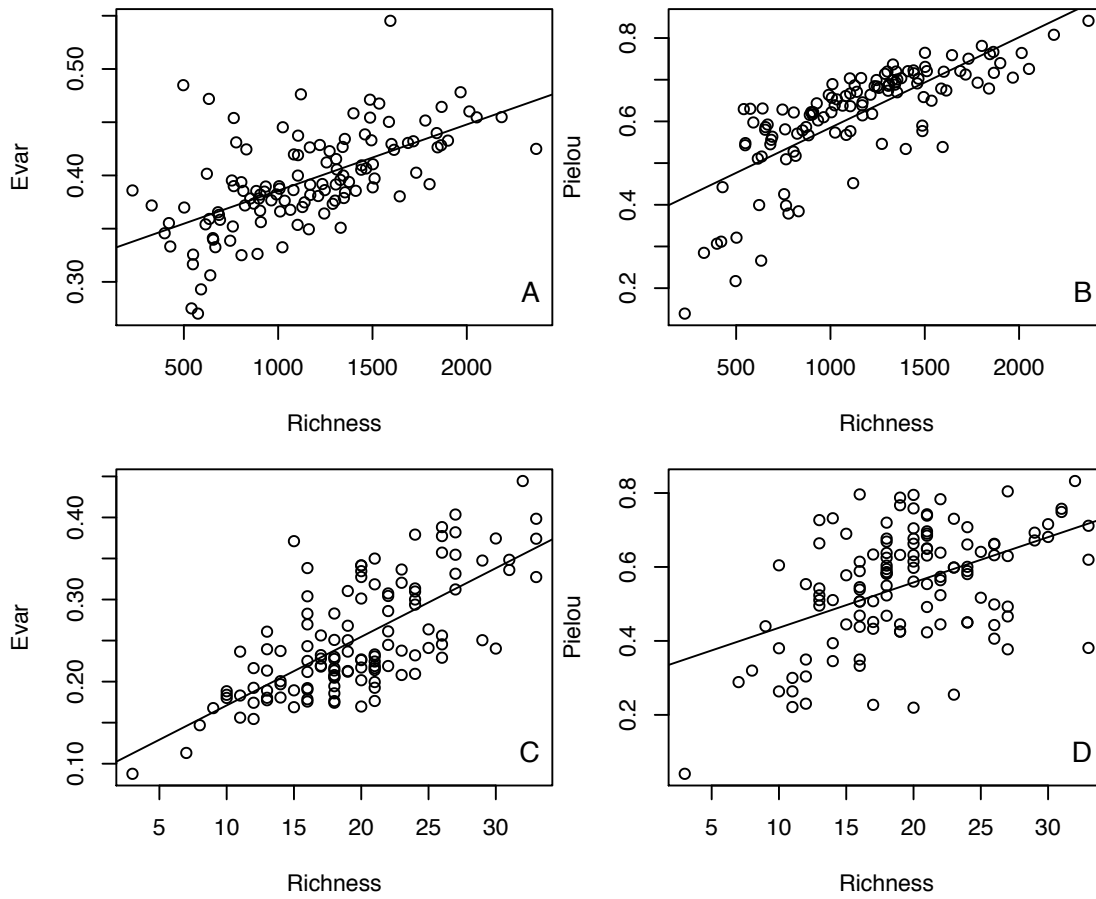


Figure A2. Partial dependence plots for all variables included in the Boosted Regression Trees (Elith, et al. 2008) model of bacterial species richness. The y-axes represent the marginal effect of the respective explanatory variable on the predicted species richness (centred to zero mean). The relative contribution (%) of each variable is shown in parentheses on the x-axes. The relative contributions are visualized in Figure 5A. The solid line is the BRT-modeled response curve to the most important variables. The dashed line is the locally weighted scatterplot smoothing (LOESS) regression (span 0.25) fitted to the response curve. TP: total phosphorus. Mountain: the mountains as a categorical variable. Shading: riparian shading (%). Substratum: median of the substratum particle size. Velocity: current velocity. Depth: streamwater depth. cDOM: chromophoric dissolved organic matter. Temperature: streamwater temperature.

