



Assessing the effectiveness of surrogates for species over time: Evidence from decadal monitoring of a Mediterranean transitional water ecosystem

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ABSTRACT

The use of higher taxa or alternative approach to species surrogacy, such as the BestAgg procedure, could represent cost-effective solutions to avoid expensive species-level identifications in monitoring activities, especially on the long term. However, whether a set of surrogates would be effective in subsequent reiteration of the same assessment remains largely unsolved. We used a long-term dataset on macro-benthic assemblages to test the hypothesis that family-level and BestAgg surrogates which are effective for a limited period of monitoring could be successfully applied to quantify community patterns also in subsequent monitoring programmes. The effectiveness of surrogates in detecting temporal variations in assemblage structure as at species level remained basically unaffected over a decade. Recognizing once and for all if species surrogacy may have a practical value for monitoring will strongly depend on future assessments of the potential of surrogates to reflect community changes and to retain this prerogative over time.

1. Introduction

Environmental and biological monitoring is at the core of applied ecological research, providing invaluable insights on patterns and processes underlying the dynamics of ecosystems, and producing sets of data that are instrumental for progresses in theoretical ecology (Lovett et al., 2007; Lindenmayer et al., 2012). Monitoring is also essential for environmental policy, since systematic collections of data are necessary to inform the adaptive management of environmental issues (Lindenmayer and Likens, 2009), whether concerning the assessment and mitigation of human impacts (Bustamante et al., 2012; Ellingsen et al., 2017), the effectiveness of conservation strategies (Fraschetti et al., 2012), the success of restoration actions (Block et al., 2001), or the surveillance of the ecological quality status of ecosystems (Borja and Dauer, 2008).

The concept of monitoring intrinsically implies performing replicated observations through time, since single assessments cannot provide a comprehensive characterization of systems being investigated. This because communities and ecosystems are not static entities, which are subject to a complex interplay of processes acting at a range of spatial, but also, temporal scales, and historical data are often a prerequisite for a deeper understanding of mechanisms driving

ecological changes (Lovett et al., 2007; Lindenmayer et al., 2012; Mieszkowska et al., 2014). However, sustaining data collection on the long term is expensive, requiring the availability of adequate and continuous funding, which often represents a critical aspect for the maintenance of effective monitoring programmes (Hewitt and Thrush, 2007) and stimulates advances in optimization strategies (Mueller and Geist, 2016; Ellingsen et al., 2017). Major cost components in monitoring activities, particularly when focusing on invertebrate taxa, concern species-level identifications of organisms (Mandelik et al., 2010). Reducing expense related to the achievement of fine taxonomic resolution, therefore, may allow allocating additional budget to extend the spatial coverage and/or the time span of routine monitoring programmes (Mueller et al., 2013).

Although several approaches have been proposed to save efforts during sample processing both reducing the number of operational units and simplifying their identification, including the use of species subsets, cross-taxon congruence, or morphological groups, the analysis of communities at taxonomic levels higher than species (e.g., genus, family) has been the mainstream procedure so far, especially in aquatic environments (Dauvin et al., 2003; Jones, 2008; Sánchez-Moyano et al., 2017). This last approach relies on the concept of taxonomic sufficiency (Ellis, 1985), which assumes that, to some extent, ecological patterns

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can be quantified at coarse levels of taxonomic resolution without substantial loss of information (Ferraro and Cole, 1995). Taxa higher than species, and particularly genera and families, have been successfully employed as surrogates for species in a wide range of environmental contexts in marine, freshwater and terrestrial ecosystems (Bevilacqua et al., 2012). However, taxonomic sufficiency implies resolving organisms to a single higher taxonomic level, irrespective of their ecological importance or actual difficulty in their identification, often leading to unnecessary and undesirable loss of taxonomic detail and related ecological information (Groc et al., 2010). More importantly, the sufficient taxonomic level for a given study is decided empirically, in the absence of any control for statistical uncertainty (Mellin et al., 2011).

An alternative approach to identify suitable sets of surrogates, the ‘Best practicable aggregation of species’ (BestAgg; Bevilacqua et al., 2013; Bevilacqua and Terlizzi, 2016), has been proposed based on evidence that the relationships between taxonomic relatedness of species and their ecological response to natural and human-driven changes could be largely neutral, and that the effectiveness of higher taxa to retain species-level information patterns might depend on numerical relationships across ranks of the Linnaean taxonomic hierarchy (Neeson et al., 2013; Rosser, 2016). BestAgg utilizes null models of decreasing information on species-level patterns at decreasing number of operational units used to substitute species, in order to identify the minimum number of surrogates, regardless of their type, needed to quantify community patterns as at species level. In this framework, surrogate selection is unconstrained to strict taxonomic criteria, allowing the use of any meaningful operational units (e.g., taxonomic, functional, morphological, mixed) in order to maximize ecological information (Groc et al., 2010; Bevilacqua et al., 2013). Hence, the approach determines statistical thresholds for the application of surrogates with associated estimates of uncertainty (Mueller et al., 2013), providing a more formal procedure for surrogate selection (Bevilacqua and Terlizzi, 2016) if compared to the classic approach of taxonomic sufficiency (Jones, 2008).

