Supplement 1

Table S1. Three parameters non-linear regressions ($\beta\text{-}diversity = a - b \times e^{-c \times Distance}$) between total β-diversity and its components based on incidence data for three matrices: all bacteria (ALL), cyanobacteria (CYA) and other bacteria (BAC) of plankton and periphyton samples. Total β-diversity measured through the Sorensen index (β_{sor}), and its respective components turnover (β_{turn}) and nestedness (β_{nes}).

			Equation	P-values	Observation
ALL	Plankton	Sorensen	$\beta_{sor} = 0.72116 - 0.43915 \times e^{-0.23652 \times Distance}$	a = < 2×10⁻¹⁶ b = 1.32 ×10⁻¹¹ c = 0.106	
		Turnover	$\beta_{turn} = 0.67320 - 0.44152 \times e^{-0.20959 \times Distance}$	a = < 2×10⁻¹⁶ b = 1.27 ×10⁻¹² c = 0.0524	
		Nestedness	-	-	Did not adjust to the model
	Periphyton	Sorensen	$\beta_{sor} = 0.75389 - 0.53210 \times e^{-0.74164 \times Distance}$	a = < 2×10⁻¹⁶ b = 4.38 ×10⁻¹³ c = 4.40 ×10⁻⁵	
		Turnover	$\beta_{turn} = 0.63783 - 0.47867 \times e^{-0.39917 \times Distance}$	a = < 2×10⁻¹⁶ b = 5.13 ×10⁻⁸ c = 0.0189	
		Nestedness	-	-	Did not adjust to the model
CYA	Plankton	Sorensen	$\beta_{sor} = 0.69146 - 0.43707 \times e^{-0.21962 \times Distance}$	a = < 2×10⁻¹⁶ b = 1.39 ×10⁻⁸ c = 0.157	
		Turnover	$\beta_{turn} = 0.55451 - 0.47225 \times e^{-0.25725 \times Distance}$	a = < 2×10⁻¹⁶ b = 7.56 ×10⁻⁸ c = 0.252	
		Nestedness	-	-	Did not adjust to the model
	Periphyton	Sorensen	$\beta_{sor} = 0.75854 - 0.61847 \times e^{-0.79470 \times Distance}$	a = < 2×10⁻¹⁶ b = 1.82 ×10⁻¹¹ c = 0.000156	
		Turnover	$\beta_{turn} = 0.59865 - 0.62812 \times e^{-0.32777 \times Distance}$	a = < 2×10⁻¹⁶ b = 1.95 ×10⁻⁸ c = 0.0277	
		Nestedness	-	-	Did not adjust to the model

Table S1: continued

			Equation	P-values	Observation
BAC	Plankton	Sorensen	$\beta_{sor} = 0.72164 - 0.43732 \times e^{-0.24513 \times Distance}$	a = < 2×10^{-16} b = 1.44 ×10^{-11} c = 0.118	
		Turnover	$\beta_{turn} = 0.65649 - 0.80310 \times e^{-4.15870 \times Distance}$	a = < 2×10^{-16} b = 0.000305 c = 0.019795	
		Nestedness	-	-	Did not adjust to the model
	Periphyton	Sorensen	$\beta_{sor} = 0.75524 - 0.52606 \times e^{-0.74049 \times Distance}$	a = < 2×10^{-16} b = 4.45 ×10^{-12} c = 0.000108	
		Turnover	$\beta_{turn} = 0.63657 - 0.46781 \times e^{-0.39878 \times Distance}$	a = < 2×10^{-16} b = 4.06 ×10^{-7} c = 0.0304	
		Nestedness	-	-	Did not adjust to the model

Table S2. Three parameters non-linear regressions ($\beta\text{-}diversity = a - b \times e^{-c \times Distance}$) between total β-diversity and its components based on abundance data for three matrices: all bacteria (ALL), cyanobacteria (CYA) and other bacteria (BAC) of plankton and periphyton samples. Total β-diversity measured through the Bray-Curtis index (β_{bc}), and its respective components balanced variation (β_{bal}) and abundance gradient (β_{gra}).

