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1. Biological Traits Analysis (BTA)

Human activities are changing the environment on local and global scales, leading to dramatic changes in the biotic structure and composition of ecological communities that can readily alter the ways in which ecosystems work (Hooper et al., 2005). Conserving these systems requires knowledge, not only of which species are present, but of how the systems work and the effects of multiple and potentially interacting threats (Bremner, 2008). To fully determine if an ecosystem is affected by anthropogenic pressures emphasis has to be given to its functioning (Elliott and Quintino, 2007; Duarte et al., 2013).

Ecosystem functioning has been assessed traditionally using taxonomy-based descriptors that although useful, may give a reductionist view of functioning since they focus on only one or a small number of traits, providing little information on ecological functions (Bremner et al., 2003). Recently, biological traits-based approaches have been considered as promising tools emerging for bio-monitoring (Borja and Elliott, 2013). Currently, little is still known about how these approaches can be useful in marine ecological assessments and management, although they have been successfully and widely applied both in freshwater and terrestrial ecosystems (Flöder and Hillebrand, 2012; Guilpart et al., 2012; Colas et al., 2014; Guisan, 2014).

From a biological viewpoint, one of the most common ways to investigate function is by looking at the characteristics (traits) of species present in the system, as these determine how species interact with their environment, and their role in maintaining and regulating ecosystem processes (Snelgrove, 1998). Biological Traits Analysis (BTA) is an analytical approach for describing functioning based on traits exhibited by members of biological assemblages (Bremner et al., 2006b). Benthic invertebrate assemblages are key to the maintenance of ecological processes (through habitat formation, nutrient cycling and as a prey to higher trophic levels), and species traits determine how they contribute to ecosystem processes. Therefore, the presence and distribution of such traits can be used to indicate aspects of functioning (Bremner et al., 2006a,b).

This multi-trait approach is built on a theoretical framework that allows the formulation of generalizations about community assembly in different environments; it is centered on the habitat templet and environmental filtering concepts (Southwood, 1977; Olff et al., 1994; Lavorel et al., 1997; Poff, 1997; Townsend and Hildrew, 1994). In essence, these state that the environment dictates community assembly through species traits, because only specific traits can persist under a given set of environmental conditions. The environment filters the regional species pool to exclude traits not suited for particular conditions and communities are assembled from species possessing traits that pass through the filter. These concepts assert direct links between species' traits and

environmental conditions that are independent of geographic scale (Bremner et al., 2006a,b; Bremner, 2008; Galparsoro et al., 2013).

BTA confers several advantages over traditional methods because it is founded on sound ecological theory ((Lavorel and Garnier, 2002, Statzner and Bêche, 2010; Bolam et al., 2014b), considers a wide range of information on traits regardless of taxonomic identity, and the links between traits and ecosystem processes (Diaz and Cabido, 2001). For instance, taxonomy-based methods do not allow the establishment of causal relationships with stressors, do not integrate natural fluctuations and fail when generalizations to different types of ecosystems are needed (regional constraints) resulting in losses of ecological information (Dolédec et al., 1999; Menezes et al., 2010). In contrast, traits-based analyses are less confounded by natural gradients showing high spatial and temporal stability over broader scales (Charvet et al., 2000; Usseglio-Polatera et al., 2000). High robustness with decreased taxonomic resolution and greater accuracy with less sampling effort have also been reported (Charvet et al., 2000; Menezes et al., 2010), illustrating a greater tendency for the approach to be more generic in terms of geographic application, high specificity regarding stressors identification and providing advanced warning of disturbance to ecosystems (Mouillot et al., 2013). These methods may thus be particularly advantageous when trying to assess and maintain ecosystem quality over broader spatial scales or in situations of limited availability of taxonomic information (Tyler et al., 2012).

BTA uses a set of different characteristics (i.e. life-history, morphological, behavioural) of species present in assemblages (Bremner et al., 2003a; Veríssimo et al., 2012). It performs well in comparison to the more traditional methods as it incorporates information on both the relative abundance/biomass of species present in communities and their biological characteristics into one analysis, and can incorporate information on a large range of traits potentially important for benthic functioning (Bremner et al., 2006a,b).

BTA has potential to identify the presence of human impacts (e.g. Charvet et al., 1998), and to separate the effects of different impact types (Usseglio-Polatera et al., 2000; Kahmen et al., 2002). This approach has been applied successfully to assess fishing effects on benthic fauna (Bremner et al., 2003, 2005; Tillin et al., 2006), to assess the functional diversity in different species assemblages (Bady et al., 2005; Hewitt et al., 2008), as well as for management and conservation purposes. For example, it revealed helpful for the designation process and management of **Marine Protected Areas (MPAs)**, when applied to a UK-proposed Special Area of Conservation (Eddystone Special Area of Conservation in the SW England) (Bremner, 2008; Frid et al., 2008).

