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RESEARCH ARTICLE

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Biological-based habitat classification approaches promote cost-efficient monitoring: An example using seabed assemblages

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Abstract

1. Seabed habitat maps can help facilitate the management of marine environments. A variety of approaches exist for seabed habitat classification. Most partition the environment according to physical environmental characteristics, with an assumption that resulting habitat classes are biologically meaningful. In the absence of comprehensive broad-scale biological data, this strategy offers a logical and pragmatic way of producing habitat maps to help manage the marine environment. Across Europe, the physical based European Nature Information System (EUNIS) classification has gained wide acceptance, with maps used to classify broadscale habitats within Marine Protected Areas and to design monitoring programmes. An alternative approach to habitat classification, made possible by increasing quantities of data, is to use the biology to identify meaningful habitats. With such contrasting approaches, the question arises as to which provides the most robust and efficient basis for biological monitoring.
2. To investigate, we compared variability in macrofaunal assemblages across different EUNIS sediment classes to those of two new habitat classification approaches developed in this study. The first of these (PHY) is based on a wide suite of physical variables known to influence the fauna. The second (BIO) uses the fauna to identify meaningful habitats. Both classifications were produced using a training dataset (9,619 grab samples) and employing k-means clustering and Random Forest Modelling. Power analysis of test set data (4,123 samples) was used to assess the number of samples required to detect a 20% change in taxon richness and total abundance across all classes of each classification approach.
3. Results showed that across all habitat classes, the BIO classification required 49% and 31% fewer samples to detect the change in richness and abundance than EUNIS level 4. Whilst offering some improvement on EUNIS, PHY still required many more samples than BIO.
4. *Synthesis and applications*. Habitat maps based on biological data have generally lower within-habitat variability in community metrics than those produced using

physical attributes alone. As a result, biologically-based habitat maps could offer a more cost-effective basis for ecological monitoring.

KEYWORDS
big data, habitat classification, habitat map, macrofauna, marine monitoring, modelling, random forest, statistical power

1 | INTRODUCTION

In 2010, the parties to the Convention on Biological Diversity adopted the Strategic Plan for Biological Diversity 2011–2020, including Target 11, which states that "by 2020, at least 17% of terrestrial and inland water and 10% of coastal and marine areas must be set aside for protection." To help meet this ambitious target, a suite of legislative packages focused on conservation, sustainable development and environmental protection has been implemented. Although significant progress has been made, there are still several challenges to address in the acquisition of robust scientific data, and in developing the ecological understanding to underpin the various policy frameworks under the convention. For marine seabed regions these challenges include improving our knowledge of the distribution of habitats and species, their fundamental ecology and how anthropogenic impacts (e.g., demersal trawling, habitat loss) and widespread environmental change due to climatic shifts affect their functioning and capacity to deliver important ecosystem services.

Effective implementation of management strategies under regulatory frameworks requires robust and targeted monitoring programs (Lovett et al., 2007). Data are often required over wide geographic areas and across a diverse range of habitats. To aid the successful implementation of monitoring programs, the shelf seas are classified into habitat units which form the basis upon which monitoring is conducted. A habitat classification system not only creates an inventory of habitats within a biogeographic region (Moss, 2008), it also reduces the spatial variability that inherently exists at large spatial scales into comparable regions (Maciejewski et al., 2016). Habitat typologies in conservation programs are essential for surveying and mapping as they enable targeted collection of information to achieve the objectives of monitoring. However, while "habitat" and "habitat type" are terms essential for all realms of ecology and have been in use in the literature for many decades, they are among the most confused in usage (Kallimanis et al., 2008). In practice, what are commonly termed habitat maps are effectively seabed classification maps. This is because the information needed to truly characterise marine habitats is not available, and the necessary use of proxies and assumptions to create a classified map for stakeholder use does not prevent the use of the term "habitat" to describe it.

The physical environment has traditionally formed the basis of seabed habitat classifications. Variations in macrofaunal assemblages have commonly been shown to correlate with a number of environmental variables across a range of spatial scales (Barrio Froján, Bolam, Eggleton, & Mason, 2012; Cooper & Barry, 2017a; Snelgrove & Butman, 1994). Areas of comparable sediment type, depth and light penetration, have thus been used to derive seabed habitat classes. The European Nature Information System (EUNIS) marine habitat classification (Davies, Moss, & Hill, 2004) was proposed in 2004 with the aim to provide a common European reference set of habitat types, within a hierarchical classification, to allow the reporting of habitat data in a comparable manner. Although this system is currently being used to underpin monitoring of seabed health, the EUNIS classification has many constraints and drawbacks for European-wide application (Galparsoro et al., 2012). In the absence of another possible approach, EUNIS is likely to be used as the basis of monitoring strategies for the foreseeable future. However, it is becoming increasingly clear that the macrofauna found within seabed sediments do not always conform to the hierarchical structure of the EUNIS marine habitat classification (Galparsoro et al., 2012). The lack of effective strata upon which to plan sampling currently poses a constraint to the development of effective macrofaunal monitoring programmes.

The implementation of a physical-based classification approach to define seabed habitats (e.g., Ierodiaconou, Monk, Rattray, Laurenson, & Versace, 2011) has several appealing advantages over a more biological-based classification (Brown, Smith, Lawton, & Anderson, 2011). The physical terrain is less likely to vary seasonally or between years and recent advances in remote acoustic approaches, when appropriately ground-truthed, are increasingly allowing relatively large areas of seabed to be mapped. However, it is, either directly or indirectly, the health of the biological component (e.g., the macrofaunal assemblages) that is generally the focus of such monitoring and, unless biological metrics are closely related to the physical environment, monitoring approaches based on physical properties are likely to result in high within-strata (i.e., habitat) variability and low statistical power to detect change. Therefore, the value of a habitat map to monitor seabed health must depend on how well the map describes variations in the faunal assemblages. To be effective, a habitat classification approach must have low variability within habitat classes.