			Equation	P-values	Observation
ALL	Plankton	Bray-Curtis	$\beta_{bc} = 0.63176 - 0.46002 \times e^{-0.32473 \times Dist}$	a = < 2×10⁻¹⁶ b = 4.18 ×10⁻⁶ c = 0.34	
		Balanced	$\beta_{bal} = 0.62628 - 0.46237 \times e^{-0.25826 \times Dist}$	a = < 2×10⁻¹⁶ b = 3.13 ×10⁻⁶ c = 0.33	
		Gradient	$\beta_{gra} = 0.007047 - 0.014680 \times e^{-11.503527 \times Dist}$	a = 2.42 ×10⁻⁶ b = 0.761 c = 0.713	Model not significant
	Periphyton	Bray-Curtis	$\beta_{bc} = 0.76977 - 0.59662 \times e^{-0.51066 \times Distance}$	a = < 2×10⁻¹⁶ b = 3.29 ×10⁻¹² c = 0.000483	
		Balanced	$\beta_{bal} = 0.75453 - 0.58771 \times e^{-0.50481 \times Distance}$	a = < 2×10⁻¹⁶ b = 2.12 ×10⁻¹¹ c = 0.00091	
		Gradient	-	-	Did not adjust to the model
CYA	Plankton	Bray-Curtis	$\beta_{bc} = 0.56383 - 0.43408 \times e^{-0.27342 \times Distance}$	a = < 2×10⁻¹⁶ b = 3.93 ×10⁻⁵ c = 0.416	
		Balanced	-	-	Did not adjust to the model
		Gradient	-	-	Did not adjust to the model
	Periphyton	Bray-Curtis	$\beta_{bc} = 0.74129 - 0.61955 \times e^{-0.39626 \times Distance}$	a = < 2×10⁻¹⁶ b = 1.56 ×10⁻⁸ c = 0.0147	
		Balanced	$\beta_{bal} = 0.67234 - 0.65909 \times e^{-0.33715 \times Distance}$	a = < 2×10⁻¹⁶ b = 1.2 ×10⁻⁶ c = 0.0578	
		Gradient	$\beta_{gra} = 0.07883 - 0.11840 \times e^{-51.84646. \times Distance}$	a = 4×10⁻¹² b = 0.771 c = 0.828	Model not significant