BTA was translated to the marine benthic environment by Bremner et al. (2003a,b) raising important questions needing further exploration and opening new research opportunities in this

field. Understanding how traits-based information could be used for bio-monitoring in marine ecosystems is crucial. The potential of traits-based approaches to form a new generation of bio-monitoring tools constitutes an important step towards effective management and conservation of aquatic systems, and will allow managers to meet obligations for protecting ecosystem function under the Marine Strategy Framework Directive (MSFD, 2008/56/EC).

2. Objectives

Based on the statement that groups of organisms sharing similar sets of traits are useful for the development of more effective monitoring and management tools to measure communities' functional diversity (Usseglio-Polatera et al., 2000), the present work aims to investigate the utility of BTA as a tool for assessing ecological function in marine ecosystems, in the scope of the European MSFD.

For that purpose, groups of benthic macroinvertebrates having similar sets of traits and that may be potentially important in terms of food-web functioning were identified. These functional groups were based on specific traits important for: (i) habitat forming (e.g., reef-building); (ii) nutrient cycling; and (iii) consumption by higher trophic levels.

This preliminary definition of the functional groups is a first step towards assessing their bio-indication potential. Following the aforementioned groups' definition, a procedure to map and relate them to habitat characteristics will be considered.

3. Study areas

Bay of Biscay

The Bay of Biscay (Iberian Atlantic coast) is a marine subregion comprised within the Atlantic Ocean ecoregion. It is included under OSPAR Region IV "Bay of Biscay and Iberian Coast" and includes several areas of the International Council for the Exploration of the Sea (ICES), including VIIIa, b, c and d2. It is a deep sea (until 5,000 m water depth), with a narrow continental shelf in the Spanish coast and a wider shelf in the French coast, especially in the north of the Bay. It is a temperate sea, with high wave exposure, due to its long (>4,000 km) fetch (González et al., 2006).

In the Bay of Biscay, two study areas were considered (Figure 1). The first study area is located on the continental shelf of the Basque country, in the southeastern part of the Bay of Biscay, northern Spain. The second area is located in the North, on the large sedimentary muddy bank known as the “Grande Vasière” (Le Loc’h et al., 2008).

Southern North Sea

The North Sea (ICES area IV) is a semi-enclosed sea situated on the continental shelf of North Western Europe between the United Kingdom, Norway and mainland Europe. Although the mean depth is 90 m, there is a strong depth gradient such that much of the south is at depths <50 m. Together with the English Channel, Skagerrak and Kattegat the area comprises the OSPAR region II “Greater North Sea”.

The North Sea has extremely diverse coastal regions with a great variety of habitats (fjords, estuaries, deltas, banks, beaches, sandbanks and mudflats, marshes, rocks and islands) that support diverse assemblages of wildlife. The seabed is mainly composed of mud, sandy mud, sand and gravel, and coastal areas are greatly affected by nutrient and sediment plumes from rivers in the south (Rees et al., 2007). The study area is located to the east of England (Figure 1).

Kattegat

The Kattegat forms together with the Danish Straits the transition zone between the North Sea/Skagerrak and the Baltic Sea. The Kattegat is included under both the HELCOM and OSPAR conventions, but for the MSFD the Kattegat is a subregion under the Atlantic Ocean ecoregion. It has a surface area, volume and average depth of 22 290 km², 533 km³ and 23.9 m, respectively, and circulation is dominated by north-flowing surface water with a salinity gradient of 15 to 30, and south-flowing deep water with salinities around 30 to 34, separated by a permanent halocline located around 15 m. Thus, the Kattegat is a relatively shallow marginal sea with estuarine character. The Kattegat is a well-monitored system and has long time series of various physical-chemical and biological components (Carstensen et al., 2003) (Figure 1).



Figure 1. Map of the case study areas. (Base map adapted from the European Atlas of the Seas, EC; http://ec.europa.eu/maritimeaffairs/atlas/maritime_atlas/)

4. Datasets

A database from the North-East Atlantic eco-region including 532 benthic taxa belonging to Bay of Biscay, southern North Sea and Kattegat areas was tested (Table 1).

Table 1. Data sets characteristics.

