

Higher Taxa Predict Plankton Beta-diversity Patterns Across an Eutrophication Gradient

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Abstract

In an attempt to speed up sample processing and minimize taxonomic identification errors, the use of higher taxa is a common strategy in biomonitoring programs. Because phytoplankton and zooplankton respond rapidly to aquatic pollution and are often used as indicators of eutrophication, in this study we tested the use of phytoplankton and zooplankton genera, families, orders and classes as surrogates for species level data. Data gathered in nine urban artificial lakes were used to test if higher-taxa were able to recover patterns of ordination generated by the phytoplankton and zooplankton species data. For phytoplankton and zooplankton, genera datasets produced ordination diagrams similar to those produced by species level. Thus, the use of higher taxa appears to be advisable for phytoplankton and zooplankton based assessments of eutrophication in urban lakes.

Key words: Phytoplankton, Zooplankton, Taxonomic Resolution, Urban Lakes.

Introduction

Only limited resources are available for biodiversity assessments (Curry *et al.* 2012). Therefore, many studies investigate ways to minimize the costs of biomonitoring programs (Carneiro *et al.* 2010; Heino & Soininen 2007; Padial *et al.* 2012; Wilson & Bayley 2012). In addition to the paucity of financial resources, comprehensive and inclusive biodiversity surveys are limited by the lack of taxonomists (Wheeler *et al.* 2004) and by the amount of time needed to process samples (Kallimanis *et al.* 2012). For instance, in environmental-impact assessments or biomonitoring programs, at least in Brazil, it is common to wait a long period to obtain a matrix of species abundance by sites. These problems make it worthwhile to examine the use of surrogates or alternatives that are not based on species-level identifications (Carneiro *et al.* 2010).

The use of the higher-taxa approach can make bioassessments more cost-effective and reduce taxonomist dependence (Marshall *et al.* 2006). However, the reliability of this approach depends on finding a strong relationship between the patterns depicted by the species and higher-taxa data (Khan 2006; Heino & Soininen 2007). Previous studies with algae (Carneiro *et al.* 2010), chironomids (Greffard *et al.* 2011), ants (Andersen 1995), spiders (Cardoso *et al.* 2004), vascular plants (Villaseñor *et al.* 2005) and birds (Kallimanis *et al.* 2012) have not found large differences between the results provided by data with different taxonomic resolutions (in most cases, genera).

Owing to the ever-growing human impacts on freshwater ecosystems, cost-effective ways of monitoring these systems are becoming increasingly important. Man-made urban lakes provide different ecological (e.g., refuges, carbon sequestration) and economic (e.g., recreation) services (Downing *et al.* 2008). Thus, the development of strategies to monitor these systems efficiently is as important as it is in natural lakes. Here, using data gathered in nine urban lakes with different trophic levels, we tested whether plankton datasets with lower levels of taxonomic resolution (genera,

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families, orders or classes) are able to predict beta diversity patterns depicted by datasets with higher taxonomic resolution (species).

Material and Methods

Study area

We sampled nine artificial lakes in the city of Goiânia (16° 40' S and 49° 15' W; Goiás, Brazil), which were created for landscaping and recreational purposes. The lakes are located in six municipal parks: Buriti Forest, Chico Mendes Botanical Garden and Flamboyant, each with two lakes; and Areião, Sullivan Silvestre and Liberdade, each with one lake. The lake area ranged from 1.76 to 29.2 km² and the maximum depth from 0.95 to 2.75 m (see Lodi *et al.* 2011). The lakes varied widely in trophic status. For instance, they were classified from oligotrophic to eutrophic according to chlorophyll-*a* concentration, and from mesotrophic to eutrophic according to total phosphorus (see Lodi *et al.* 2011; Table 1).