Table S2: continued

|			Equation	P-values	Observation
BAC	Plankton	Bray-Curtis	$\beta_{BC} = 0.66033 - 0.46604 \times e^{-0.25384 \times Distance}$	a = < 2×10^{-16} b = 4.47 ×10^{-6} c = 0.332	
		Balanced	$\beta_{bal} = 0.62775 - 0.49251 \times e^{-0.25013 \times Distance}$	a = < 2×10^{-16} b = 1.01 ×10^{-6} c = 0.292	
		Gradient	$\beta_{gra} = 0.037358 - 0.401055 \times e^{-34.309210 \times Distance}$	a = < 2×10^{-16} b = 0.870 c = 0.663	Model not significant
	Periphyton	Bray-Curtis	$\beta_{bc} = 0.78503 - 0.59269 \times e^{-0.60700 \times Distance}$	a = < 2×10^{-16} b = 2.18 ×10^{-9} c = 0.00183	
		Balanced	$\beta_{bal} = 0.74951 - 0.57982 \times e^{-0.58426 \times Distance}$	a = < 2×10^{-16} b = 7.89 ×10^{-8} c = 0.00639	
		Gradient	$\beta_{gra} = 0.03595 - 0.02722 \times e^{-0.2181 \times Distance}$	a = 1.75 ×10^{-12} b = 0.807 c = 0.932	Model not significant
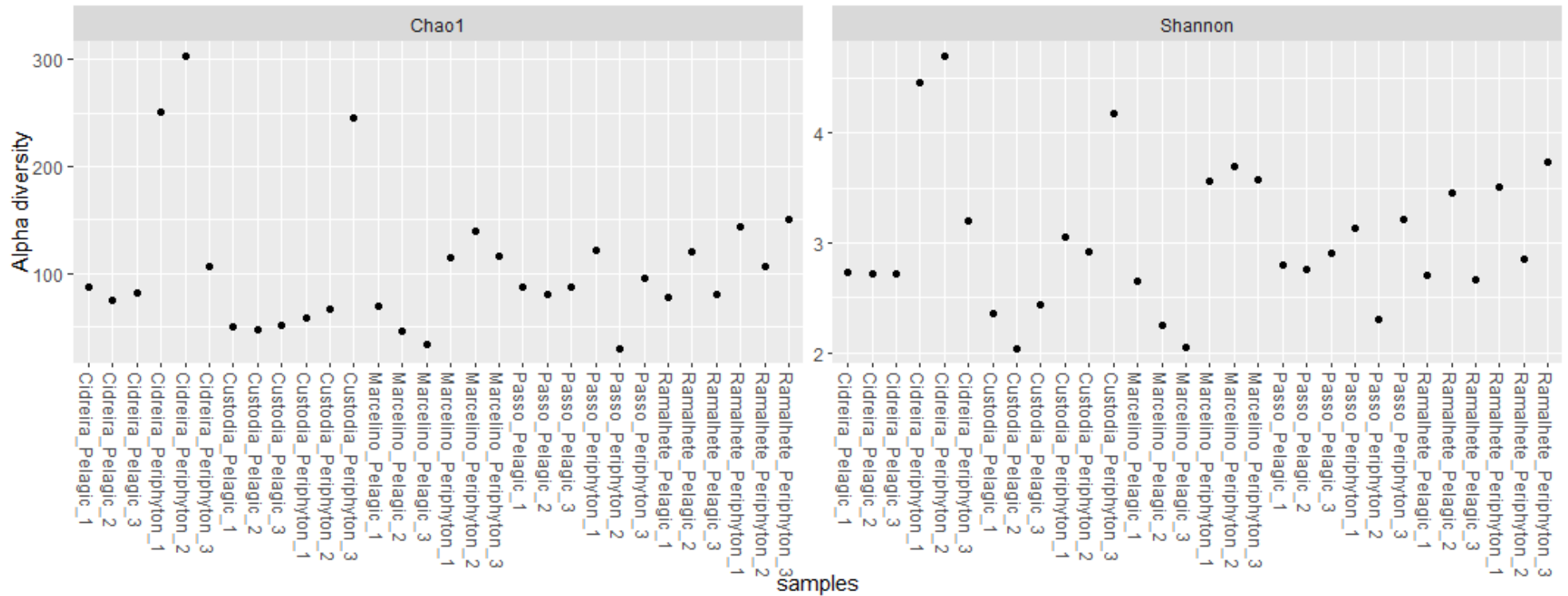