Bay of Biscay (AZTI)		Kattegat (AU)	
Years	2003- 2012		1989-2002
Months	Feb and March		April and May
Grab type and area	Van veen 0.1 m ²		Haps 143 cm ²
N° replicates	3		14 replicates
N° stations	17		6
Type of data	Density		Density
Bay of Biscay (CNRS)		North Sea (CEFAS)	
Years	2001		2000-2003
Months	May		May and June
Grab type and area	Benne hamon 0.25 m ²		Day grab/Mini hamon 0.1m ²
N° replicates	3		3
N° stations	14		47
Type of data	Density		Density

5. Traits data compilation and numerical matrices construction

The main constraints when conducting traits analysis are (i) the time needed to gather the relevant information, (ii) the information availability on the required species traits to construct the “taxa by stations” data matrix and (iii) the contradictory information that might come from different sources. As reported in previous studies (e.g. Marchini et al., 2008; Statzner and Bêche, 2010; van der Linden et al. 2012), collecting such detailed information on the biology of species is often a hard task and a full data matrix, where traits information for all taxa is available, is rarely achieved.

The *a priori* selection of biological traits is a fundamental step when performing BTA, because the number and type of traits available are numerous and different choices may provide different pictures of the functioning in assemblages (Bremner et al., 2006b). However, there is still no accepted methodology for selecting the most appropriate biological traits for a given study (Bolam et al., 2014a,b). So, from the wide variety of existing traits, selection has to be a compromise between their efficacy to describe variability in ecological functioning and the time and effort needed to gather the information for the taxa. Since certain types of traits may be more relevant in some circumstances than others (Bremner, 2008), traits included here were selected considering the context and goal of the present investigation thus, the ones potentially most important and meaningful for the purpose of this study. The selection, which is restricted by considerations such as the availability of information or their potential ecological relevance, was based on the choices adopted in previous studies that were successful in evaluating ecosystem functioning by means of BTA (e.g. Bremner et al., 2003; 2006 a,b; Tillin et al., 2006; Bremner, 2008; Cooper et al., 2008; Hewitt et al., 2008; Marchini et al., 2008; Villnäs et al., 2011; Aarnio et al., 2011; Tyler et al., 2012; Van der Linden et al., 2012; Veríssimo et al., 2012; Bolam et al., 2014a,b). Hence, trait selection took into account: (i) the traits' perceived importance to ecosystem functioning according to the literature; (ii) expert judgment and personal knowledge on the investigated benthic community; and (iii) the availability of information on the traits for the macrobenthic species present in the datasets which often heavily determines the final traits list.

Five biological traits were selected covering different aspects of life history, morphology and behaviour of each taxa. Each trait was divided into several categories adding up to a total of 20 (Table 2). Some traits are important for benthic function, some are useful indicators of management-related change and others serve to indicate both. For example, the traits **longevity** and **size** are representative of the movement of organic matter within the benthic system, with

long-lived and large organisms holding matter within the system and short-lived small species contributing to higher turnover. These traits could also be indicative of disturbance within the system, with small-sized and short-lived species increasing in both abundance and species number as disturbance increases (Pearson and Rosenberg, 1978). **Feeding habit** is another key trait in this respect. In addition to being a descriptor of movement of energy and matter through the food web, feeding traits determine species' abilities to utilize/tolerate different hydrodynamic conditions, with a switch from predominantly suspension feeders to surface deposit feeders indicating a potential reduction in hydrodynamism (Rosenberg, 1995). **Development mechanism** captures energy/materials transfer pathways and the nature of connections between benthos and pelagos while, as it is associated with different modes of recruitment, it may also give insights on potential recovery patterns (with different types of recruitment conferring different recovery potentials, e.g. communities recruiting mainly by pelagic dispersal are theoretically likely to recover from disturbance more quickly than those with predominantly benthic recruitment; Thrush and Whitlatch, 2001). **Living habit** trait describes a particular activity of the assemblage that can alter a species ability to survive different environmental conditions and may also indicate a particular habitat formation (eg. *Tube-dweller*).

Traits used to study marine benthic communities are mostly of a categorical type (divided into *a priori* defined categories). In BTA, even if a trait is measured in a continuous scale, it will be used as a categorical one (e.g. "body size" is divided into <1cm, 1-3cm, 3-10cm; 10-20cm; >20cm) and thus a coding procedure must be used to link taxa to traits (Usseglio-Polatera et al., 2000; Törnroos and Bonsdorff, 2012). Furthermore, many taxa may display multi-faceted behaviour depending on specific maturity stage, conditions and resources available, and therefore, it is difficult to assign them to a single category (Usseglio-Polatera et al., 2000; Paganelli et al., 2012). To address this, taxa were coded for the extent to which they display the categories of each trait using a "Fuzzy coding" procedure (Chevenet et al., 1994) on scale 0-3 (0: no affinity for a trait category; 3: total affinity for a trait category).

