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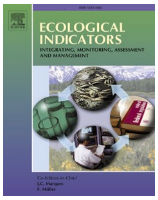

The reliability of low taxonomic and numerical resolutions for biodiversity monitoring is site specific and dependent on the statistical method

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ABSTRACT

Ecologists are challenged to detect and offer measures to mitigate the ever-growing impacts on ecosystems (e.g., eutrophication and global warming). An important part of the challenge is to get the necessary biodiversity data over large spatial extents and continuously over time. This challenge is even more evident when one considers the scarcity of research funds and specialized personnel to conduct biomonitoring programs. Thus, by necessity, most of them are based on some sort of shortcut, including the use of higher taxa, presence-absence data and a limited number of taxonomic groups. However, there is a scarcity of studies evaluating the reliability of these shortcuts in temporal analyses of community structure. Here, using zooplankton communities monitored over a period of 85 months in a tropical reservoir, we tested whether data with low taxonomic and numerical resolutions were able to predict beta diversity and ordination patterns generated with species abundance data. The results of two methods, commonly used to measure the relationships between multivariate data (Mantel and Procrustes tests), indicated a high correlation between datasets with low and high taxonomic resolutions. However, the Mantel test results indicated that resemblance matrices derived from presence-absence data were, in general, poorly correlated with those matrices derived from abundance data. Finally, based on the simple correlation between ordination axes derived from data with different taxonomic and numerical resolutions, we found that none of the shortcuts provided reliable results for the different sites analyzed. We suggest that further studies should raise the bar for the proposal of shortcuts and that high-resolution data are key to achieve biomonitoring goals.

1. Introduction

Biodiversity knowledge is key to assist conservation policy and management (Kallimanis et al., 2012; Socolar et al., 2016) and, therefore, to mitigate the current biodiversity crisis (Bevilacqua et al., 2012; Mueller et al., 2013 and references therein). However, the now well-known biodiversity shortfalls, which include, *inter alia*, the lack of formal description ("Linnean Shortfall") and of information on the geographic distribution of many species ("Wallacean Shortfall"; for a review, see Hortal et al., 2015) are hurdles to evidence-based conservation (Sutherland et al., 2004). In addition, data on temporal dynamics of biodiversity are scarce for most biological groups and regions (Magurran et al., 2010). Thus, filling the gap in the biodiversity knowledge has become a major challenge for researchers and practitioners (Wheeler et al., 2004; Butchart, 2011).

There is a consensus that the most effective ways to minimize the biodiversity shortfalls consist in carrying out biodiversity monitoring programs and surveys (Balmford and Gaston, 1999, Balmford et al., 2000; Kallimanis et al., 2012; Henderson and Magurran, 2010). However, we have a shortage of taxonomists, working side by side with ecologists, which delays the minimization of the biodiversity shortfalls (Hopkins and Freckleton, 2002; but see Joppa et al., 2011). Moreover, a rapid solution to the scarcity of highly skilled personnel is hindered by persistent underfunding (Mallet and Willmott, 2003; Wilson, 2004;

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Drew, 2011; Bebber et al., 2014). Thus, given the pace of human-related threats to biodiversity, different forms of shortcuts for evidence-based conservation have been used (e.g., Rodrigues and Brooks, 2007; Heino, 2010; Bennett et al., 2014).