Development of accurate biological-based seabed maps for the UK covering large spatial scales has, until recently, been hindered by a lack of suitable data. However, Cooper and Barry (2017a) recently compiled a comprehensive big dataset of macrofaunal data (33,198 samples from 777 surveys) and used these data to produce a baseline assessment for UK shelf waters. This large dataset Cooper and Barry (2017b) was created by integrating empirical data acquired from both governmental and non-governmental sector (e.g., marine aggregates, offshore wind, oil and gas) monitoring efforts. The availability of this resource opened the possibility to produce a macrofaunal-based map of the UK continental shelf. In this study, we generate a full coverage map of benthic

TABLE 1 Explanatory variables used in the study. Data sources: A (ICES climatology of surface and near-bed temperature and salinity 1971–2000 [Berx & Hughes, 2009]); B (Data from MODIS satellite sensor [Gohin et al., 2005]); C (Defra DEM 500m pixel resolution [Astrium Oceanwise, 2011]); D (POLCOM model [Holt & James, 2001; Aldridge, Parker, Bricheno, Green, & van der Molen, 2015]); E (Stephens & Diesing, 2015)

Variable		Detail	Raster resolution *xy* (m)	Data source
1	Sal	Mean annual near-bed salinity (ppt)	10500 × 11100	A
2	Temp	Mean annual near-bed temperature (°C)	10500 × 11100	A
3	Chl *a*	Mean annual chlorophyll *a* concentration (2002–2010)	1120 × 1110	B
4	SPM	Mean annual concentration of mineral origin suspended particulate matter ($g \cdot m^{-3}$) (2002–2010)	1120 × 1110	B
5	Depth	Bathymetry (m)	499 × 488	C
6	WOV	Peak wave orbital velocity ($m \cdot s^{-1}$)	11100 × 12400	D
7	AvCur	Average current velocity ($m \cdot s^{-1}$)	11100 × 12400	D
8	Stress	Peak wave/current stress($N \cdot m^{-2}$)	11100 × 12400	D
9	Gravel	Proportion of gravel (%) from sediment particle size data	498 × 492	E
10	Sand	Proportion of sand (%) from sediment particle size data	498 × 492	E
11	Mud	Proportion of silt/clay (%) from sediment particle size data	498 × 492	E

faunal assemblages, based on the point sample data and faunal groups identified in Cooper and Barry (2017a). We then compare variability in commonly used metrics of community structure (i.e., taxon richness, total abundance and community composition) across the different classes of this biologically informed habitat classification with those of three physical-based habitat classification approaches, including EUNIS levels 3 and 4 (EUNIS 3 and EUNIS 4 hereafter) and a newly-created physical-based classification. For these various approaches, the numbers of samples needed per habitat type to detect a given change in taxon richness and total abundance are compared. We discuss the implications of our findings for developing more efficient monitoring programmes to assess the status of benthic assemblages.

2 | MATERIALS AND METHODS

2.1 | The dataset and study area

The extensive dataset used in this study is available from the Cefas Data Hub https://doi.org/10.14466/cefasdatahub.34 (Cooper & Barry, 2017b). In summary, the dataset comprises 33,198 macrofaunal samples (777 surveys) with associated data for a range of physical environmental variables (Table 1) including: salinity (Sal), near-bed temperature (Temp), chlorophyll *a* (Chl *a*), sediment particulate matter (SPM), water depth (Depth), wave orbital velocity (WOV), average current (AvCur), bed stress (Stress) and sediment composition (% Mud, % Sand, % Gravel). Samples were collected using grabs or cores and subsequently processed for macrofauna and sediment particle size composition. Macrofaunal processing involved sieving sediments over a 0.5 or 1 mm sieve, with all extracted macrofauna identified to the lowest possible taxonomic level and enumerated. Colonial taxa were recorded as present and given a value of 1 in the dataset.

From the 33,198 samples, we selected a subset of 20,635 for which data were considered comparable (i.e., sample acquired using a 0.1 m^2 grab, processed using 1 mm sieve and not taken from a known impacted site) and for which a full suite of accompanying environmental variables was available. To address spatial autocorrelation in the data (see correlograms in supporting information Figures S3 and S4), samples closer than 50 m were removed from the dataset, reducing the overall number of samples to 13,742. This subset was then split, at random, into separate training (70%, 9,619 samples) and test (30%, 4,123 samples) sets, with training data used for development of physical and biological habitat classifications (see Section 2.2) and test data used solely for comparing the performance of each habitat classification approach (see Sections 2.3 and 2.4). For each test set sample, values of richness and total abundance were calculated, together with habitat class association under each habitat classification approach (EUNIS 3, EUNIS 4, PHY and BIO—see below). To take account of taxonomic differences between surveys, macrofaunal data were analysed at family level, with the dataset including 635 families. In addition, raster layers for each physical environmental variable were used in modelling (Table 1). Data for EUNIS classes were sourced from the 2016 version of the UKSeaMap (http://jncc.defra.gov.uk/ukseamap; Populus et al., 2017). The spatial extent of this study (Figure 1) was defined by the common area of extent of the raster and UKSeaMap layers. All analyses were undertaken using the statistical package R (R Core Team, 2017). The R script and associated files used in this study are available from the Cefas Data Hub https://doi.org/10.14466/cefasdatahub.56 (Cooper, Bolam, Downie, & Barry, 2019).