Information for assigning taxa to functional traits and used to construct the 'taxa by traits' data matrix, was obtained from different published sources including online databases such as BIOTIC developed by the Marine Life Information Network - UK (<http://www.marlin.ac.uk/biotic/>) and POLYTRAITS (<http://polytraits.lifewatchgreece.eu>), scientific journals, and fully referenced traits databases provided by traits experts (J. Bremner, S. Bolam and C. Garcia). When reliable information was missing, expert judgment and/or data from the nearest phylogenetic neighbour were considered. As previously reported by several authors (e.g. Usseglio-Polatera et al., 2000; Tyler et al., 2012), it is difficult to undertake a BTA at the species level due to the lack of information on many traits for a large set of species (inexistent data or not published) and higher

taxonomic levels have been frequently considered (e.g., Usseglio-Polatera et al., 2000; Tyler et al., 2012; Bolam et al., 2014a,b). In the present work, traits information was collected for the lowest possible taxonomic level (species) and only later adjusted to a higher level “genus” so that we could achieve a good completion of the traits categories. The list with the biological traits assigned to each genus can be consulted in the Supplementary Material (**Annex 1**) to this report, in the file **MS18_FCdata_IMAR.xlsx**.

To conduct BTA, three different types of data matrices are usually required (Figure 2): a) ‘taxa by station’ (taxa abundance or biomass for each sampling station); b) ‘taxa by traits’ (biological traits for each taxon); and c) ‘traits by station’ (biological traits in each sampling station). The final ‘traits by station’ matrix is a result of the cross-product between the other two matrices (Figure 2). To achieve this, trait categories for each taxon present at a station are multiplied by their abundance/biomass at that station, and then summed over all taxa present at each station to obtain a single value for each trait category in each station (Bremner et al., 2006b). The resulting ‘traits by station’ data matrix can then be subjected to multivariate analysis, or each matrix can be analysed individually.

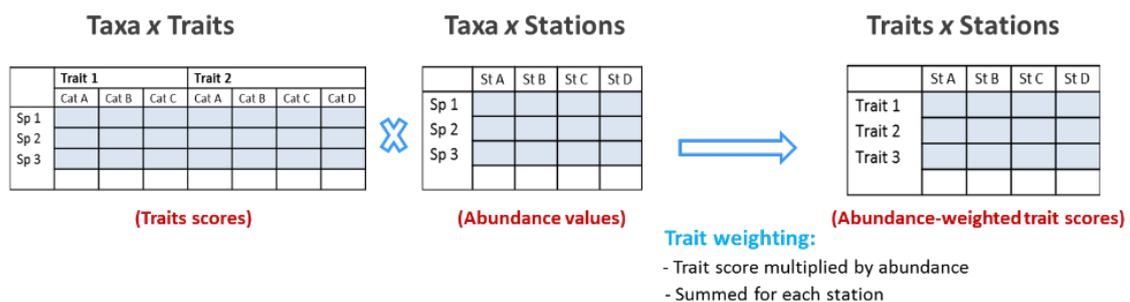


Figure 2. Numerical matrices used for BTA.

Table 2. List of biological traits and categories of benthic invertebrates used in the present study, including their respective definitions.

Traits and Categories	Definitions
Feeding mode <i>Deposit feeder</i> <i>Filter/suspension feeder</i> <i>Scavenger/opportunist</i> <i>Predator</i>	Mode of food capture (Tyler et al., 2012); The method by which a species feeds, encapsulating resource type rather than specific dietary components (Webb et al., 2009) Any organism which feeds on fragmented particulate organic matter from the substratum (MarLIN, 2006) Any organism which feeds on particulate organic matter, suspended in the water column (MarLIN, 2006) Any organism that actively feeds on dead organic material (e.g. crabs, whelks) (MarLIN, 2006) An organism that feeds by preying on other organisms, killing them for food (MarLIN, 2006)
Body size < 1 cm 1-3 cm 3-10 cm 10-20 cm > 20cm	Maximum linear dimension (cm) of adults (Webb et al., 2009; Tyler et al., 2012)
Longevity < 1 year 1-3 years 3-10 years > 10 years	Longest recorded life span of the adult stage (Webb et al., 2009; Tyler et al., 2012; Bolam et al., 2014a,b)
Larval development <i>Planktotrophic</i> <i>Lecitotrophic</i> <i>Direct (benthic)</i>	Larval development mode (Webb et al., 2009; Tyler et al., 2012) Feeding at least in part on materials captured from the plankton (MarLIN, 2006; Törnroos and Bonsdorff, 2012); larvae feed and grow in water column, generally pelagic for several weeks (Bolam et al., 2014a,b) Development at the expense of internal resources (i.e. yolk) provided by the female (MarLIN, 2006; Törnroos and Bonsdorff, 2012); larvae with yolk sac, pelagic for short periods (Bolam et al., 2014) Development without a larval stage (direct) (MarLIN, 2006; Törnroos and Bonsdorff, 2012; Bolam et al., 2014a,b)
Living habit <i>Tube-dweller</i> <i>Burrow-dweller</i> <i>Free-living</i> <i>Attached to substratum</i>	How organisms live (Törnroos and Bonsdorff, 2012) Builds and dwells in a tube(s) (MarLin, 2006; Törnroos and Bonsdorff, 2012) Living within a burrow (MarLIN, 2006) Living without attachment or restriction (MarLIN, 2006); in or on sediment, in water column (Törnroos and Bonsdorff, 2012) Adherent to a substratum (MarLIN, 2006)