The rationale underlying species surrogacy, irrespective of the approach employed, is that community patterns can be quantified equally well using operational units other than species, while reducing costs and time needed for fine taxonomic identifications (Ellis, 1985; Ferraro and Cole, 1995; Warwick, 1993). Once such operational units (i.e., surrogates for species) are properly identified from baseline data, they are assumed to be effective in comparable systems, or in reiteration of the same study such as, for instance, in repeated monitoring programmes (Olsgard and Somerfield, 2000; Mueller et al., 2013). Most of studies on surrogates, nonetheless, explored their performance in quantifying spatial changes in assemblage structure (e.g., Olsgard et al., 1998; Olsgard and Somerfield, 2000; Bevilacqua et al., 2009; Terlizzi et al., 2009; Heino, 2014), with limited efforts to extend the application of a given set of surrogates from a local to a wider geographic context (e.g., Bevilacqua et al., 2015). Very few works have examined the effectiveness of surrogates to reflect temporal variations (e.g., Musco et al., 2011; Cabral et al., 2017), and no attempts have never been done, except for rare short-term evaluations (e.g., Magierowski and Johnson, 2006; Thiault et al., 2015), to assess whether the ability of a given set of surrogates to reproduce species-level patterns is maintained over time. Here, we used long-term data on macro-benthic assemblages from a coastal lagoon system to test the hypothesis that surrogates defined on the basis of a given period of monitoring can be successfully applied to quantify patterns of temporal variation also in successive monitoring programmes.

2. Material and methods

2.1. Study area and sampling design

The study focused on a decadal dataset of soft bottom macro-

benthos from the Valli di Comacchio (N Adriatic Sea), a complex of shallow (depth range 0.5–1.5 m) brackish lagoons extending over 100 km² in the southern part of the Po River delta (NE Italy). Data were collected yearly during several sampling campaigns carried out from 1997 to 2006 (Munari and Mistri, 2010), with four (every 3–4 months) times of sampling (hereafter referred to as dates) per year, except for 1999, 2000, 2005, and 2006, in which only three dates were available. In each date, four stations representative of the whole lagoon system were sampled. One sample, consisting of three replicate Van Veen grabs (0.06 m²) of soft sediments, was collected in each station, for a total of 144 samples. Samples were sieved (0.5 mm-mesh size) and macro-invertebrates were sorted, identified at the species level and counted.

2.2. Simulated monitoring programmes

The identification of surrogates requires exhaustive pilot assessments at species level, able to characterize the structure of assemblages under study and to provide data as representative as possible of their spatial and temporal patterns of variation (Terlizzi et al., 2003; Heino and Soininen, 2007). In our case, preliminary multivariate analyses using species-level data showed that at least four years of sampling were needed to detect significant intra- and interannual variations in macro-invertebrate assemblages (see Table A1 in Appendix A), suggesting that, in the investigated system, a five-years programme may be sufficient for routine monitoring of temporal variations at species level and, seemingly, long enough also for the identification of successful surrogates. Therefore, we split our ten-years dataset in two halves, simulating the realistic situation in which two rounds of monitoring of five years each have been carried out to assess temporal trends in macro-invertebrate assemblages of the lagoon system. The first five years of the dataset, from 1997 until 2001, represented the ‘pilot’ study that was employed to define and validate surrogates for species. Data from 2002 until 2006, instead, were used as a ‘test’ study to assess whether surrogates would have been effective for quantifying community patterns in a successive monitoring programme.

2.3. Defining surrogates for species

Surrogates for species were defined based on pilot data (1997–2001) following the BestAgg procedure (Bevilacqua et al., 2013; Bevilacqua and Terlizzi, 2016), and the traditional approach of taxonomic sufficiency (Ellis, 1985; Olsgard et al., 1998; Dauvin et al., 2003). BestAgg focuses on determining to which extent the original S species in a data matrix can be aggregated (i.e., grouped and their abundance summed) into a smaller number of G surrogates, irrespective of their type (i.e., whether taxonomic, morphological, functional, or even mixed), before a substantial loss of information on species-level community patterns occurred. For a given sampling design, and for any term of interest in the analysis, the BestAgg procedure generates a null model of decreasing information, quantified as the Spearman’s correlation ρ between the species-level matrix and the corresponding aggregated matrix, at increasing level of species aggregation, expressed as $\varphi = G/S$. The null model is built by random aggregations of the original S species in decreasing numbers of G groups, and obtaining 1000 randomly-aggregated matrices for each set of G groups. For each aggregated matrix, the correlation value (ρ) with the original species-level matrix is then calculated, and a distance-based permutational multivariate analysis of variance (PERMANOVA; Anderson, 2001) is also performed to test for the main term of interest in the analysis (in this case the variability among years). This allows assessing that the information retained in the surrogate matrices and, consequently, the ability of surrogates to reflect species-level community patterns, is correlated to φ . In addition, the null model identifies the minimum number of surrogates G_{min} , sufficient to obtain results consistent with those obtained using species, with a probability of type-I error (i.e., the probability of considering G_{min} as sufficient when actually it is not) of

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