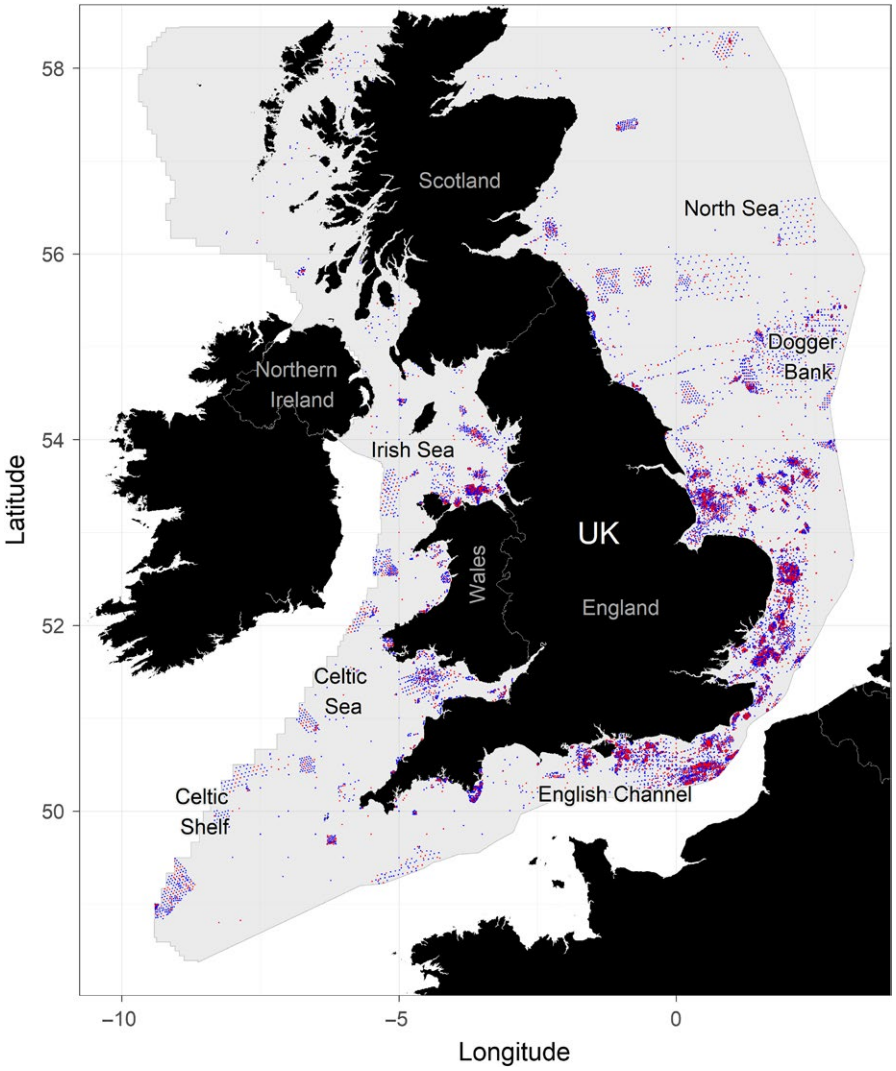

FIGURE 1 Study area (grey polygon) and positions of the 13,619 grab samples used in the study (blue: training set samples; red: test set samples)

2.2 | Habitat map derivation

2.2.1 | Clustering

Two new habitat maps based on physical (PHY) and macrofaunal (BIO) data were produced through an initial clustering of data from point samples followed by predictive Random Forest modelling (Breiman, 2001). Faunal clustering followed the approach of Cooper and Barry (2017a), using 4th root-transformed family level abundance data, to ensure the appropriate weighting of colonial and rarer taxa and with samples partitioned into 12 cluster groups. The number of faunal cluster groups in Cooper and Barry (2017a) was decided on the basis of an "elbow plot" (Thorndike, 1953). Clustering was performed in R using the k-means function (MacQueen algorithm). Physical clustering also followed the approach of Cooper and Barry (2017a), but with the addition of sediment variables (% gravel and % mud). These sediment variables came from direct measurements (i.e., particle size analysis of grab sampled sediments) rather than from raster layers as for other physical variables. Prior to clustering, physical variables were assessed for collinearity and skewness before normalising to bring them on to a common scale. As a result of strong correlations (i.e., $\rho > 0.75$) between Chl *a*/SPM and Gravel/Sand, Chl *a* and Sand were excluded from use in clustering (physical variables) or modelling (physical and faunal clusters). $\text{Log}_{(x+0.1)}$ transformations were applied to SPM, Depth, Stress, % Gravel and % Mud to address right skewness.

2.2.2 | Modelling

Full coverage maps for PHY and BIO clusters were produced using the Random Forest approach from the R package "randomForest" (Liaw & Wiener, 2002), with predictor variables (see Table 1) used to model the spatial distribution of PHY and BIO cluster groups. Random Forest was selected because of its suitability for predicting factor-type response variables and its ability to account for the multiple interactions and nonlinear relationships between the response and predictor variables (Rodriguez-Galiano, Ghimire, Rogan, Chica-Olmo, & Rigol-Sanchez, 2012; Strobl, Malley, & Tutz, 2009). In addition, our own research on this dataset showed that it performed better than multinomial models for prediction (results

not shown). In this procedure, sample coordinates are used to extract predictor variables from each of the nine raster layers: Sal, Temp, SPM, Depth, WOV, AvCur, Stress, % Gravel and % Mud. The resulting data frame was then split into separate model "training" (90%, 8,657 samples) and "test" (10%, 962 samples) subsets, with samples assigned at random and in proportion to the number of samples within each cluster group. The model was then fitted on the model training set, with performance (percentage of samples where predicted and actual faunal cluster groups agree) assessed using the model test set. Model results were output as a raster layer. While our approaches for the PHY and BIO are based on rather different data, we will refer to the resulting classification units as "habitats."

2.3 | Habitat classifications and biological variability

The extent to which different habitat classification approaches (i.e., EUNIS 3, EUNIS 4, PHY, BIO) act as proxies for the biology was examined. Analyses were based on comparison of within-class variability for: (a) univariate metrics taxon richness and total abundance, using measures of residual sum of squares (RSS) and coefficient of variation (CV); and (b) assemblage composition, using similarity percentage (SIMPER) from the Primer 7 package (Clarke, Gorley, Somerfield, & Warwick, 2014). Comparisons were made between EUNIS 3 and a simplified version of BIO, each with four habitat classes and between EUNIS 4, PHY and BIO, each with 12 classes. For the simplified version of BIO, the 12 habitat classes were collapsed into 4 high level groups (A–D), based on the underlying dendrogram from Cooper and Barry (2017a) showing the relationship between faunal cluster groups. This dendrogram was based on a group average hierarchical clustering of the distances between cluster centres, giving an indication of the relatedness of the cluster groups.