6. Data Analysis

Fuzzy Correspondence Analysis (FCA) is a parametric linear ordination method that uses eigenanalysis to investigate differences between samples (Bremner et al, 2006), in this case based

on the biological traits exhibited by species present in the assemblages. It resembles a Correspondence Analysis and is suitable for fuzzy-coded data (Chevenet et al., 1994). FCA provides the variability contained in every axis and the correlation ratios of each biological trait along the principal axes. It also allows plotting the scores of trait category on two-dimensional factor maps, reducing the n-dimensional space represented by all the categories of taxa traits and thus, summarizing the complex patterns embedded in the original dataset.

To identify relevant functional groups we followed a similar procedure to that described in Usseglio-Polatera et al. (2000), and the “**taxa by traits**” matrix was ordinated using FCA. Functional groups of genera with similar sets of traits were then defined by cluster analysis based on the **Ward’s linkage method** (Ward, 1963), using Euclidean distances and the scores of taxa on the first two axes of the FCA. Following, the groups identified were plotted on the FCA first factorial plane at the weighted average of their taxa.

For each functional group, a biological trait profile was created indicating for each trait the proportion of categories displayed by the group. Using the “**taxa by stations**” matrix (density of genera per sample), the proportion of each group in each sea was assessed.

The R software packages ADE-4 and STATS (Thioulouse, 1997; R Development Core Team 2009) were used to perform the analyses.

Table 3. Labels for the traits categories used in statistical analyses.

TRAITS	CATEGORIES	CODES
Body size (cm)	<1	S<1
	1-3	S1_3
	3-10	S3_10
	10-20	S10_20
	>20	S>20
Longevity (years)	<1	L<1
	1-3	L1_3
	3-10	L3_10
	>10	L>10
Larval development	Planktotrophic	Plan
	Lecitotrophic	Lec
	Direct	Dir
Living habit	Tube-dweller	Td
	Burrow-dweller	Bd
	Free-living	Fl
	Attached	Att
Feeding mode	Deposit	Dep
	Filter/suspension	F_S
	Scavenger/opportunist	S_O
	Predator	Pred

7. Results and discussion

The first two axes of the **FCA performed on the biological traits by taxa table** accounted for 28% of the total variance in biological traits (F1 = 17% and F2 = 11%, respectively).

The correlation ratios allowed the identification of the traits that were best explained by the first two FCA axes. These ratios represent the proportions of the total variance explained by each axis to depict the separation among categories of a trait (Chevenet et al., 1994). The total variance of coordinates on each axis is indicated by the eigenvalues (Figure 3).

Along the F1 axis, trait categories “longevity” and “larval development” showed the highest correlation ratios with 58 to 49% of the variance explained (Table 4). “Living habit” and “body size” were also well separated in this axis but to a weaker extent (37 and 31%, respectively). The second axis (F2) was mainly correlated with “living habit” and “feeding mode” (62 and 44%) (Table 4). The following axes (F3 and F4; Table 4) were correlated mainly with “longevity” and “living habit” and did not provide any additional information, and thus, they were not considered for further analysis.

Overall, the F1 axis separated short-lived, direct developers, from medium-long lived, planktotrophic organisms, and to a lesser extent, small-sized, free-living/tube-dwellers from large-sized, attached/burrow-dwellers (Table 4; Figure 4c). The F2 axis discriminates free-living, predator/scavenger taxa from burrower/tube dwellers with deposit/filter-suspension feeding modes (Table 4; Figure 4c).

Table 4. Correlation ratios of each biological trait with axes F1 and F2 of the FCA. Values in bold indicate which traits are best explained by the first two axes.