Two shortcuts for biomonitoring involve the use of low taxonomic (e.g., the use of genera instead of species, e.g., Ellis, 1985; Jiang et al., 2017; Gerwing et al., 2020) and numerical resolutions (e.g., presence/absence data instead of abundance data; e.g., Blanchet et al., 2016; Sgarbi et al., 2020). A strong relationship between data with different taxonomic resolutions (or different numerical resolutions) would be a necessary, but not sufficient, condition to adopt this strategy, for example, in a long-term biomonitoring program (Heino, 2010). However, most studies evaluating the reliability of these approaches are based on snapshot surveys (Ferraro and Cole, 1992; Dauvin et al., 2003; Anderson et al., 2005; Bacci et al., 2009; Carneiro et al., 2010; Groc et al., 2010; Smale et al., 2010; Souza et al., 2016; Pitacco et al 2019). Thus, we are left with the question whether the validation of shortcuts based on spatial data (i.e., from snapshot surveys) also validates their use in biomonitoring studies, which are focused on the temporal dimension. For example, considering a spatial dataset (i.e., from a snapshot survey), a strong relationship between ordination scores generated with different taxonomic or numerical resolutions does not necessarily indicates that this relationship will also occur when the samples were taken over time. For example, the use of data with low resolutions may be insufficient to detect important temporal changes in community structure. In fact, there are only a few studies that evaluated the capacity of low-resolution data (e.g., genera and presence-absence data) to recover temporal patterns generated by high-resolution data (e.g., species abundance; see Carneiro et al., 2010; Vieira et al., 2017).

Here, we evaluated the capacity of low-resolution data (genera and families or presence-absence data) to represent high-resolution data (species abundance) in a Brazilian reservoir focusing on the temporal dynamics of zooplankton communities. Based on previous studies (see above), one would predict a high capacity of data with low taxonomic and numerical resolutions in recovering temporal community patterns obtained by high-resolution data (species abundance). To the best of our knowledge, few other studies evaluated the potential of low-resolution data (higher taxa and presence-absence data) in recovering temporal patterns in community structure obtained with high-resolution data (species abundance).

2. Material and methods

2.1. Datasets

This study was based on a dataset obtained at the Ribeirão das Lajes Reservoir (State of Rio de Janeiro, Brazil). Our zooplankton samples were obtained monthly, at six sampling sites, between August 2001 and December 2009. However, sampling was not conducted between July 2003 and October 2004. In short, our zooplankton dataset contained 510 (6 sites × 85 months) samples. A full description of the study area and methods can be found elsewhere (Lopes et al., 2017; Lopes et al., 2018; Lopes et al., 2019).

2.2. Data analysis

We carried out different analyses to test the effects of reducing the taxonomic and numerical resolutions of our zooplankton dataset. Thus, for each sampling site, we created sampling months-by-taxa matrices with different taxonomic (species, genera and families) and numerical (abundance and presence-absence) resolutions. With these matrices, we calculated resemblance matrices using the coefficients of Bray-Curtis (for abundance data) and Sørensen (for presence and absence data; see Legendre and Legendre, 2012). Afterwards, based on each resemblance matrix, we used a Principal Coordinate Analysis (PCoA) to ordinate the sampling months.

We used three methods to test the relationships between the data with different resolutions. First, considering a distance-based approach, we used the Mantel test (Mantel, 1967; Manly, 2007) to evaluate the relationships between the resemblance matrices generated with different taxonomic and numerical resolutions (e.g., between the Bray-Curtis distance matrices generated with species and genera abundance data or between the Sørensen distance matrices generated with species and genera presence-absence data). Second, the relationships between the scores derived from the PCoAs (using the different resemblance matrices) were tested using the Procrustes analysis (Jackson, 1995a; Peres-Neto and Jackson, 2001). Third, we estimated the Pearson correlation coefficient between the first PCoA axis scores derived from the species abundance ($A1_S$) data and the first PCoA axis scores derived from the genera abundance ($A1_G$) data [$cor(A1_S,A1_G)$]. We repeated this procedure considering the second axis (A2) scores [$cor(A2_S,A2_G)$]. The whole procedure was repeated when the PCoA axes scores were derived from data with different numerical resolutions [i.e., abundance (AB) and presence-absence (PA) data: $cor(A1_{AB},A1_{PA})$ and $cor(A2_{AB},A2_{PA})$].