Values of taxon richness and total abundance were identified for each sample. Within group residual sums of squares (RSS) and variances were calculated for each group. The performance of the habitat classification approaches was summarised by summing the RSS values for each group (Total RSS, below) and dividing by the total number of observations minus the number of groups (g). This generates the mean residual sum of squares (MSS) = Total RSS/(3,989 − g).

For comparative purposes, MSS values were also calculated for a random and an optimal scenario. The random scenario was established by carrying out 1000 replications of randomly assigning samples to groups, whilst the optimal scenario was established through k-means clustering of the data. This gives an indication of how the habitat classification approaches perform against a method based on no habitats (i.e., the random scenario) and the best that could be done if our prime objective was to achieve the lowest within cluster sum of squares, irrespective of faunal or habitat values (i.e., the k-means clustering).

Coefficients of variation, which provide a standardized measure of variability where group means are different, were calculated by dividing the group standard deviation by the group mean. Values of CV were plotted for taxon richness and abundance, allowing a comparison of variability across the different habitat classification approaches.

2.4 | Power analysis

Power analysis was used to determine the total number of required samples (n_{req}) to detect a 20% change in taxon richness and total abundance across each of the classes of the different habitat classification approaches. The choice of metric and magnitude of change (i.e., 20%) was to test the concept and was not based on any ecologically meaningful or management relevant target. For richness, values of n_{req} were calculated for 90% power with a statistical significance level of 0.05, using the comparison of a two-sample *t* test. The *t* test assumption of normality was reasonably well met by the richness data. For abundance, where the data had an approximate log-normal distribution, n_{req} was determined by simulation—using the same power parameters as for richness. This essentially involved a *t* test on the logged data using the emon package in R (Barry, Maxwell, Jennings, Walker, & Murray, 2017). We chose two-sided tests given that monitoring programmes are likely to be aimed at detecting both ecological degradation and enhancement.

Power comparisons were made between EUNIS 3 and the simplified version of BIO, and between EUNIS 4, PHY and BIO. Thus, all comparisons were based on an equitable number of habitat classes. Note that from the original 14 EUNIS 4 classes, two (A5.34 and A5.43) were excluded from analysis due to small number of samples (1 and 10).

3 | RESULTS

3.1 | Habitat maps

The four habitat maps based on different classification methods are shown in Figure 2. It is not the purpose of this paper to present a description of the nature and distribution of the various physical and ecological habitats across the study area. For a detailed description of UKSeaMap plots (i.e., Figures 2a and 2b) see Populus et al. (2017). The physical characteristics of the 12 physical cluster habitat classes (Figure 2c) are presented in supporting information Figure S1. The 12 classified regions represent distinct physical areas. For example, the large region in the northern North Sea and off the west coast of Scotland, classified as Group 4 (Figure 2c), is characterised by deep water, low annual average bed temperatures, low SPM and chlorophyll, weak bottom currents and muddy sediments. In contrast, the mid English Channel, classified as Group 2 (Figure 2c), is typified by relatively shallow water, warm annual average near bed water temperatures, high bottom current flow and bed stresses and gravelly sediments.

In contrast to the first three approaches (Figure 2a–c), the strata presented in Figure 2d (BIO) are derived solely from clustering of the macrofaunal data. Thus, the boundaries delineate areas of contrasting faunal characteristics. The faunal characteristics (dominant taxa and assemblage abundance and diversity)