Data sampling

Subsurface phytoplankton samples (*ca.* 40 cm depth) were stored in 100-ml dark bottles and fixed with Lugol-acetic solution. Phytoplankton density was estimated according to the method of Utermöhl (1958), with a Zeiss inverted microscope, at a magnification of 400×. Members of the phytoplankton community were classified to species level, and subsequently these species were aggregated in genera, families, orders and class levels.

For zooplankton sampling, we used a water pump to filter *ca.* 500 L of water through a 64-µm plankton net. The filtered material was fixed in a 4% formaldehyde solution, buffered with calcium carbonate. Samples were examined microscopically in adapted Sedgwick-Rafter chambers for identification (to the lowest possible taxonomic level) and counting of microcrustaceans, rotifers and testate amoebae. Counting was undertaken by the analysis of three subsamples obtained with a Hensen-Stempel pipette (3 mL). At least

100 individuals per subsample were counted (see Lodi *et al.* 2011). Similarly to phytoplankton, different matrices, with decreasing taxonomic resolution, were created.

Data analysis

For each group (phytoplankton and zooplankton), five data matrices were created, using different taxonomic resolutions (species, genus, family, order and class). All data were log(*X* + 1) transformed prior to analyses. We used the Bray-Curtis coefficient to calculate dissimilarities between the lakes for each matrix. The correlation between the Bray-Curtis distance matrix generated with the species data and the distance matrices generated with the lower taxonomic-resolution datasets was tested by the Mantel procedure. High *r*-values indicate that the Bray-Curtis distance matrices generated by the datasets with low taxonomic resolutions are highly correlated with the distance patterns generated by the species datasets.

Although the Mantel test is the most common method used to identify the association between two biological distance matrices, we also used a Procrustean analysis for this purpose (Jackson 1995). The Procrustean analysis is more powerful than the Mantel test to detect matrix association (Peres-Neto & Jackson 2001). Prior to the Procrustean analysis, we performed a Principal Coordinate Analysis (PCoA) to ordinate the lakes (Legendre & Legendre 1998). In the Procrustean analysis, a pair of data matrices (the scores from two ordinations generated, for example, by species and genera) is compared by using a rotational-fit algorithm that minimizes the sum of squared residuals between the two matrices (resulting in a badness-of-fit statistic called *m*²-value). The *m*² statistic reflects the lack of overlap between two ordinations. As we used a transformation of the *m*² statistic value $\left[r = \sqrt{1 - m^2} \right]$, values of 1 indicate total overlap between the matrices (e.g., the results of two ordinations are the same) and values closer to 0 indicate a greater difference between ordination patterns. *P*-values were evaluated after 1,000 random permutations. A schematic representation of the analyses used in our study is given in Figure 1.

Results

We identified 127 species of phytoplankton and 53 species of zooplankton. Ratios between phytoplankton species richness and the number of other taxa considering lower taxonomic resolutions were: 1.98 (genus), 4.23 (family), 7.93 (order) and 12.7 (class). Ratios between zooplankton species richness and the number of taxa considering lower taxonomic resolutions were 2.4 (genus), 2.8 (family), 8.8 (order) and 13.2 (class).

For zooplankton, the ordination patterns generated from the genera, families, orders and classes datasets were significantly correlated with the ordination pattern generated from the species dataset. Similarly, the Bray-Curtis distance matrices

Table 1. Limnological data of nine urban lakes in Goiânia City.

Variables	Unity	Mean	Min	Max
Area	km ²	13.2	1.76	29.2
Chlorophyll- <i>a</i>	µg/L	5.67	0.00	11.52
Conductivity	µS/cm	105.13	30.60	183.30
Depth	m	1.57	0.95	2.75
pH		7.68	6.60	9.81
Temperature	°C	29.10	26.90	30.70
TN	µg/L	0.53	0.14	1.12
TP	µg/L	31.44	12.96	85.73
Transparency	m	0.66	0.35	1.05
Turbidity	NTU	7.79	4.64	12.16