In the analyses described above, high coefficients (Mantel's *r*, Procrustes' *r* and the correlation coefficients between ordination axes) would indicate that the temporal patterns in community structure were similar for the different taxonomic and numerical resolutions. For example, a high Mantel's *r* for the comparison between the Bray-Curtis distance matrices generated with species and genera abundance would indicate that the changes in community structure between sampling months (i.e., temporal beta diversity) were similar independently of the taxonomic resolution used. Likewise, a high Procrustes' *r* for the comparison between the PCoA scores derived from the Bray-Curtis (abundance data) and Sørensen (presence-absence data) distance matrices would indicate that the ordination patterns of the sampling months, obtained with different numerical resolutions, were similar. High correlation coefficients (ignoring the sign because of a property called "axis reflection", see Jackson, 1995b; Mehlman et al., 1995; Peres-Neto et al., 2003) would indicate that the temporal variation in community structure, as shown by both axes, would be similar even after reducing the taxonomic (or numerical) resolution of the data. Thus, both the Procrustes correlation and the simple correlation would give similar results. On the other hand, low the correlation coefficients may indicate two situations that should be further evaluated. First, a low correlation may indicate that the temporal pattern in community structure was substantially modified by reducing the taxonomic (or numerical) resolution of the data. Second, it may be caused by a "change" in the order of the axes in each dataset (i.e., "axis reordering"; e.g., Peres-Neto et al., 2003). For example, the temporal variation in community structure depicted by the first PCoA axis scores from the species abundance data may be depicted instead by the second PCoA axis scores from the genera abundance data (or vice-versa). Axis reordering after the reduction of data resolution, if unchecked, may be problematic when only the first axis of an ordination analysis is used to described temporal change in community structure. In order to evaluate whether low correlation coefficients between the corresponding axes (e.g., the correlation coefficient between $A1_S$ and $A1_G$ and between $A2_S$ and $A2_G$) were caused by axes reordering, we calculated the correlation coefficients between, for example, $A1_S$ and $A2_G$ and between $A2_S$ and $A1_G$. After, we identified axis reordering when the correlations between the corresponding axes (e.g., between $A1_S$ and $A1_G$ and between $A2_S$ and $A2_G$) were smaller than the correlations between the first and the second axes (e.g., between $A1_S$ and $A2_G$ and between $A2_S$ and $A1_G$).

All analyses were repeated for each sampling site and, therefore, we were able to verify whether the results were spatially consistent. The analyses were performed in the R programming environment (R Core Team, 2020) using the packages listed in Table 1.

3. Results

We found that the patterns of temporal beta diversity, as given by the

Table 1
Packages used to perform the analyses in the R programming environment and their references (R Core Team, 2020).

	Package	Function	Reference
Sørensen coefficient	betapart	beta.pair	Baselga and Orme (2012)
Bray-Curtis coefficient	vegan	vegdist	Oksanen et al. (2013)
Mantel test	ecodist	mantel	Goslee and Urban (2007)
Principal Coordinate Analysis	stats	cmdscale	R Core Team (2020)
Procrustes Analysis	vegan	protest	Oksanen et al. (2013)
Correlation coefficient	stats	cor	R Core Team (2020)

Mantel's test results, were mostly preserved after reducing the taxonomic resolution of the data from species to genera or from species to families (Table 2). Considering the results of the Procrustes analyses, the ordination patterns generated by genera and families were also similar to those generated by species abundance data (Table 2). However, the results of the correlation coefficients indicated that the temporal dynamics of PCoA axes scores, as given by genera abundance data, were not always similar to those depicted by species abundance data. For example, the first PCoA axis scores derived from species abundance data, at site 1, were highly correlated with the first PCoA axis scores derived from genera abundance data [$\mathrm{cor}(A1_S,A1_G) = 0.987$; Fig. 1a,b and Fig. 2a]. However, we found a low correlation between the second axes, respectively, derived from species and genera abundance data [$\mathrm{cor}(A2_S,A2_G) = 0.437$; Fig. 1c,d and Fig. 2b). These results indicate that whereas genera data were enough to represent the temporal patterns in the community structure along the first axis, they were not along the second axis. Indeed, genera data were not able to represent a clear trend in community structure, as revealed by species abundance data (compare Fig. 1c with Fig. 1d). Similar results were found for sites 3, 4, 5 and 6. Finally, we found a high correlation between species and genera data, considering the different measures, in site 2 only. The results for the comparison between species and families indicated that the effect of reducing the taxonomic resolution was also substantial for sites 1, 4 and 5 (see results of the correlation coefficients; Table 2). Axis reordering was detected in sites 3 and 5 in the analyses between species and genera and in sites 4 and 5 in the analyses between species and families. However, even after taking axis reordering into account (e.g., by calculating the correlations between $A1_S$ and $A2_G$ and between $A2_S$ and $A1_G$), we found relatively low (<0.75) correlation values (Table 2).