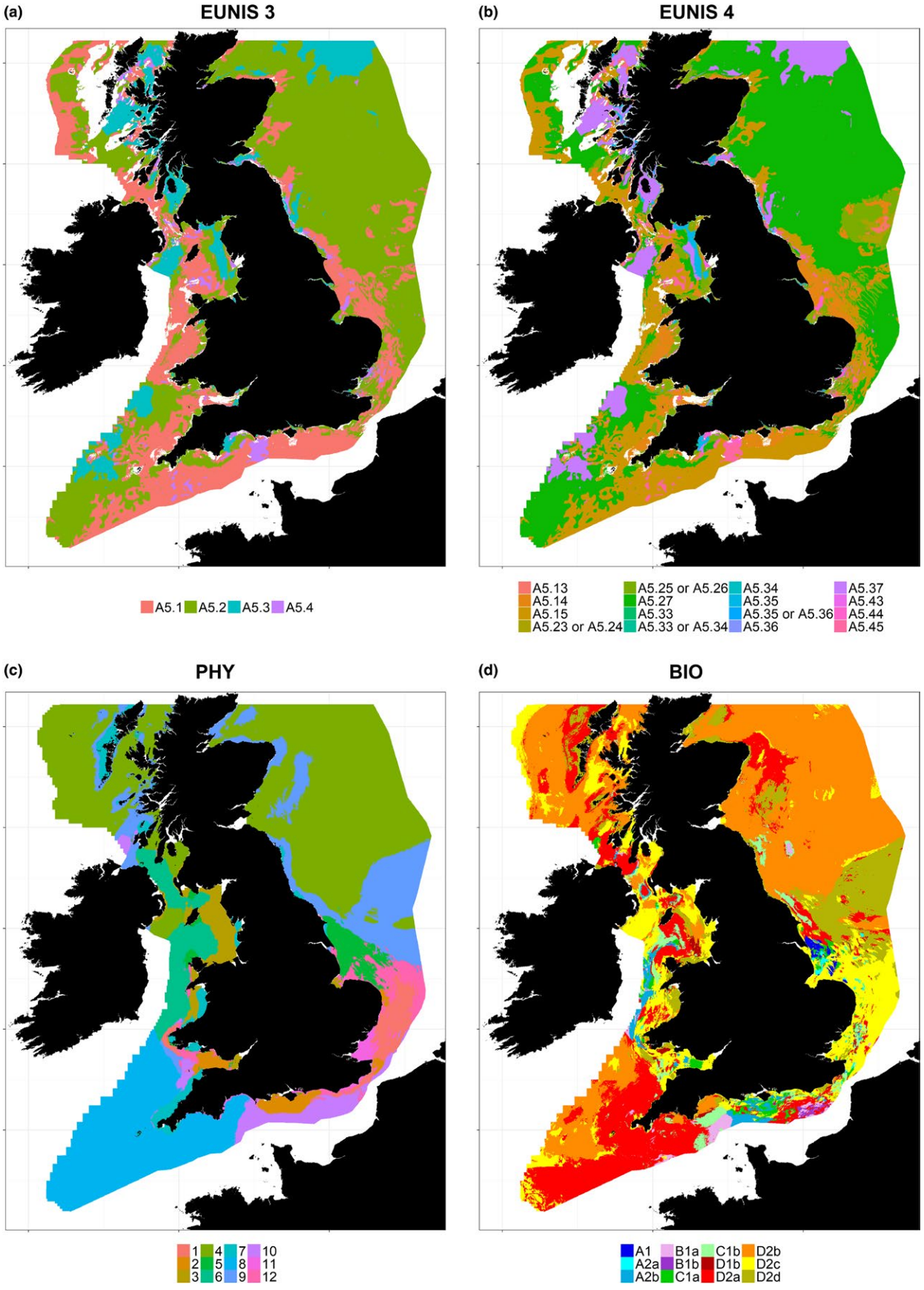

FIGURE 2 Habitat classification maps for: (a) EUNIS level 3 (EUNIS 3), (b) EUNIS level 4 (EUNIS 4), (c) Physical clusters derived in this study (PHY) and (d) faunal clusters (BIO). Habitat names for EUNIS codes are shown in supporting information Table S1

TABLE 2 Mean residual sum of squares by taxon richness and total abundance for habitat classification approaches EUNIS 3 and a simplified version of BIO, each with four habitat classes. Also shown are results for a RANDOM and OPTIMAL scenario. The values shown for the groups are the within group variances. Numbers of samples are shown in parentheses. The final row shows the MSS over all the groups. Note that for the RANDOM groupings, only the mean MSS over the 1,000 replicates is shown because the group values are different for each randomisation

GROUP	RANDOM	EUNIS 3	BIO	OPTIMAL
Richness				
1		437.8 (2,222)	507.5 (356)	26.3 (1,283)
2		163.3 (1,393)	323.0 (292)	26.5 (1,637)
3		121.3 (190)	326.5 (493)	37.3 (715)
4		306.1 (184)	231.2 (2,848)	96.7 (354)
MSS	378.9	320.6	274.0	34.5
Abundance				
1		211,448.6 (2,222)	331,829.1 (356)	5,530.4 (3491)
2		104,440.3 (1,393)	15,650.9 (292)	41,175.8 (428)
3		14,564.5 (190)	189,635.6 (493)	4,330,427.7 (8)
4		120,755.2 (184)	141,429.6 (2,848)	262,489.6 (62)
MSS	163,307.9	160,405.9	155,002.4	20,859.4

of each of the 12 assemblage types are provided in supporting information Table S1. Test set samples (see section 2.2.2) showed the modelled layer correctly predicted the faunal group association in 59% of cases, with a further 12% matched to the nearest cluster group (see faunal dendrogram in Cooper & Barry, 2017a). Whilst defined boundaries are based solely on the macrofauna data, it is possible to describe the habitat characteristics (physical parameters) associated with each of the 12 groups using information presented in the boxplots shown in supporting information Figure S2. For instance, faunal cluster group D2b, widely found across the northern North Sea and Celtic Shelf, is typically associated with deep water, low bottom temperature, muddy habitats with low bottom current flows, high salinity and low chlorophyll.

TABLE 3 Mean residual sum of squares by taxon richness and total abundance for habitat classification approaches EUNIS 4, PHY and BIO, each with 12 habitat classes. Also shown are results for a RANDOM and OPTIMAL scenario. The values shown for the groups are the within group variances. Numbers of samples are shown in parentheses. The final row shows the MSS over all the groups. Note that for the RANDOM groupings, only the mean MSS over the 1,000 replicates is shown because the group values are different for each randomisation

GROUP	RANDOM	EUNIS 4	PHY	BIO	OPTIMAL
Richness					
1		314.0 (45)	321.4 (606)	669.3 (66)	3.0 (329)
2		466.5 (945)	421.7 (374)	438.5 (106)	3.1 (567)
3		414.3 (1,232)	241.3 (271)	373.7 (184)	5.1 (196)
4		127.2 (127)	128.9 (262)	325.7 (149)	1.9 (226)
5		159.2 (604)	610.1 (427)	313.9 (143)	4.0 (586)
6		165.1 (662)	433.8 (111)	370.8 (248)	46.8 (34)
7		216.9 (9)	207.4 (107)	264.7 (245)	4.0 (469)
8		95.7 (49)	224.3 (250)	273.6 (130)	7.9 (187)
9		29.3 (8)	117.2 (480)	251.6 (547)	3.9 (614)
10		111.5 (124)	407.2 (571)	94.0 (380)	15.5 (111)
11		416.4 (72)	229.5 (144)	210.3 (1,266)	3.9 (214)
12		223.0 (112)	135.1 (386)	111.7 (525)	2.1 (456)
MSS	378.1	315.9	303.1	235.6	4.3
Abundance					
1		26,222.9 (45)	193,717.8 (606)	497,474.7 (66)	4,242.0 (91)
2		352,717.0 (945)	63,336.3 (374)	387,413.0 (106)	121,398.3 (14)
3		102,999.1 (1,232)	358,957.2 (271)	172,755.1 (184)	26,102.5 (28)
4		338,896.8 (127)	7,908.9 (262)	20,551.3 (149)	174.0 (1,432)
5		147,566.8 (604)	751,421.3 (427)	10,493.7 (143)	549.7 (383)
6		19,309.6 (662)	17,147.7 (111)	108,758.2 (248)	1,741.2 (176)
7		31,515.2 (09)	19,761.1 (107)	271,855.0 (245)	6,760.6 (57)
8		17,729.2 (49)	6,396.9 (250)	730,709.6 (130)	4,330,427.7 (8)
9		2,627.9 (8)	16,585.4 (480)	226,604.7 (547)	271.8 (958)
10		10,696.8 (124)	19,310.1 (571)	48,520.1 (380)	1,011.9 (212)
11		246,029.6 (72)	123,168.7 (144)	85,243.0 (1,266)	394.6 (598)
12		31,299.8 (112)	31,929.9 (386)	90,612.9 (525)	13,135.7 (32)
MSS	162,973.6	157,617.8	154,009.3	148,921.1	8,833.4