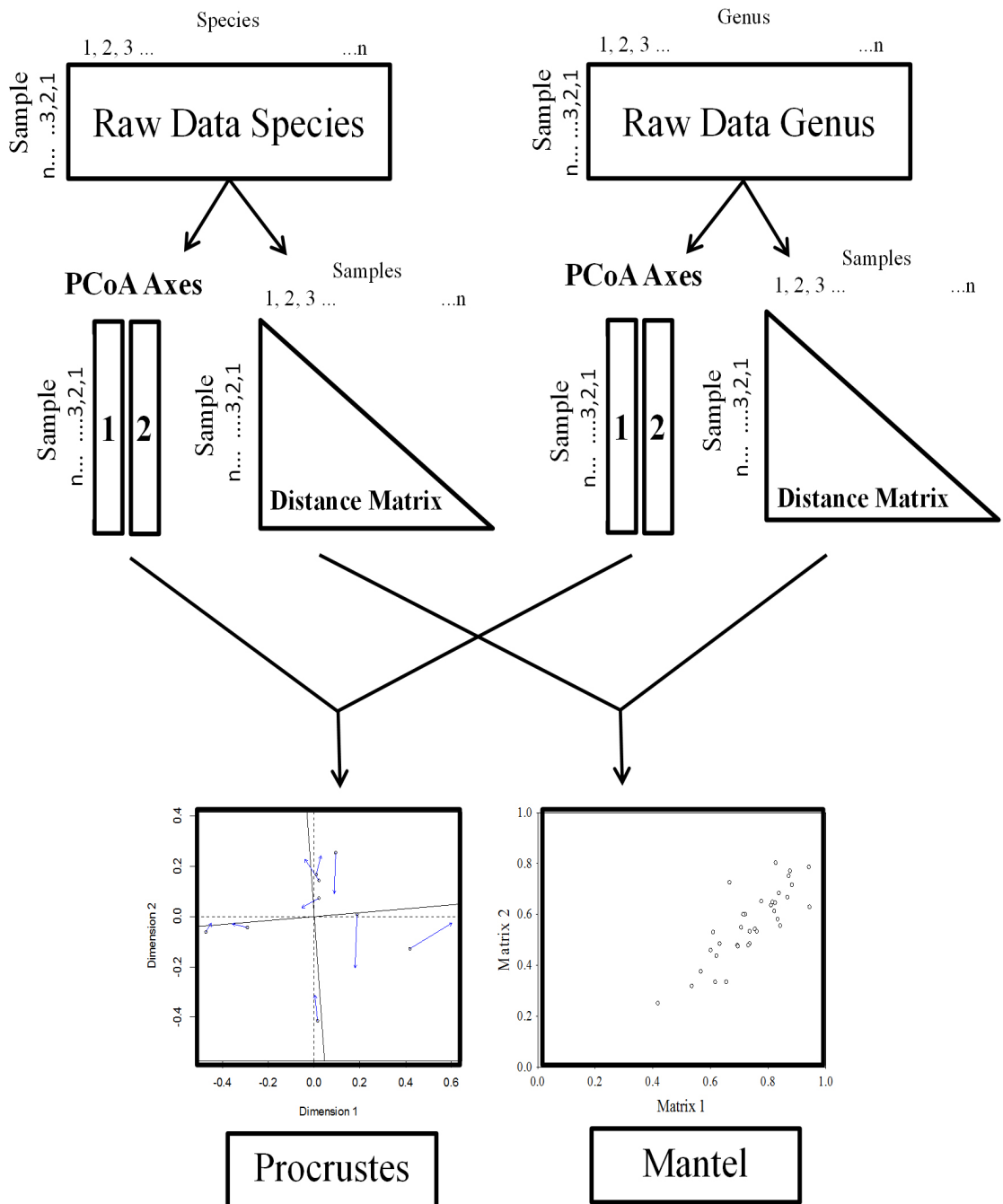


Figure 1. Schematic representation of the analytical procedures used in this study (see details in methods).

calculated from the genera and families datasets were significantly correlated with the Bray-Curtis distance matrix generated with the species dataset. For phytoplankton, we found significant relationships only between ordination patterns generated from the species and genera datasets. In addition, for phytoplankton, the Bray-Curtis distance matrix generated with the species dataset and those distance matrices generated with genera, families, orders and classes datasets were significantly correlated (Table 2).