After converting abundance into presence-absence data and considering the results of the Mantel test, we found strong relationships (i.e., > 0.75) between the datasets in all sites (Table 3). Similar results were obtained with the Procrustes analysis (except for the result in site 4). However, the correlation coefficients indicated that the effects of reducing the numerical resolution on community temporal dynamics were negligible at sites 1 and 6 only (Table 3). For example, even after taking axis reordering into account (in sites 2 and 3), we found correlation values lower than 0.75 for one of the comparisons (e.g., correlations between $A1_{AB}$ and $A2_{PA}$ = 0.721 and 0.626, in sites 2 and 3, respectively).

Table 2
Mantel' *r*, Procrustes' *r* and the correlations between Principal Coordinate axes scores quantifying the strength of the relationships between data with different taxonomic resolutions. All results were based on the Bray-Curtis coefficient (using abundance data). The analyses were repeated for each sampling site. The correlations between the first axes scores and between the second axes scores (for species and genera (or families) data) are shown in column A1,A1 and A2, A2, respectively. Underlined values indicate the correlations between the ordination scores after taking axes reordering into account.

	Sites	Mantel	Procrustes	A1,A1	A2,A2
Species to Genera	1	0.723	0.800	0.987	0.437
	2	0.846	0.914	0.899	0.917
	3	0.842	0.880	0.652	0.685
	4	0.845	0.877	0.699	0.800
	5	0.843	0.812	0.672	0.650
	6	0.870	0.860	0.616	0.779
Species to Families	1	0.729	0.808	0.984	0.468
	2	0.790	0.922	0.919	0.904
	3	0.800	0.869	0.895	0.816
	4	0.816	0.880	0.628	0.741
	5	0.802	0.866	0.738	0.674
	6	0.844	0.855	0.794	0.929

4. Discussion

We tested whether patterns of zooplankton community dynamics over time were captured by data with reduced taxonomic and numerical resolutions. According to Procrustes' *r*, we found that data with low taxonomic (genera or families) and numerical (presence-absence data) resolutions were, in general, sufficient to represent the community dynamics depicted by data with high resolution (species abundance data). However, contrary to previous studies (e.g., Sgarbi et al., 2020; Giehl et al., 2014; Santos Ribas and Padial, 2015; Vieira et al., 2017), we found that presence-absence data were not sufficiently correlated with abundance data, considering the different metrics (i.e., Mantel, Procrustes and correlation between axes), in four of the six sites analyzed. Furthermore, if all metrics are considered, none of the shortcuts (i.e., using low taxonomic or numerical resolutions) were reliable for all sampling sites.

In general, studies addressing the reliability of strategies to simplify biomonitoring programs (which come with different names, such as, higher taxa, taxonomic sufficiency, etc.) are based on spatial (snapshot) data obtained in a single point in time (but see Carneiro et al., 2010; Vieira et al., 2017). Here, we focused on the temporal dimension of biomonitoring programs as most of them are mainly designed to evaluate how biological communities change over time in response to human-induced threats, conservation and restoration measures. By doing so, we found that the strength of relationship between high and low-resolution data was contingent on the sampling site and on method used to evaluate that relationship. This result contrasts with many previous studies that tested the reliability of the low-resolution data (higher taxa or presence-absence data) in community analyses (e.g., Bowman and Bailey 1997; Carneiro et al., 2010; Valente-Neto et al., 2016; Valente-Neto et al., 2018; Gerwing et al., 2020; Oliveira Jr et al., 2020).