TABLE 4 Number of samples required (n_{req}) to detect a 20% change in mean levels of taxon richness and total abundance for each habitat class as defined by the four different seabed classification approaches. Assessment based on power analysis for a two-sided, two sample *t* test (power = 0.9 and significance level = 0.05). *n* = total number of samples in test dataset for each habitat, delta = change to be detected (20% *of* mean value), *SD* = standard deviation. Also shown are coefficients of variation (CV) and outputs from SIMPER analysis showing the within group percentage similarity

			Taxon richness						Total abundance						Assemblage Sim	
Classification	Group	*n*	Mean	SD	CV	delta	n_{req}	Total n_{req}	Mean	SD	CV	delta	n_{req}	Total n_{req}	%	Mean %
EUNIS 3	A5.1	2,222	33.9	20.9	0.62	6.8	202	759	214.3	459.8	2.15	42.9	1077	4,329	23.82	23.93
	A5.2	1,393	17.9	12.8	0.71	3.6	268		105.2	323.2	3.07	21.0	1,072		19.23	
	A5.3	190	20.9	11.0	0.53	4.2	148		107.5	120.7	1.12	21.5	926		27.06	
	A5.4	184	34.0	17.5	0.52	6.8	141		248.9	347.5	1.40	49.8	1,254		25.60	
BIO	A	356	47.5	22.5	0.47	9.5	120	587	447.4	576.0	1.29	89.5	1,010	3,240	33.46	30.86
(simplified)	B	292	49.4	18.0	0.36	9.9	71		187.9	125.1	0.67	37.6	309		42.80	
	C	493	36.1	18.1	0.50	7.2	133		220.5	435.5	1.97	44.1	818		28.57	
	D	2,848	21.5	15.2	0.71	4.3	263		128.5	376.1	2.93	25.7	1,103		18.64	
EUNIS 4	A5.13	45	20.6	17.7	0.86	4.1	389	3,375	99.0	161.9	1.64	19.8	970	13,539	21.76	24.00
	A5.14	945	34.4	21.6	0.63	6.9	208		286.3	593.9	2.07	57.3	1,254		24.21	
	A5.15	1,232	33.9	20.4	0.60	6.8	190		163.2	320.9	1.97	32.6	891		25.34	
	A5.23 or A5.24	127	15.3	11.3	0.74	3.1	288		176.3	582.1	3.30	35.3	1,514		21.93	
	A5.25 or A5.26	604	16.1	12.6	0.78	3.2	325		112.1	384.1	3.43	22.4	1,200		20.18	
	A5.27	662	20.1	12.9	0.64	4.0	215		85.3	139.0	1.63	17.1	874		20.07	
	A5.33	9	26.8	14.7	0.55	5.4	160		210.8	177.5	0.84	42.2	1,035		24.97	
	A5.35	49	21.2	9.8	0.46	4.2	114		154.5	133.2	0.86	30.9	840		33.94	
	A5.36	8	3.9	5.4	1.40	0.8	1,025		21.3	51.3	2.41	4.3	1,649		12.59	
	A5.37	124	21.4	10.6	0.49	4.3	129		87.0	103.4	1.19	17.4	489		30.96	
	A5.44	72	30.2	20.4	0.68	6.0	242		347.7	496.0	1.43	69.5	2211		22.37	
	A5.45	112	36.4	14.9	0.41	7.3	90		185.3	176.9	0.95	37.1	612		29.64	
PHY	1	606	25.6	17.9	0.70	5.1	259	2,907	176.1	440.1	2.50	35.2	1,279	11,982	22.81	25.82
	2	374	31.3	20.5	0.66	6.3	227		182.9	251.7	1.38	36.6	1,404		23.81	
	3	271	24.3	15.5	0.64	4.9	217		230.7	599.1	2.60	46.1	1,280		23.70	
	4	262	26.9	11.4	0.42	5.4	95		98.7	88.9	0.90	19.7	334		31.34	
	5	427	36.4	24.7	0.68	7.3	244		418.7	866.8	2.07	83.7	1,579		26.12	
	6	111	37.2	20.8	0.56	7.4	166		152.8	130.9	0.86	30.6	800		29.49	
	7	107	23.4	14.4	0.62	4.7	201		139.4	140.6	1.01	27.9	899		25.71	

(Continues)

TABLE 4 (Continued)

			Taxon richness						Total abundance						Assemblage Sim	
Classification	Group	*n*	Mean	SD	CV	delta	n_{req}	Total n_{req}	Mean	SD	CV	delta	n_{req}	Total n_{req}	%	Mean %
	8	250	28.3	15.0	0.53	5.7	149		94.2	80.0	0.85	18.8	454		27.17	
	9	480	22.0	10.8	0.49	4.4	129		101.9	128.8	1.26	20.4	472		28.06	
	10	571	41.0	20.2	0.49	8.2	129		159.6	139.0	0.87	31.9	639		33.42	
	11	144	16.3	15.1	0.93	3.3	458		198.7	351.0	1.77	39.7	1,807		19.11	
	12	386	10.6	11.6	1.10	2.1	633		58.4	178.7	3.06	11.7	1035		19.09	
BIO	A1	66	61.9	25.9	0.42	12.4	93	1,717	780.6	705.3	0.90	156.1	1,192	9,368	41.75	32.59
	A2a	106	38.6	20.9	0.54	7.7	156		529.7	622.4	1.17	105.9	1,364		32.91	
	A2b	184	47.5	19.3	0.41	9.5	88		280.5	415.6	1.48	56.1	599		37.67	
	B1a	149	51.4	18.0	0.35	10.3	66		196.5	143.4	0.73	39.3	315		42.06	
	B1b	143	47.3	17.7	0.37	9.5	75		178.9	102.4	0.57	35.8	274		44.36	
	C1a	248	33.1	19.3	0.58	6.6	179		206.0	329.8	1.60	41.2	939		26.11	
	C1b	245	39.1	16.3	0.42	7.8	92		235.2	521.4	2.22	47.0	622		33.68	
	D1	130	32.8	16.5	0.50	6.6	135		389.9	854.8	2.19	78.0	1,320		28.38	
	D2a	547	30.4	15.9	0.52	6.1	145		145.0	476.0	3.28	29.0	562		26.25	
	D2b	380	27.7	9.7	0.35	5.5	66		154.7	220.3	1.42	30.9	428		32.14	
	D2c	1,266	15.2	14.5	0.95	3.0	479		94.0	292.0	3.11	18.8	1,280		16.30	
	D2d	525	20.4	10.6	0.52	4.1	143		111.0	301.0	2.71	22.2	473		29.48	