Discussion

Considering both analytical approaches (i.e., Procrustes and Mantel), our results suggest that the patterns of beta diversity depicted by plankton species-level data would be satisfactorily recovered by using genera datasets. Although other taxonomic levels also showed significant congruence values with the phytoplankton and zooplankton species-level patterns, the values of the statistics were low

Table 2. Strength of the congruence between data with high (species) and low (Genus, Family, Order, Class) taxonomic resolutions as determined by Procrustean analysis and Mantel's test.

	Procrustes				Mantel			
	Zooplankton		Phytoplankton		Zooplankton		Phytoplankton	
	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>
Genus	0.91	0.001	0.91	0.002	0.92	0.000	0.93	0.000
Family	0.85	0.002	0.52	0.23	0.56	0.003	0.93	0.000
Order	0.73	0.013	0.46	0.37	0.27	0.083	0.70	0.005
Class	0.72	0.012	0.37	0.62	0.29	0.063	0.61	0.006

(for phytoplankton, using Procrustean analyses or for zooplankton, using Mantel's tests), indicating a low ability to predict species-level patterns. Congruence values above 0.75 indicate high concordance between the results generated by different taxonomic levels, i.e., a higher taxonomic level can be a satisfactory surrogate for another (Lovell *et al.* 2007). Other studies with algae also found high congruence values and a decrease in congruence with decreasing taxonomic resolution (Carneiro *et al.* 2010; Gallego *et al.* 2012; Heino & Soininen 2007; Rimet & Bouchez 2012). Similar findings were reported by Nielsen *et al.* (1998) for rotifer communities, whereas another study, also regarding rotifer communities, indicated that only the use of genera recovered the species-level patterns (Azemar *et al.* 2010).

A recurrent, cost-inefficient situation that happens in biomonitoring programs is related to the long time required in the processing of samples due to the identification of rare species. After, these same species are often removed from the dataset for modeling purposes (e.g., using canonical analyses). Moreover, species-level data are noisier than low resolution taxonomic data (Heino 2008). Therefore, the use of datasets with low taxonomic resolutions can minimize the problem of the long time required to identify species that are present in low abundance and that, in most cases, are removed from modeling purposes.

The higher-taxa approach is cost-efficient, less time-consuming and less dependent of experts (Kallimanis *et al.* 2012). Also, higher taxa are more taxonomically stable, and more reliable for comparative purposes; the database is less compromised by identification errors, particularly at the species level (Rimet & Bouchez 2012). Genera identification is simpler than species identification, mainly for certain algae groups that must be identified by more sophisticated tools (Sánchez-Moyano *et al.* 2006). The use of higher taxa is also recommended to detect aquatic pollution (Khan 2006). For instance, in comparisons using phytoplankton (Gallego *et al.* 2012) and benthic diatoms (Rimet & Bouchez 2012), the performance of predictive models to reconstruct nutrient concentrations was equivalent from order to species levels. Therefore, it is possible to evaluate the relationship between human disturbance and biological response using a coarser taxonomic resolution (Birk *et al.* 2012). A study with macroinvertebrates also found that species, genera

and families datasets exhibited similar relationships with environmental predictors (Heino 2008).

In conclusion, our results support the use of genera to depict patterns of variation in community composition across eutrophication gradients, for instance, using unconstrained ordination analyses. Although some information would be lost, the use of genera might imply an increase in long-term data comparability and a reduction in the costs of biomonitoring programs. Also, the resources saved by adopting a higher taxa approach could be used to guarantee the continuity of these programs or their spatial extent.

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