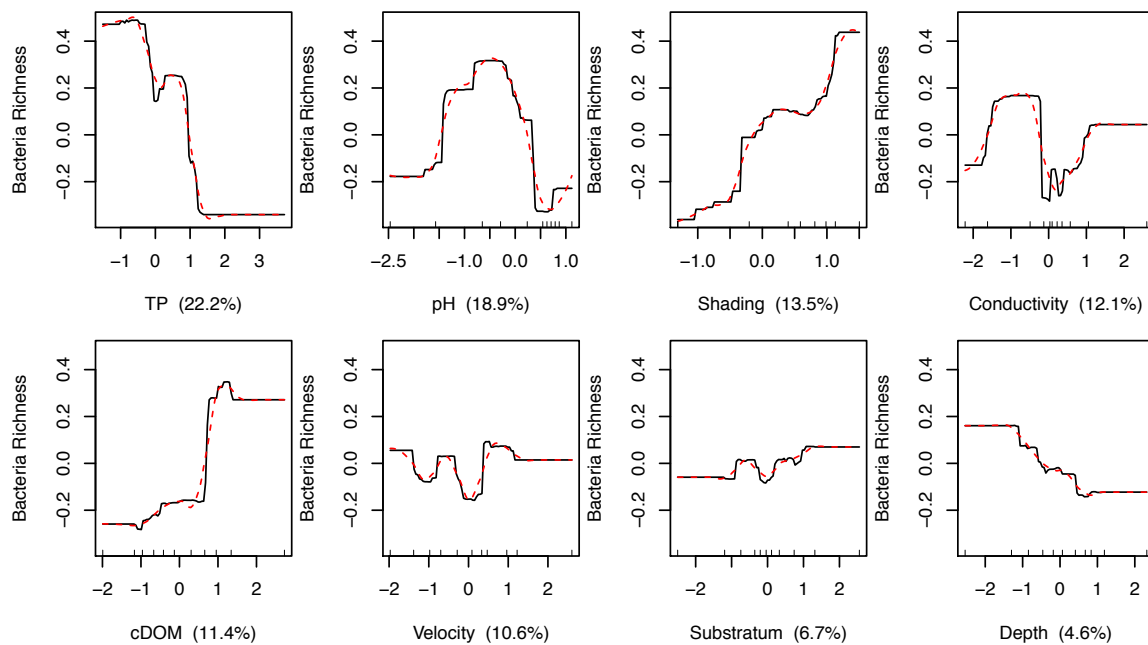


Figure A3. Partial dependence plots for all variables included in the Boosted Regression Tree model of bacterial species evenness. The y-axes represent the marginal effect of the respective explanatory variable on the predicted species richness (centred to zero mean). The relative contribution (%) of each variable is shown in parentheses on the x-axes. The relative contributions are visualized in Figure 5B. The solid line is the BRT-modeled response curve to the most important variables. The dashed line is the LOESS smoother (span 0.25) fitted to the response curve. The abbreviations of environmental variables are shown in Figure A2.

