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Methods for describing ecological functioning of marine benthic assemblages using biological traits analysis (BTA)

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Abstract

Biological traits analysis (BTA) is a method recently proposed for describing ecological functioning of marine benthic assemblages. It incorporates information on species' distributions and the biological characteristics they exhibit, to produce a summary of the biological trait composition of assemblages. The approach provides a link between species, environments and ecosystem processes, and is potentially useful for the investigation of anthropogenic impacts on ecological functioning. As part of the development of BTA for application to marine systems, two aspects of the approach were investigated here: (1) the comparative applicability of three analytical tools proposed for conducting BTA and (2) the sensitivity of the approach to the number and type of traits selected for analysis. The three tools, fuzzy correspondence analysis (FCA), co-inertia analysis (CoI) and non-metric multidimensional scaling (nmMDS) portrayed trait composition of benthic assemblages in similar ways, however nmMDS had less power to discriminate between assemblages with varying trait composition than FCA or CoI. For the thirteen biological traits considered, the number of traits selected for analysis affected the ability of BTA to describe relationships between assemblages, more so than the identity of the traits themselves. Ultimately, selection of biological traits for inclusion in BTA will be based on a trade-off between their efficacy for describing variability in ecological functioning and the time and effort required to gather information on the biological characteristics of the taxa studied. The choice of analytical tool is a balance between the power of the tool to describe changes in trait composition and the ease with which results can be interpreted. nmMDS is appropriate for providing a general picture of functioning in marine assemblages, whereas FCA and CoI have greater power to detect the effects of human impacts, but are more difficult to interpret. Including as many traits as possible will lead to the most useful description of ecological functioning, as will selecting traits sensitive to anthropogenic impacts or closely linked to important ecosystem processes.

Keywords: Biological traits; Biomonitoring; Ecosystems; Anthropogenic impacts

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1. Introduction

With the advent of an ecosystem approach to marine monitoring and management, the importance of developing methods to investigate ecological functioning is receiving increasing attention. Several approaches have been proposed for assessing functioning of benthic assemblages, including trophic group analysis (Roth and Wilson, 1998; Desrosiers et al., 2000), functional group analysis (Mancinelli et al., 1998; Bonsdorff and Pearson, 1999; Padilla and Allen, 2000; Pearson, 2001) and integrative indices such as the index of biotic integrity (Borja et al., 2000), the ecological evaluation index (Orfanidis et al., 2003) and the ecofunctional quality index (Fano et al., 2003).

One of the most promising of the recently proposed approaches is biological traits analysis (BTA) (Statzner et al., 1994). Biological traits analysis uses a series of life history, morphological and behavioural characteristics of species present in assemblages to indicate aspects of their ecological functioning (here defined as the maintenance and regulation of ecosystem processes, after Naeem et al. (1999). The roles performed by benthic species are important for regulating ecosystem processes (Snelgrove, 1998) and these roles are determined by the biological traits species exhibit. For example, certain types of feeding and movement exhibited by benthic invertebrates (primarily deposit feeding and burrowing activities) can disrupt sediments, increasing the depth of oxygen and detritus penetration and consequently enhancing organic matter decomposition (Pearson, 2001). Other traits, such as tube-building, have been implicated in the transport of toxins into and through sediments (Aller, 1983). Changes in the patterns of trait expression within assemblages, in terms of changes in the relative abundance/biomass of taxa exhibiting the traits, can be used to indicate the effects of human impacts on ecological functioning.

Biological traits can be shared by organisms that differ widely in their taxonomic identity (Usseglio-Polatera et al., 2000), so BTA can be applied to different taxonomic groups (Doledec and Statzner, 1994) and also over large geographic ranges, where gradients in species composition make traditional species-based assessments difficult (Charvet et al., 2000; Statzner et al., 2001). In freshwater systems, where the approach was initially developed, there is mounting evidence that BTA has the capacity to both identify the presence of an anthropogenic impact (Charvet et al., 2000) and separate the contrasting effects of different impact types (Doledec et al., 1999). It has advantages over other approaches to describing ecological functioning as it incorporates information on both the relative abundance/biomass of species present in assemblages and their biological characteristics into one analysis and can incorporate information on a large range of traits potentially important for functioning.

The approach can be used to address ecological functioning in marine ecosystems. It performs well in comparison to more traditional assessment methods (Bremner et al., 2003) and initial marine applications suggest it can be used to provide a view of the effects of anthropogenic impacts such as fishing on benthic assemblage functioning (Bremner et al., 2004). Marine ecosystems differ in their nature from the freshwater systems where the approach was initially developed and methodologies devised for freshwater BTA may not necessarily be the most informative for open marine systems. A useful step in the development of marine BTA is therefore an appraisal of the methods involved, which could, ultimately, lead to standardisation of protocols for application to a range of environments and anthropogenic impacts.

BTA uses multivariate ordination to describe patterns of biological trait composition over entire assemblages (i.e. the types of trait present in assemblages and the relative frequency with which they occur). Several ordination tools are available for this purpose. The two most widely used are fuzzy correspondence analysis (FCA, Chevenet et al., 1994) and co-inertia analysis (CoI, Doledec and Chessel, 1994).

FCA is a parametric linear ordination method that uses eigenanalysis to investigate differences between samples, based on the biological traits exhibited by species present in the assemblages, weighted by their abundance or biomass. CoI is also based on eigenanalysis, however it differs from FCA in that it investigates patterns in species' distributions and their biological traits separately, searching for covariation between them (Doledec and Chessel, 1994). Both FCA and CoI allow the traits that contribute most to differences in functioning between assemblages to be