We also show that the Procrustes statistics, a common measure used to evaluate the reliability of low-resolution data in biomonitoring, may lead to misleading results. Specifically, we found that although the Procrustes' *r* indicated, in different sampling sites, a high similarity between the ordination plots (generated with different resolutions), the correlations between axes indicated otherwise. For example, the Procrustes' *r* for the comparison between species and genera datasets, at the first sampling site, was high ($r = 0.800$). However, the correlation coefficient revealed that the clear temporal trend in community composition (as shown by the second PCoA axis scores using species data) would be undetected with the use of genera data. We found similar results (i.e., high Procrustes' *r*, but low correlation between the axes) for other sampling sites and for the tests focused on numerical resolution. Thus, our results cast doubts on the validity of shortcuts for biomonitoring when the inferences are based on the Procrustes analysis. Indeed, Paunonen (1997) indicated that: "One of the problems noted with those methods, as with any such statistical optimization procedure, is that they capitalize on chance and, as a result, can produce excessively high coefficients of congruence between the rotated and the targeted solutions" (e.g., in our case, matrices of genera and species, respectively). Other studies have also indicated that Procrustes analysis tends to produce unreliable results (Horn and Knapp, 1973; see also references in Paunonen, 1997).

The powerful Procrustean procedures, aimed to maximize the superimposition between two ordination plots (i.e., minimizing the badness-of-fit, as given by the statistic m^2), may correctly indicate a strong congruence between the distributions of sampling scores (i.e., a

