

Supplemental Materials

Table S2. Pairwise angles between PC1 axes calculated on body shapes of species in each of the six habitat groups (above diagonal) and associated p-values (below diagonal). Bolded values designate comparisons between corresponding habitats.

	freshwater benthic	freshwater demersal	freshwater pelagic	marine benthic	marine demersal	marine pelagic
freshwater benthic	-	19.7	34.1	29.8	25.3	32.9
freshwater demersal	0.052	-	36.8	46.9	9.9	39.2
freshwater pelagic	0.163	0.696	-	36.4	33.5	12.8
marine benthic	0.017	0.122	0.037	-	48	29.8
marine demersal	0.016	<0.001	0.029	0.227	-	35.2
marine pelagic	0.041	0.082	<0.001	0.036	0.082	-

Table S3. Trait loadings on PC1 by group for the three different methods, PCA, phylogenetic PCA, and PACA. Loadings on PC1 for the entire dataset are in the last column.

method	trait	freshwater_benthic	freshwater_demersal	freshwater_pelagic	marine_benthic	marine_demersal	marine_pelagic	all
PACA	Head depth	-0.108	-0.618	0.383	-0.478	-0.449	-0.341	-
	Lower jaw length	-0.149	-0.157	0.112	0.098	0.206	0.455	-
	Max body depth	-0.351	-0.413	0.331	-0.283	-0.444	-0.299	-
	Max fish width	0.668	0.011	-0.697	-0.361	0.034	-0.438	-
	Min caudalpeduncle depth	-0.426	-0.351	-0.384	-0.322	-0.408	-0.002	-
	Min caudalpeduncle width	-0.284	-0.184	-0.092	-0.295	-0.396	-0.422	-
	Mouth width	0.176	-0.080	-0.246	-0.236	0.082	-0.075	-
	Standard length	-0.322	0.508	0.169	0.552	0.476	0.460	-
PCA	Head depth	-0.513	-0.451	-0.273	0.440	-0.439	0.392	-0.433
	Lower jaw length	-0.009	0.163	0.392	0.092	0.305	-0.349	0.222
	Max body depth	-0.527	-0.520	-0.461	0.305	-0.481	0.444	-0.482
	Max fish width	0.069	0.228	-0.196	0.276	0.173	0.300	-0.008
	Min caudalpeduncle depth	-0.456	-0.377	-0.412	0.441	-0.324	0.342	-0.425
	Min caudalpeduncle width	-0.270	-0.244	-0.136	0.373	-0.308	0.243	-0.325
	Mouth width	0.042	0.274	-0.034	0.217	0.281	0.072	0.105
	Standard length	0.415	0.415	0.576	-0.498	0.418	-0.506	0.483
Phy-PCA	Head depth	-0.226	0.110	-0.088	-0.033	-0.043	0.179	-
	Lower jaw length	-0.247	0.691	-0.011	-0.012	-0.093	-0.097	-
	Max body depth	-0.013	-0.214	-0.027	-0.020	0.070	0.024	-
	Max fish width	-0.080	0.225	0.143	0.026	-0.421	0.182	-
	Min caudalpeduncle depth	-0.068	-0.034	-0.036	-0.452	0.034	0.021	-
	Min caudalpeduncle width	-0.910	-0.097	-0.972	-0.890	-0.075	-0.067	-
	Mouth width	-0.205	0.635	0.139	-0.023	-0.891	0.953	-
	Standard length	0.087	0.033	-0.070	-0.002	0.082	-0.103	-

Table S4. Percent variance explained by PC1 for each habitat.

Ecosystem	Habitat	perc. var.
freshwater	benthic	34.2
	demersal	37.8
	pelagic	34.8
marine	benthic	44.7
	demersal	45.4
	pelagic	45.7

Table S5. Angles between the first components of each PCA method within each habitat (PCA = standard PCA; PACA = phylogenetically-aligned PCA; PhyPCA = phylogenetic PCA)

Ecosystem	Habitat	PCA_PACA	PACA_PhyPCA	PCA_PhyPCA
freshwater	benthic	64.4	76.4	64.9
	demersal	33.2	84.8	63.3
	pelagic	78.5	85.0	83.9
marine	benthic	15.1	65.0	56.6
	demersal	17.1	86.4	71.3
	pelagic	26.1	73.6	73.7