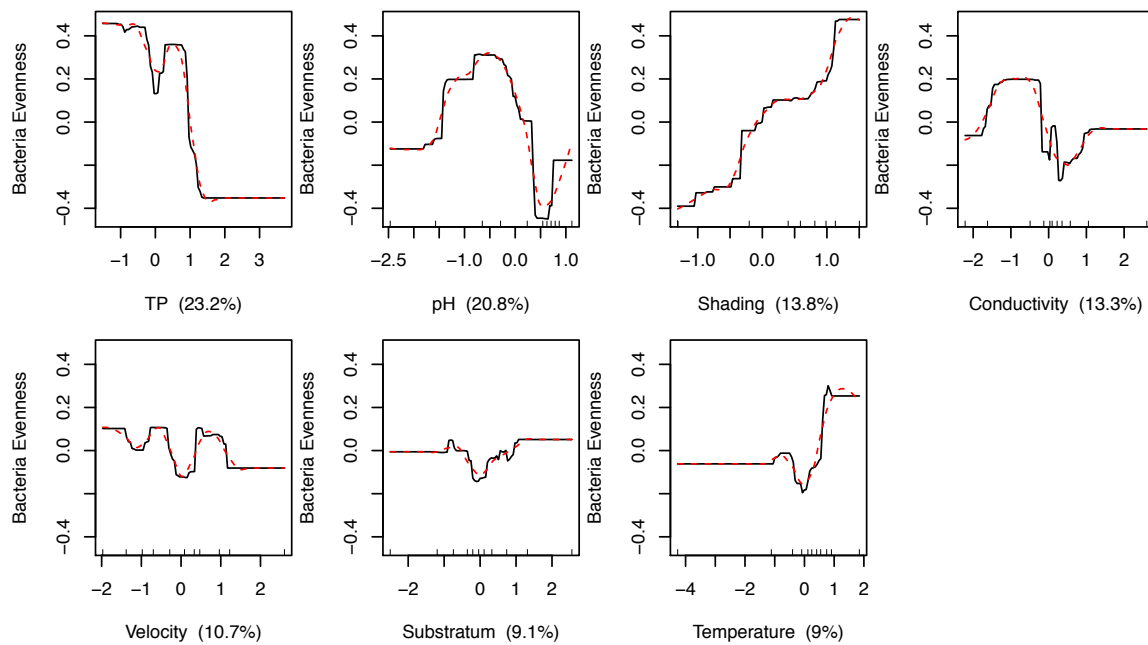


Figure A4. Partial dependence plots for all variables included in the Boosted Regression Tree model of species richness of diatoms. The y-axes represent the marginal effect of the respective explanatory variable on the predicted species richness (centred to zero mean). The relative contribution (%) of each variable is shown in parentheses on the x-axes. The relative contributions are visualized in Figure 5C. The solid line is the BRT-modeled response curve to the most important variables. The dashed line is the LOESS smoother (span 0.25) fitted to the response curve. The abbreviations of environmental variables are shown in Figure A2.