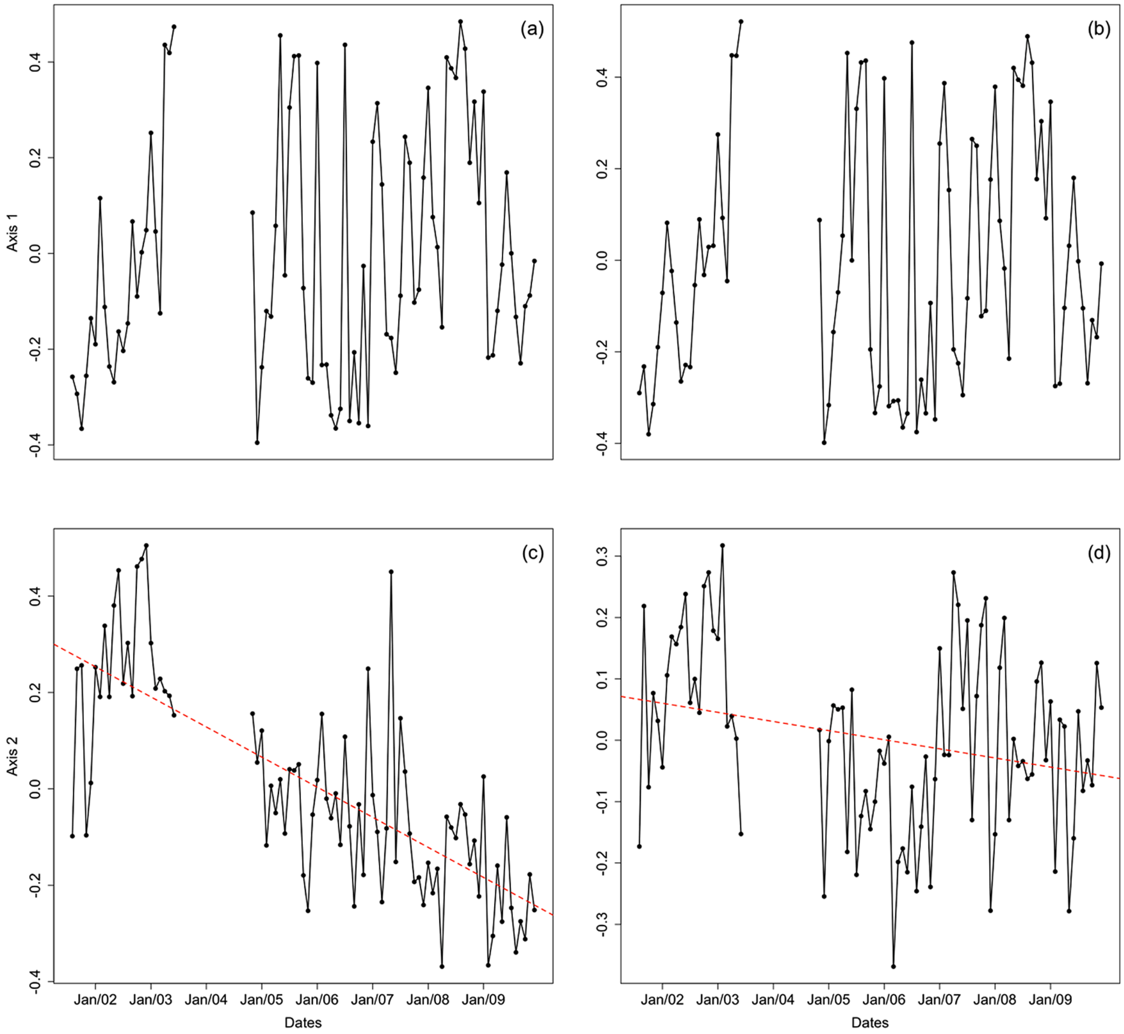

Fig. 1. Temporal variation of the first two Principal Coordinate scores (at the first sampling site) obtained with species (a,c) and genera abundance data (b,d).

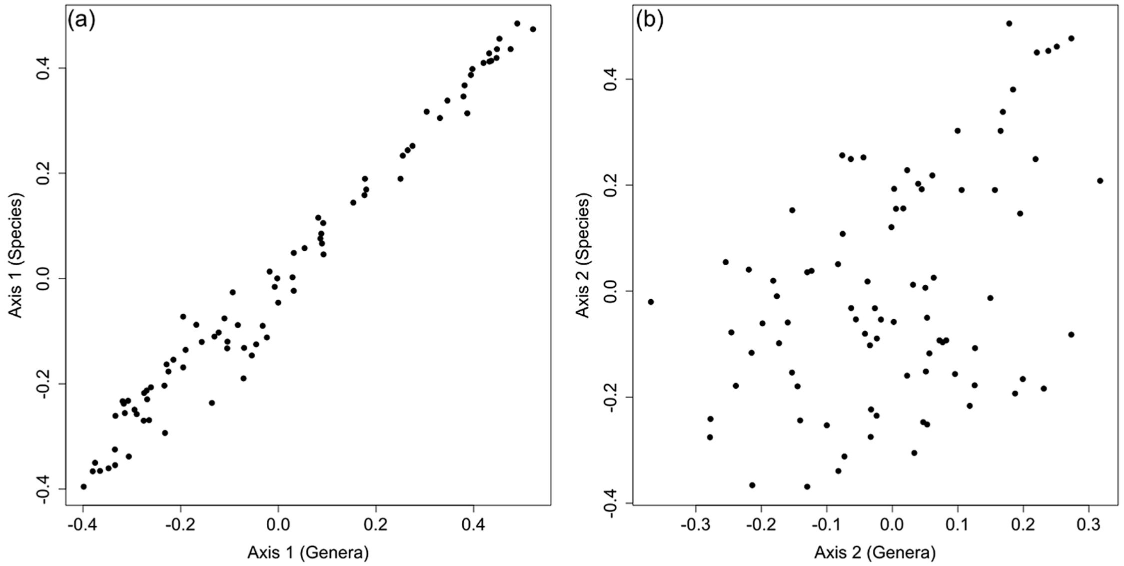

Fig. 2. Relationship between the first Principal Coordinate scores (at the first sampling site) obtained with species and genera abundance data (a). The same is shown for the second Principal Coordinate scores (b).

Table 3
Mantel' *r*, Procrustes' *r* and the correlations between Principal Coordinate axes scores quantifying the strength of the relationships between data with different numerical resolutions. The analyses were repeated for each sampling site. The correlations between the first axes scores and between the second axes scores (for species and genera (or families) data) are shown in column A1,A1 and A2, A2, respectively. Underlined values indicate the correlations between the ordination scores after taking axes reordering into account.