Table S6. Pairwise angles between PC1 axes calculated on body shapes of species in each of the six habitat groups using log-shape ratios.

	freshwater benthic	freshwater demersal	freshwater pelagic	marine benthic	marine demersal	marine pelagic
freshwater benthic	-	-	-	-	-	-
freshwater demersal	17.7	-	-	-	-	-
freshwater pelagic	34.8	37.8	-	-	-	-
marine benthic	35.4	48.7	31.7	-	-	-
marine demersal	23.1	9.9	34	48.3	-	-
marine pelagic	36.6	40.1	10.6	30.5	35	-

Table S7. Pairwise correlations between the covariance matrices of each habitat.

	freshwater benthic	freshwater demersal	freshwater pelagic	marine benthic	marine demersal	marine pelagic
freshwater benthic	-	-	-	-	-	-
freshwater demersal	0.754	-	-	-	-	-
freshwater pelagic	0.616	0.709	-	-	-	-
marine benthic	0.864	0.778	0.643	-	-	-
marine demersal	0.722	0.899	0.689	0.704	-	-
marine pelagic	0.64	0.634	0.902	0.669	0.675	-

Table S8. Pairwise Krzanowski correlations between rate matrices for each regime using family averages.

	freshwater benthic	freshwater demersal	freshwater pelagic	marine benthic	marine demersal	marine pelagic
freshwater benthic	-	-	-	-	-	-
freshwater demersal	0.654	-	-	-	-	-
freshwater pelagic	0.478	0.543	-	-	-	-
marine benthic	0.791	0.774	0.588	-	-	-
marine demersal	0.624	0.889	0.588	0.66	-	-
marine pelagic	0.554	0.632	0.669	0.64	0.757	-

Table S9. Pairwise Krzanowski correlations between rate matrices for each regime using the subtree pruning procedure.

	freshwater benthic	freshwater demersal	freshwater pelagic	marine benthic	marine demersal	marine pelagic
freshwater benthic	-	-	-	-	-	-
freshwater demersal	0.696	-	-	-	-	-
freshwater pelagic	0.922	0.763	-	-	-	-
marine benthic	0.747	0.717	0.806	-	-	-
marine demersal	0.656	0.923	0.67	0.689	-	-
marine pelagic	0.741	0.904	0.839	0.765	0.842	-