3.2 | Habitat classifications and biological variability

Values of MSS (Tables 2 and 3) suggest that variability for taxon richness and total abundance was lower within all habitat classification approaches than for the random scenario. Furthermore, the values of MSS over all groups for all the classification methods (EUNIS 3, BIO for 4 groups; EUNIS 4, PHY and BIO for 12 groups) are all statistically significantly different ($p \approx 0.001$) to the random allocations (i.e., none of the 1,000 random MSS values were lower than the observed classification value). Thus, all four approaches, albeit to varying degrees, provide some reduction in variability relative to a random scenario. However, variability in both richness and abundance was noticeably lower for BIO in comparison with EUNIS 3 and EUNIS 4. Whilst improving on EUNIS 4 (richness only), variability within the PHY classification was still higher than for BIO (Table 3).

Coefficients of variation for richness and total abundance by habitat class were generally higher for EUNIS and lower for BIO, with intermediate values seen for PHY (Table 4, Figures 3a and 3b). Irrespective of the habitat classification approach, total abundance was much more variable than taxon richness.

In terms of assemblage composition (i.e., taxon identity), SIMPER analysis showed generally lower levels of within group similarity for EUNIS compared to BIO, with intermediate levels for PHY (Figure 3c). In other words, within-habitat variability in macrofaunal assemblage composition is reduced for the BIO classification compared with PHY and especially EUNIS.

3.3 | Power analysis

Of all the habitat classification approaches, power analysis shows that EUNIS would require the highest number of samples to detect a

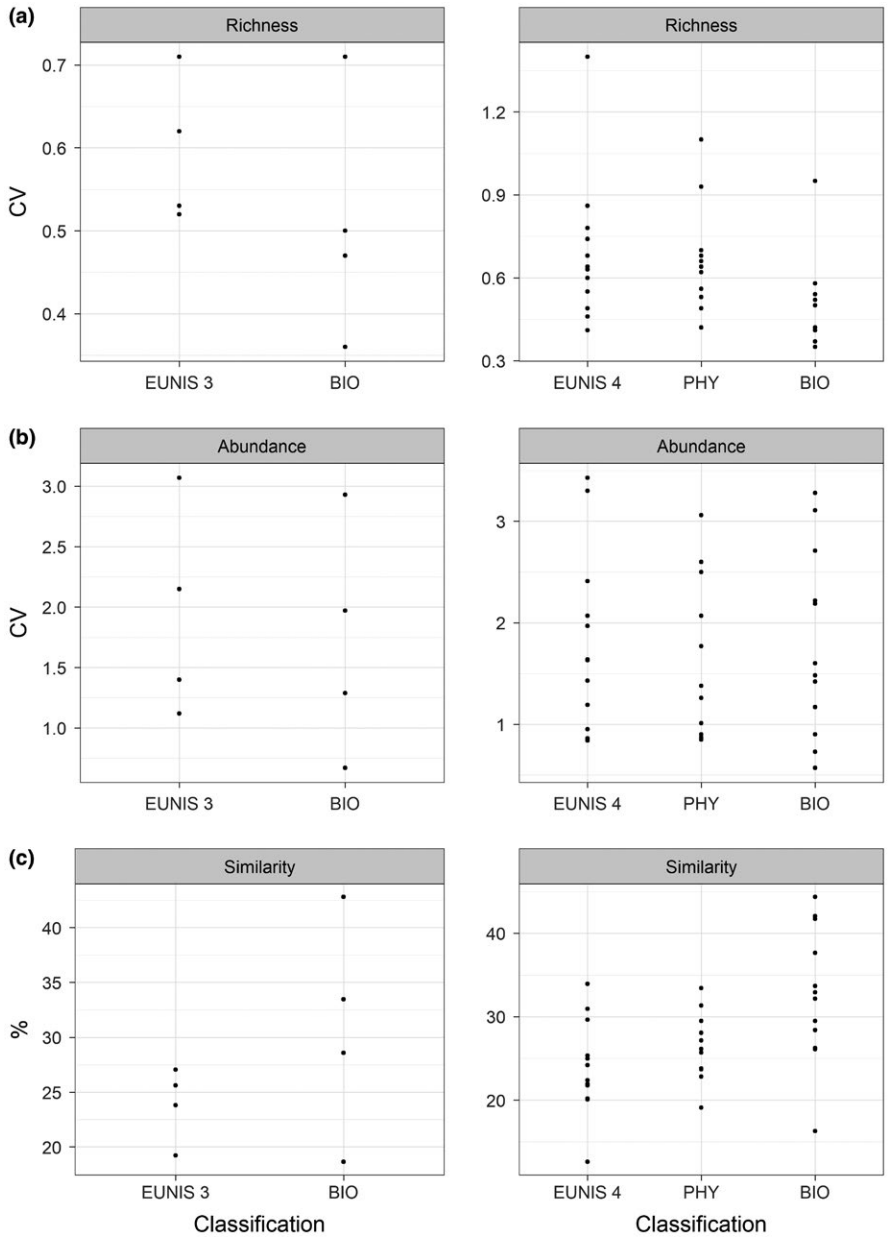

FIGURE 3 Variability within habitat classes based on: (a) coefficient of variation for taxon richness, (b) coefficient of variation for total abundance and (c) multivariate assemblage similarity. Left side plots relate to the EUNIS 3—BIO comparison, whilst right side plots relate to the comparison of EUNIS 4, PHY and BIO classifications