Fig. S1. Chao1 and Shannon-Weaver alpha diversity of and plankton (pelagic) and periphyton samples from five coastal shallow lakes in Brazil (original OTUs, not rarefied).
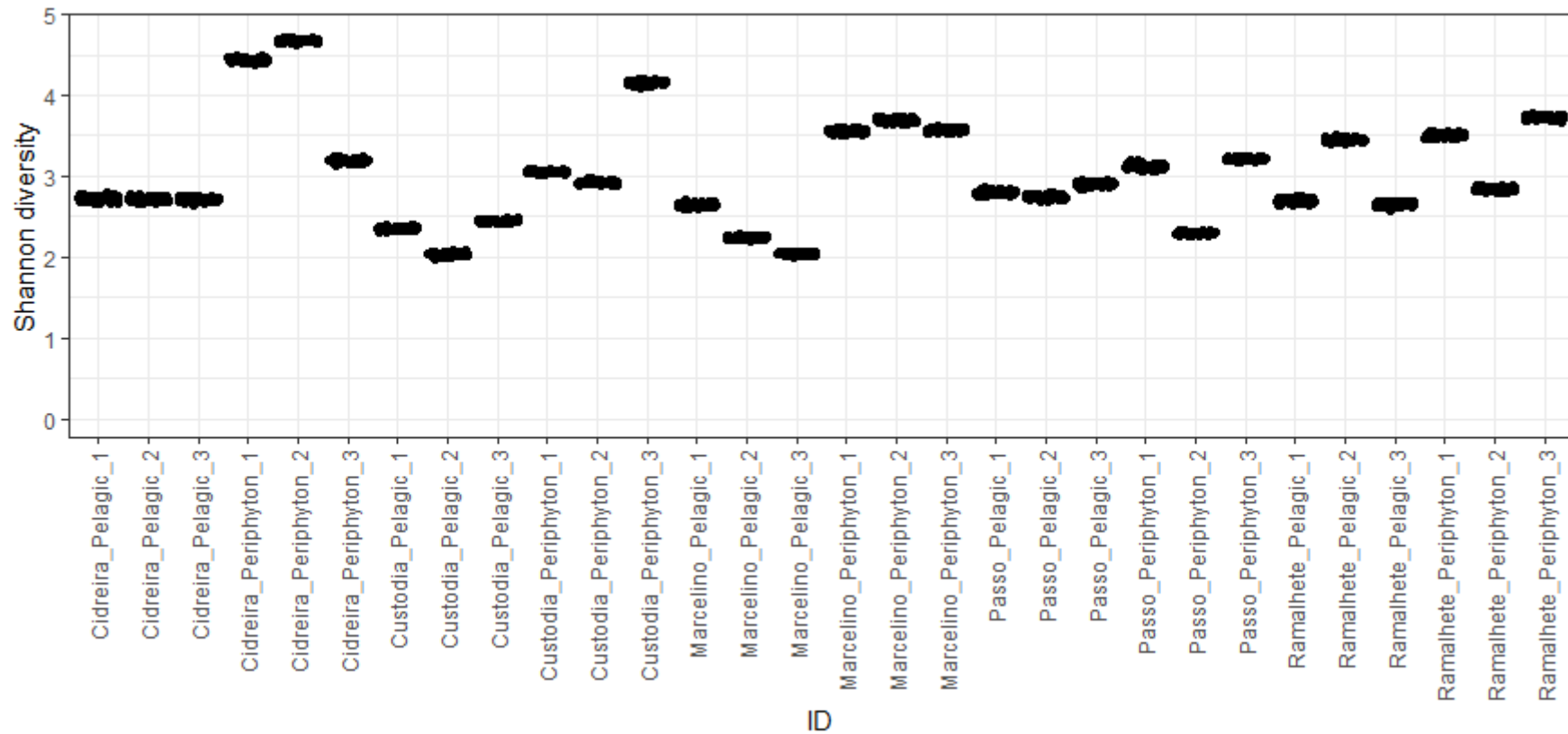
Fig. S2. Shannon-Weaver alpha diversity of OTUs calculated for 100 rarefying iterations using the *mirlyn* package and a library size = 5,000 sequences (slightly more conservative than our cut size of our minimum library size of 8,790 sequences) for plankton (pelagic) and periphyton samples from five coastal shallow lakes in Brazil.
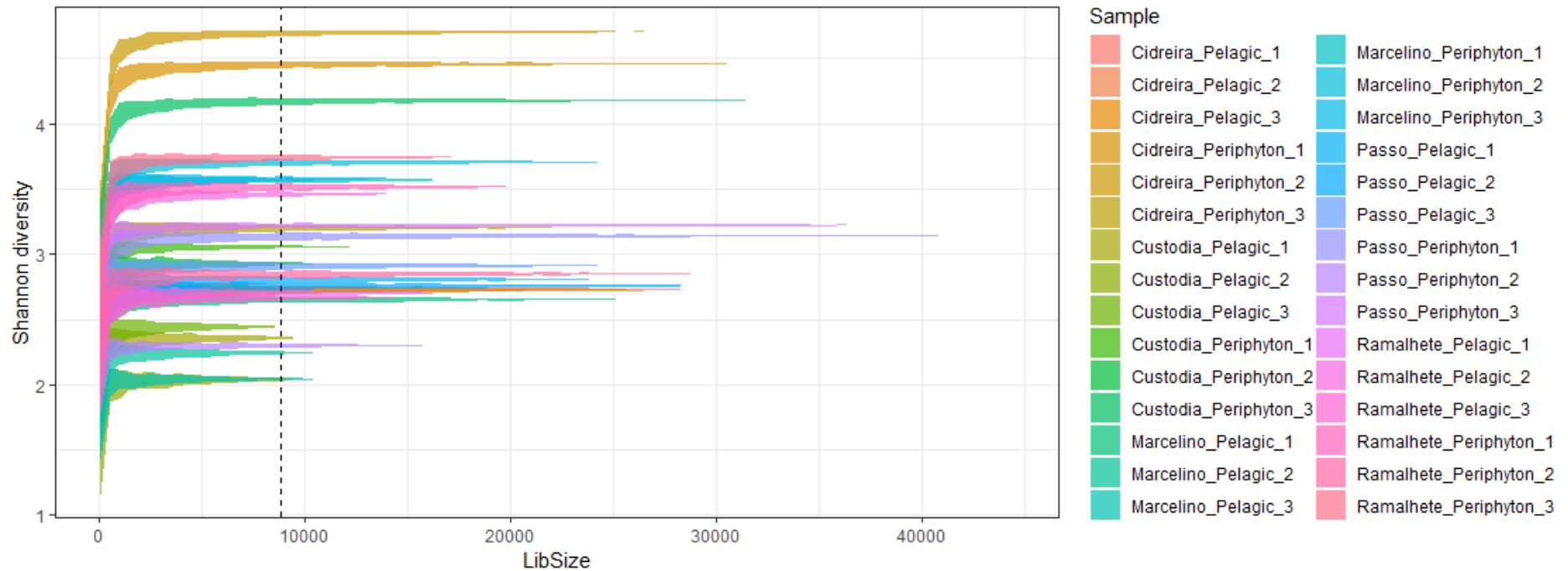
Fig. S3. Shannon-Weaver alpha diversity of OTUs calculated for 100 rarefying iterations using the *mirlyn* package and varying library sizes for plankton (pelagic) and periphyton samples from five coastal shallow lakes in Brazil. The dashed vertical line corresponds to our minimum library size of 8,790 sequences