Traits	F1	F2	F3	F4
Feeding	0.26	0.44	0.19	0.11
Body size	0.31	0.09	0.23	0.20
Living habit	0.37	0.62	0.27	0.53
Larval development	0.49	0.18	0.15	0.12
Longevity	0.58	0.06	0.42	0.05
Eigenvalues	0.40	0.28	0.25	0.20

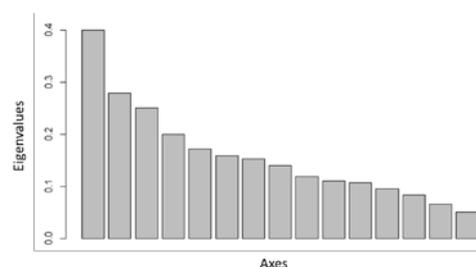


Figure 3. Histogram of eigenvalues.

The **cluster analysis (Ward's linkage method)** performed on the FCA output (i.e. taxa scores on the first two axes), suggested the existence of 5 distinct groups of taxa clearly separated on the F1-F2 factorial plane and characterized by different sets of traits (Figure 4 c, d and e). Each functional group displayed a distinctive profile of biological traits. Figures 4 and 5 describe and allow to characterize these groups.

Groups A and B present the most distinct profile along F1 axis (negative and positive sides, respectively). Group A is mainly composed of medium-sized organisms, filter/suspension feeders with planktotrophic development and medium-long lifespan. These have an attached or burrower living habits. Bivalvia and cnidaria are the main contributors to this group (Figure 4 b, c and e). Group B consists mainly of small-sized, short-lived organisms with direct development, living without attachment and exhibiting deposit - predatory feeding modes. Amphipods, isopods and several polychaetes taxa contribute to this group (Figure 4 b, c and e).

Groups C and D are well discriminated along the second axis (negative and positive ends of F2, respectively). Group C includes taxa exhibiting a wide variety of sizes and larval development modes although the lecithotrophic mode is slightly predominant, and presenting short to medium longevity. These are mainly tube dwellers and burrowers, feeding on particulate organic matter from the substrate or suspended in the water column. Polychaeta taxa are dominant. Group D is characterized by taxa with small to medium size and a short-medium lifespan. Free-living, planktotrophic and a predatory - scavenger/opportunist modes prevail. Taxa in this group comprised mainly gastropods, decapods and polychaetes (Figure 4 b, c and e).

For a detailed description of the biological features of each group please see Figure 5.