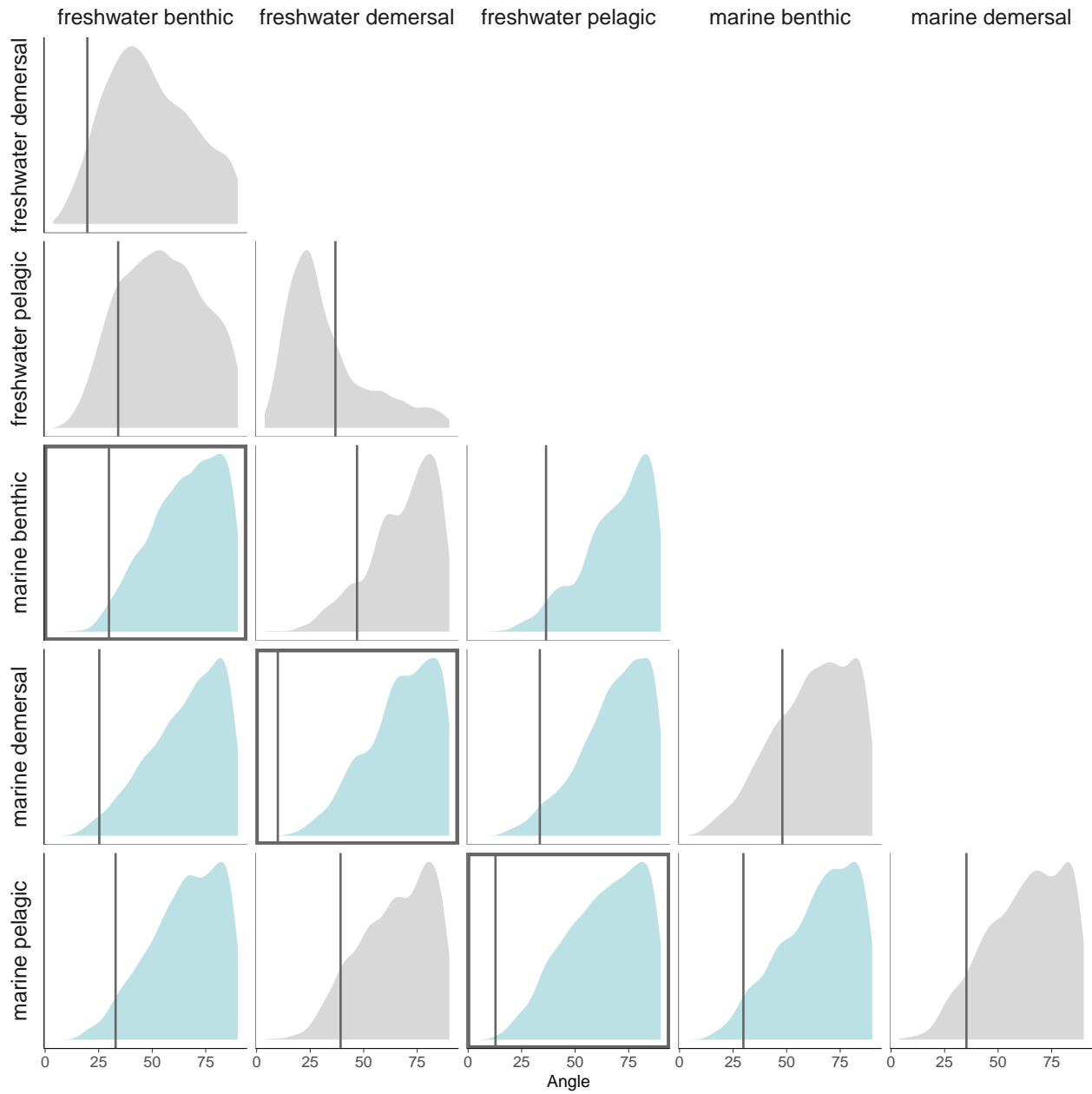


Figure S1. Distributions of pairwise angles from the 1000 simulated datasets for all six habitat groups. Empirical angles are designated by the vertical black line in each plot and distributions in blue indicated statistical significance ($p < 0.05$; see Table S1). Pairwise plots surrounded by a black box indicate the comparisons between corresponding habitats across freshwater and marine systems.