Sites	Mantel	Procrustes	A1,A1	A2,A2
1	0.953	0.988	0.962	0.964
2	0.898	0.844	0.721	0.958
3	0.893	0.813	0.626	0.935
4	0.918	0.737	0.910	0.483
5	0.919	0.828	0.931	0.651
6	0.944	0.936	0.804	0.833

low m^2 or a high Procrustes' *r*, given by $\sqrt{1\text{-}m^2}$). Accounts of these procedures (e.g., standardization, mirror reflection, rotation and dilation of the distribution of the scores) can be found elsewhere (e.g., for introductory and mathematical descriptions see Borg and Lingoes, 1987; Peres-Neto and Jackson, 2001, respectively). However, excessive congruence tends to increase with decreasing sample size (i.e., the number of sampling units in the ordination plots; see Paunonen, 1997). This is so because, with low sample sizes, those powerful Procrustean procedures are likely to incorrectly indicate a high congruence, even when the distributions of the sampling scores differ markedly. However, considering our relatively large sample size (i.e., 85 months), the unduly high values of Procrustes' *r*, as compared to the correlation coefficients, are unlikely to be explained by this effect.

Our results, based on the temporal dimension of biomonitoring and on different metrics, showed that the reliability of shortcuts for biodiversity analysis is not as high as previously reported (e.g., Landeiro et al., 2012; Slimani et al., 2019; Oliveira Jr et al., 2020). Caro (2010) discuss some difficulties in applying the higher-taxa approach considering spatially based studies. Among these difficulties, the strength of the relationship between data with different taxonomic resolutions may vary geographically. For example, it is expected that this strength is lower in areas with low values of the ratio between number of higher taxa and the number of species (e.g., genus richness/species richness; see Caro, 2010; Oliveira Jr et al., 2020). Indeed, the lowest relationship between data with different taxonomic resolutions (for the different statistical approaches) was found at the first sampling site, which has the lowest average ratio in our dataset. In other words, this is, in average, the richest sampling site in the reservoir, as well as the site with the highest community turnover and environmental variability (Lopes et al., 2019). Thus, we speculate that the higher taxa approach is especially unlikely to be valid in areas with high environmental variability, which may select for different species over time (but not for genera). As our study shows, the strength of relationship between data with different numerical resolutions can also be local specific (even within a single water body). In general, since the strengths of the relationships between data with different resolutions are site-specific, the reliability of these approaches should be tested before using them in biomonitoring programs.

We also found that the results of Procrustes analysis, often used in studies of taxonomic and numerical resolution (e.g., Carneiro et al., 2010; Timms et al., 2013; Giehl et al., 2014; Valente-Neto et al., 2016; Minor et al., 2017; Erdozain et al., 2019), may indicate an unduly high congruence between ordination scores. Procrustes analysis is also often used in studies of community concordance or cross-taxon congruence (e.g., Jackson and Harvey, 1993; Paszkowski and Tonn 2000, Bini et al., 2007; Bini et al., 2008; Paavola et al., 2006; Corte et al., 2017; de Morais et al., 2018; Godoy et al., 2019). Thus, we also suggest that the results of these studies, even those showing a high Procrustes' *r*, should be viewed with caution. Although further studies are needed, we advocate the use of the correlation coefficient between axes as a more conservative metric to measure the strength of relationship between data with different resolutions in biomonitoring programs. Finally, at least for the system we studied, we show that high resolution data are key to biomonitoring.

CRediT authorship contribution statement

Vanessa G. Lopes: Conceptualization, Methodology, Software, Formal analysis, Investigation, Resources, Visualization, Writing – original draft. **Christina W. Castelo Branco:** Investigation, Resources, Visualization, Project administration, Funding acquisition. **Betina Kozlowsky-Suzuki:** Investigation, Resources, Visualization, Project administration, Funding acquisition. **Luis Mauricio Bini:** Conceptualization, Methodology, Software, Formal analysis, Investigation, Supervision.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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