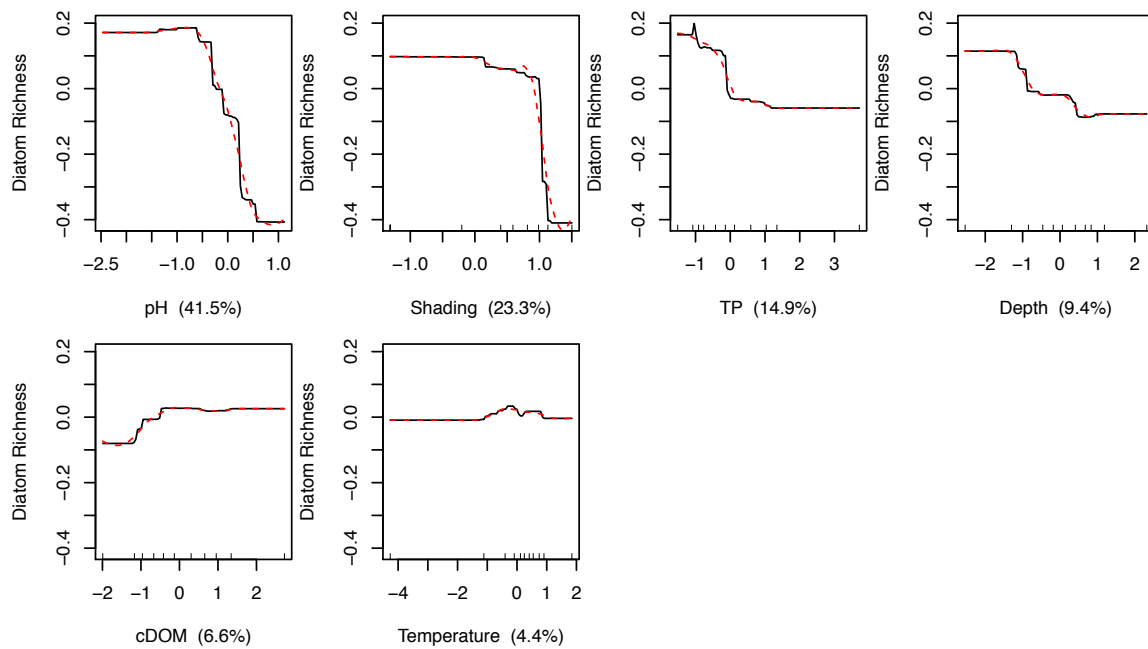
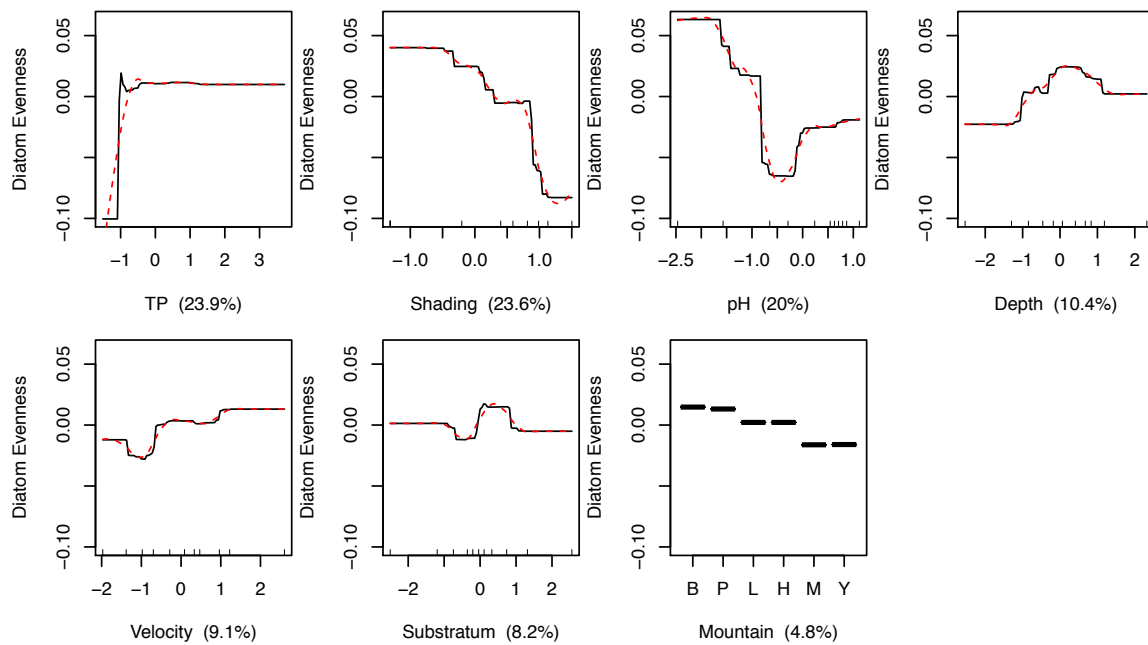


Figure A5. Partial dependence plots for all variables included in the Boosted Regression Tree model of species evenness of diatoms. The y-axes represent the marginal effect of the respective explanatory variable on the predicted species richness (centred to zero mean). The relative contribution (%) of each variable is shown in parentheses on the x-axes. The relative contributions are visualized in Figure 5D. The solid line is the BRT-modeled response curve to the most important variables. The dashed line is the LOESS smoother (span 0.25) fitted to the response curve. The abbreviations of environmental variables are shown in Figure A2.



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