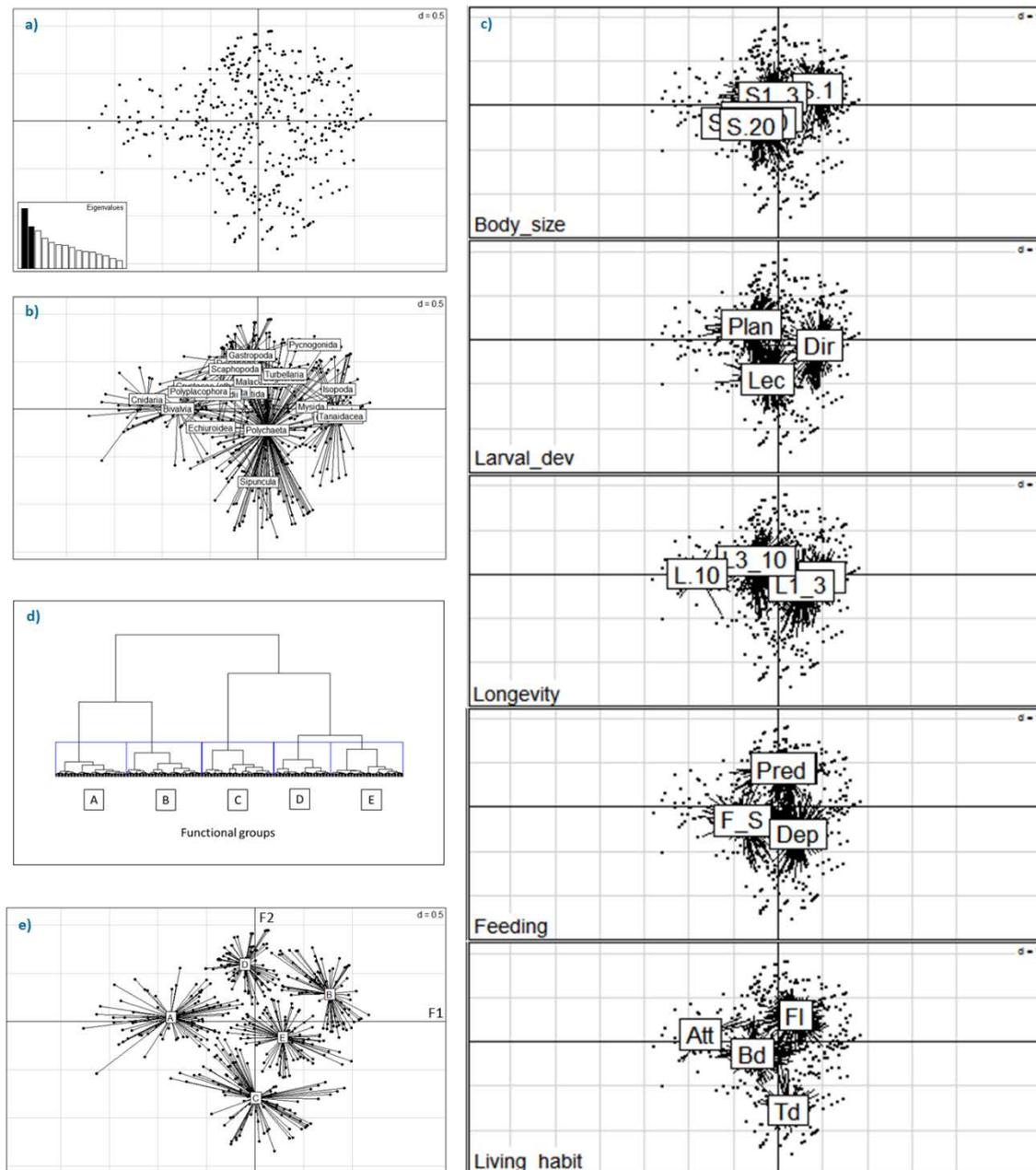


Figure 4. Ordination and classification of biological traits and taxa.

(a) Histogram of eigenvalues and distribution of genera (dots) on the first two FCA axes.

(b) Distribution of genera on the F1-F2 factorial plane grouped according to the main taxonomic unit (squared labels) and positioned at the weighted average of their component genera.

(c) Ordination of the traits categories on the first two axes of the FCA. Each category is placed at the weighted average of the taxa positions representing the category, where **Living habit**: Td = Tube dweller; Bd = Burrow-dweller; Fl = free-living; Att = attached; **Feeding mode**: Dep = Deposit; F_S = Filter/suspension; S_O = Scavenger/opportunist; Pred = Predator; **Larval development**: Plan = Planktotrophic; Lec = Lecitotrophic; Dir = Direct; **Longevity**: L# = longevity by age category (years) (<1; 1-3; 3-10; <10); **Body size**: S# = size by dimension category (cm) (<1; 1-3; 3-10; 10-20; >20).

(d) Dendrogram resulting from the Cluster analysis (Ward's linkage method on Euclidean distances). The blue squares define faunal groups characterized by different sets of traits.

(e) Distribution of the groups on the F1-F2 factorial plane of the FCA. Functional groups (A, B, C, D and E) are positioned at the weighted average of their taxa. The link of the average location of each group to the respective taxa are indicated by the lines.