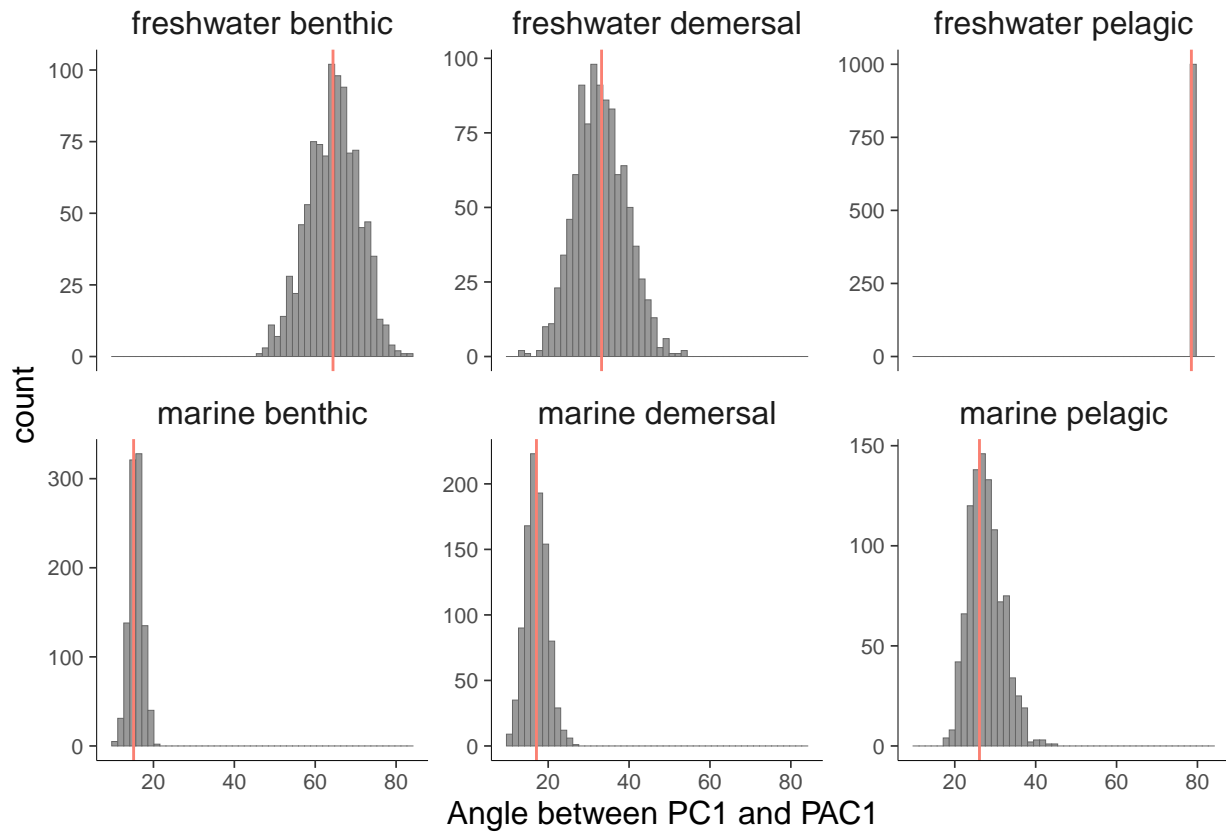


Figure S2. Distribution of angles between PC1 and PAC1 from each habitat group resampled with 477 species for 1,000 iterations. This was to determine if differences in group size are biasing our angle estimates. Red lines represent the empirical angle from the full dataset for each habitat group.