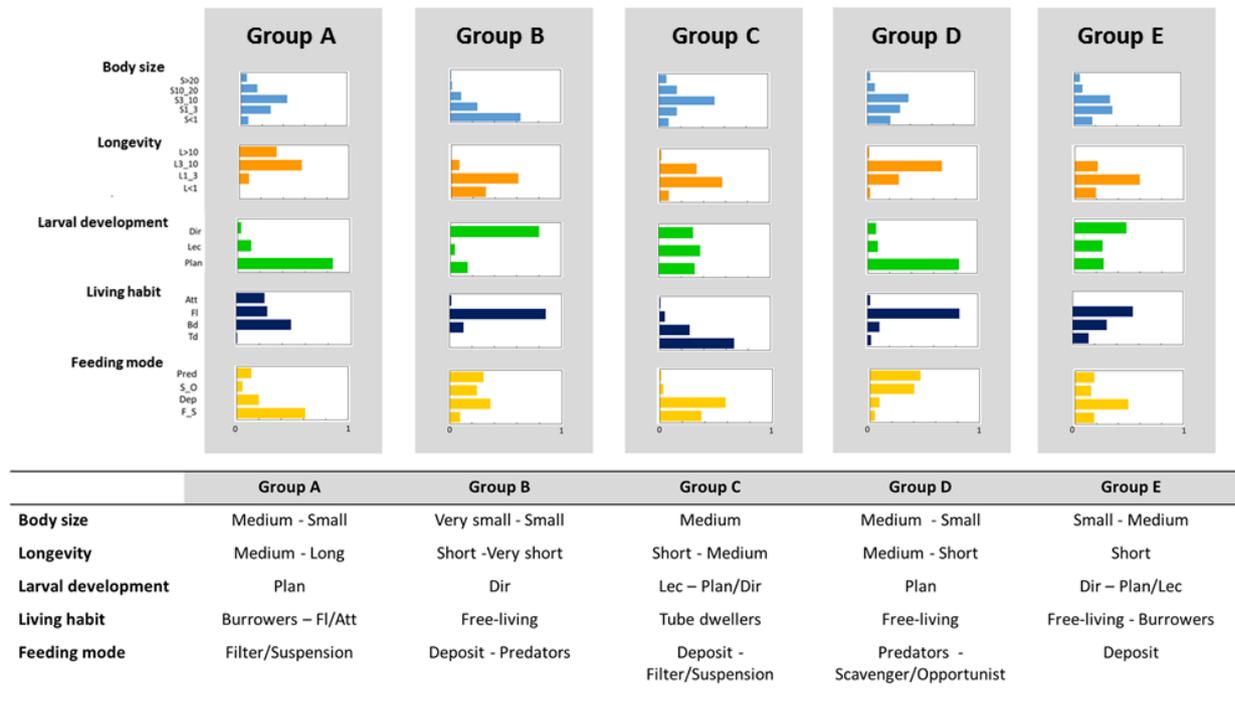


Figure 5. Biological traits profile of each group. Proportions of traits categories exhibited by the groups are shown. For traits categories labels please see Table 3.

The proportion of each group was also analysed for each case study and is presented in Figure 6. Groups A and C are well represented in all areas and the less dominant is group D. The Bay of Biscay is the most “balanced” of the three seas, the proportions of most groups are similar (except group D). The North Sea and Kattegat are more “unbalanced” in comparison. In the North Sea group C dominates, and then group A. In the Kattegat groups A, C and E are dominant and groups B/D mostly absent.

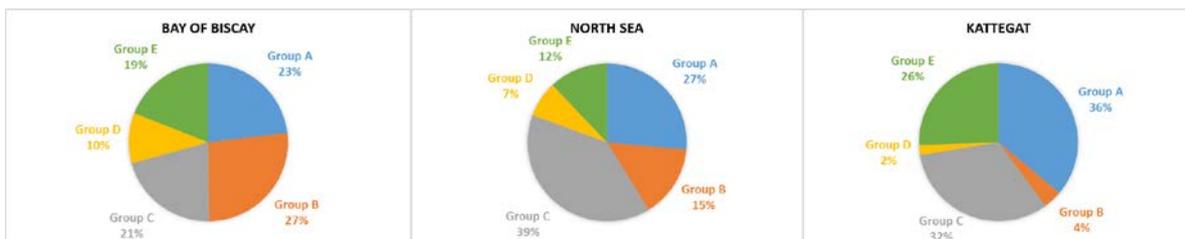


Figure 6. Proportions of the five functional groups in the Bay of Biscay, southern North Sea and Kattegat.

8. Conclusions

- The use of functional groups of taxa has been recommended in order to overcome potential trade-offs among species traits and should allow a more effective use of macroinvertebrates traits in community ecology (Statzner et al., 1997; Usseglio-Polatera et al., 2000).
- Through multivariate analyses (ordination and classification), 5 groups of benthic macroinvertebrates were identified based on traits for the Bay of Biscay, southern North Sea and Kattegat areas.
- Most of the traits were important in determining the ordination of taxa according to the combinations of their traits (high correlation ratios along F1 and/or F2 axes). In particular, lifespan, larval development mode, living habit and feeding mode.
- Assessment of the groups' performance as potential indicators of functioning will be further considered in the future research of the WP4.

9. Recommendations for future work

- Under the MSFD, a benthic functional indicator for the food-web descriptor (D4) is lacking.
- The conceptual development of BTA as an indicator for food-web health is currently underway.
- Setting the benthic functional groups was a first step in that direction but further work is needed to propose it as an operational indicator for the MSFD.
- Our results show that BTA has potential to become operational, however, a number of issues still need to be addressed:
 - (i) Baseline levels and targets must be determined, and a method for this must be proposed?
 - (ii) The scale of the assessment and monitoring requirements have to be established (e.g, the frequency of sampling);
 - (iii) Testing against pressures needs to be carried out to define trends of variation.

10. References

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11. List of Annexes

Annex 1 – MS18_FCdata_IMAR