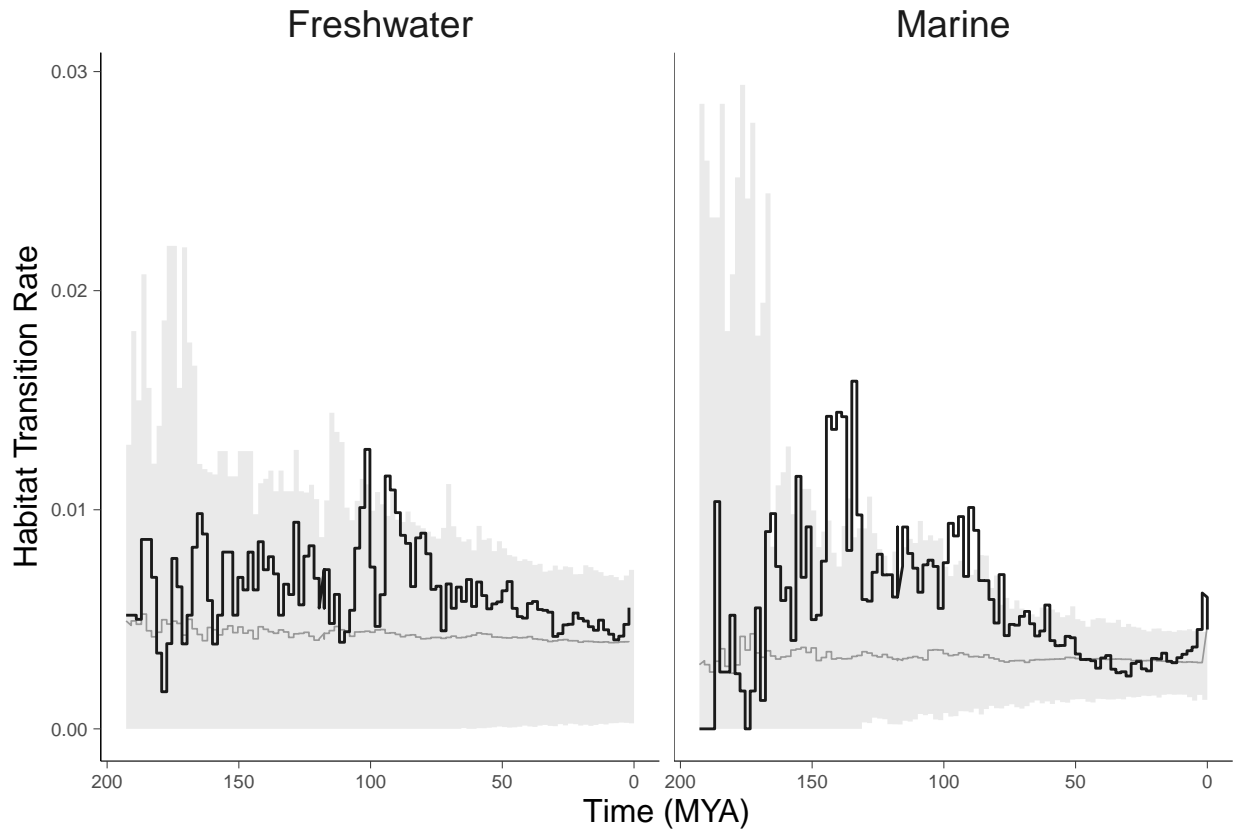


Figure S3. Rate of habitat transitions through time averaged across 100 stochastic character maps. Grey lines and the shaded regions designate the expectation under a constant rate and the associated 95% confidence interval, respectively.

- freshwater_benthic
- freshwater_demersal
- freshwater_pelagic
- marine_benthic
- marine_demersal
- marine_pelagic

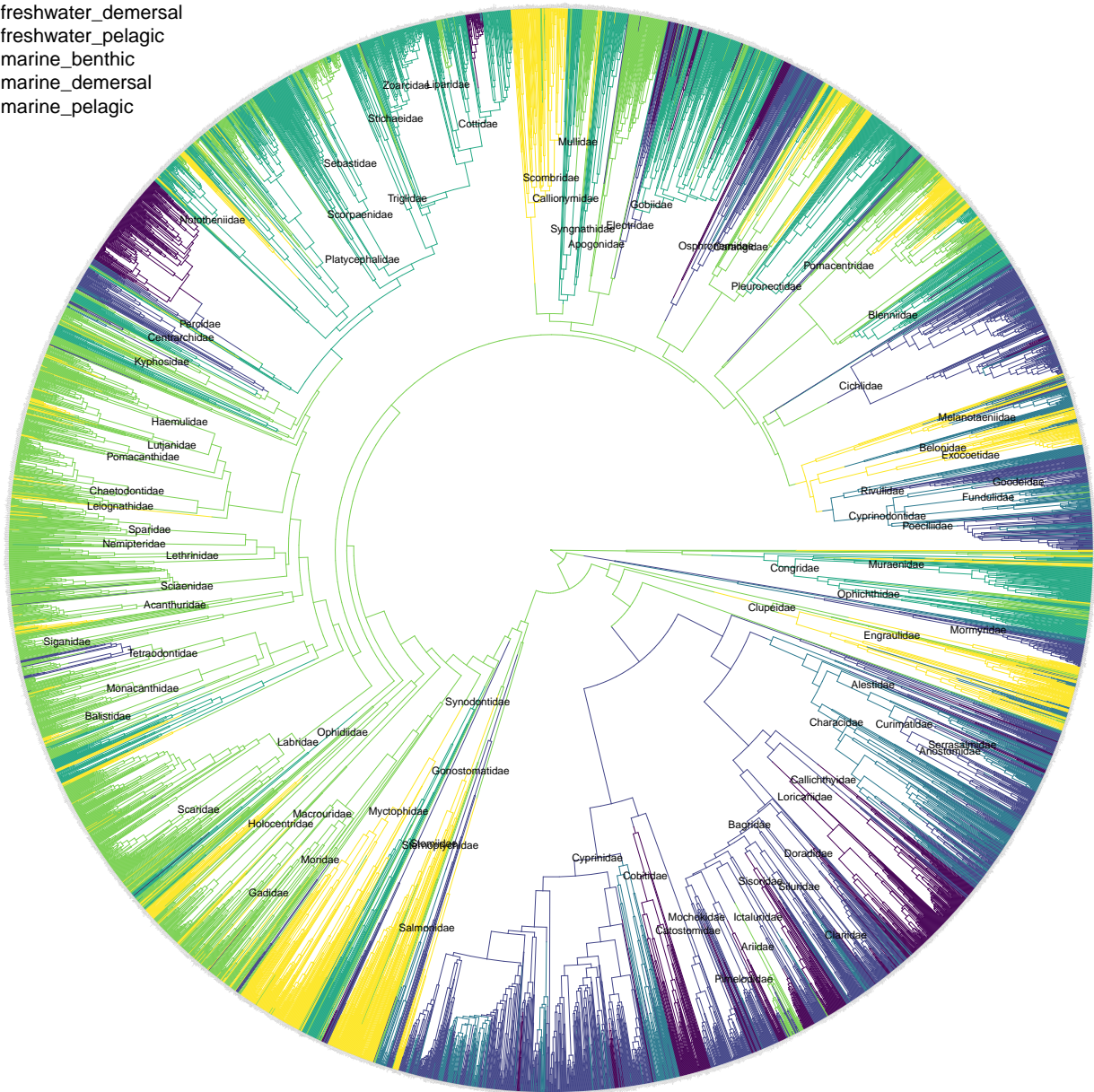


Figure S4. Representative stochastic character map with all six habitat states reconstructed. Select family names printed at the node corresponding to the most recent common ancestor of the species present in the dataset. Pruned phylogeny from Rabsoky et al. (2018).

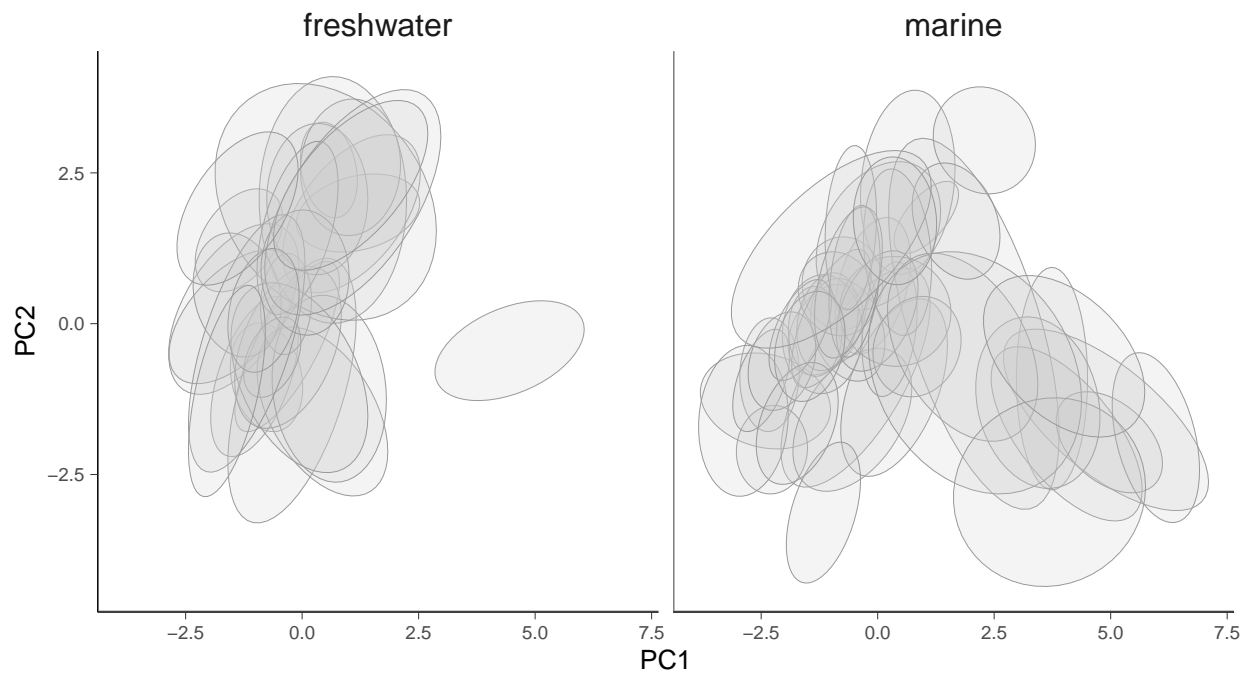


Figure S5. Visualization of 95% data ellipses for each family by ecosystem.