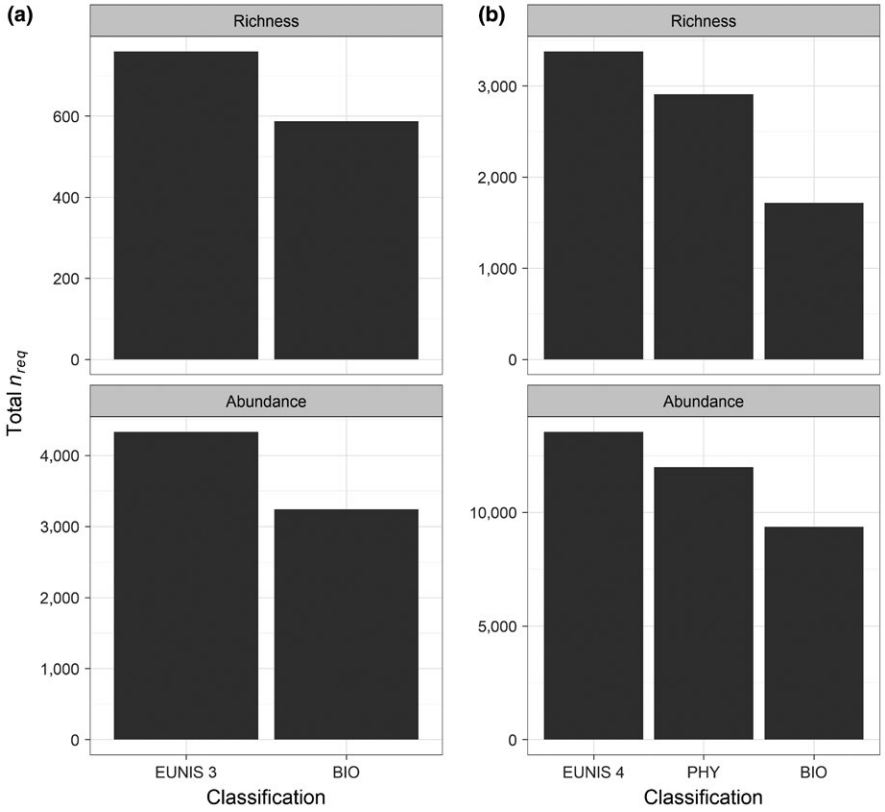

FIGURE 4 Bar charts showing the total number of samples (n_{req}) required to detect an arbitrary 20% change in taxon richness (top) and total abundance (bottom) across all habitat classes of different habitat classification approaches. Part (a) relates to the EUNIS 3 - BIO comparison (four habitat classes), whilst part (b) relates to the comparison of EUNIS 4, PHY and BIO classifications (12 habitat classes)

20% change in taxon richness and total abundance across all habitat classes (Table 4, Figure 4).

For the EUNIS 3—BIO comparison, the number of samples required to detect a 20% change in taxon richness and abundance would be 759 and 4,329 for EUNIS 3 and 587 and 3,240 for BIO. Thus, sampling effort under BIO would be 23% and 25% lower for richness and abundance respectively (Figure 4a).

For the EUNIS 4—BIO comparison (i.e., the 12 habitat approaches), the number of samples required to detect a detect a 20% change in taxon richness and abundance would be 3,375 and 13,539 for EUNIS 4 and 1,717 and 9,368 for BIO. Thus, sampling effort under BIO would be 49% and 31% lower for richness and abundance respectively (Figure 4b).

Whilst offering some improvement on EUNIS 4, the number of samples required to detect a 20% change in taxon richness and abundance using PHY was still 35% and 19% higher than for BIO (Figure 4b).

4 | DISCUSSION

A habitat classification approach based on biology reduces within-habitat variability, in terms of taxon richness, total abundance and multivariate similarity. As a result, fewer samples are generally required to detect a comparable magnitude of change. Compared to EUNIS 4, the faunal (BIO) classification approach required 49% fewer samples to detect a 20% change in taxon richness and 31% fewer samples to detect a 20% change in total abundance. Despite the inclusion of a greater number of variables considered to be important for structuring benthic faunal communities, the habitat classification based on clustering of physical variables (PHY) offered little improvement upon the UKSeaMap EUNIS approach. Several previous studies have highlighted problems with the EUNIS classification system, and the extent to which it is able to discriminate between different seabed faunal assemblages (Galparsoro et al., 2012). Despite these issues the system continues to be widely used, underpinning the identification of MPAs and their associated habitats and marine monitoring.

The lower number of samples required to detect change using the faunal cluster (BIO) classification map can be explained by lower variability in taxon richness and total abundance, although the generally lower group means and thus values of delta under EUNIS, may also be a factor. However, it is important to note that the lower group means for certain EUNIS classes can be explained by the inclusion of multiple assemblage types, both rich and sparse, within the same EUNIS class (Figures 5a and b). For instance, both EUNIS classes A5.1 (Sublittoral coarse sediment) and A5.4 (Sublittoral mixed sediments) include all 12 faunal cluster classes from highly diverse A1 assemblages (mean taxon richness = 70, mean abundance = 1,122) through to sparse D2c assemblages (mean taxon richness = 8, mean abundance = 26). The same issue arises for the PHY classification, although perhaps to a lesser extent (Figure 5c). This contrasts to the BIO classification where each class tends to have a more dominant assemblage type (Figure 5d). Thus, it is fundamentally the differences in the capacity of the various approaches to capture the true variability in macrofaunal assemblages into discrete habitats which is responsible for the observed differences in power to detect change.

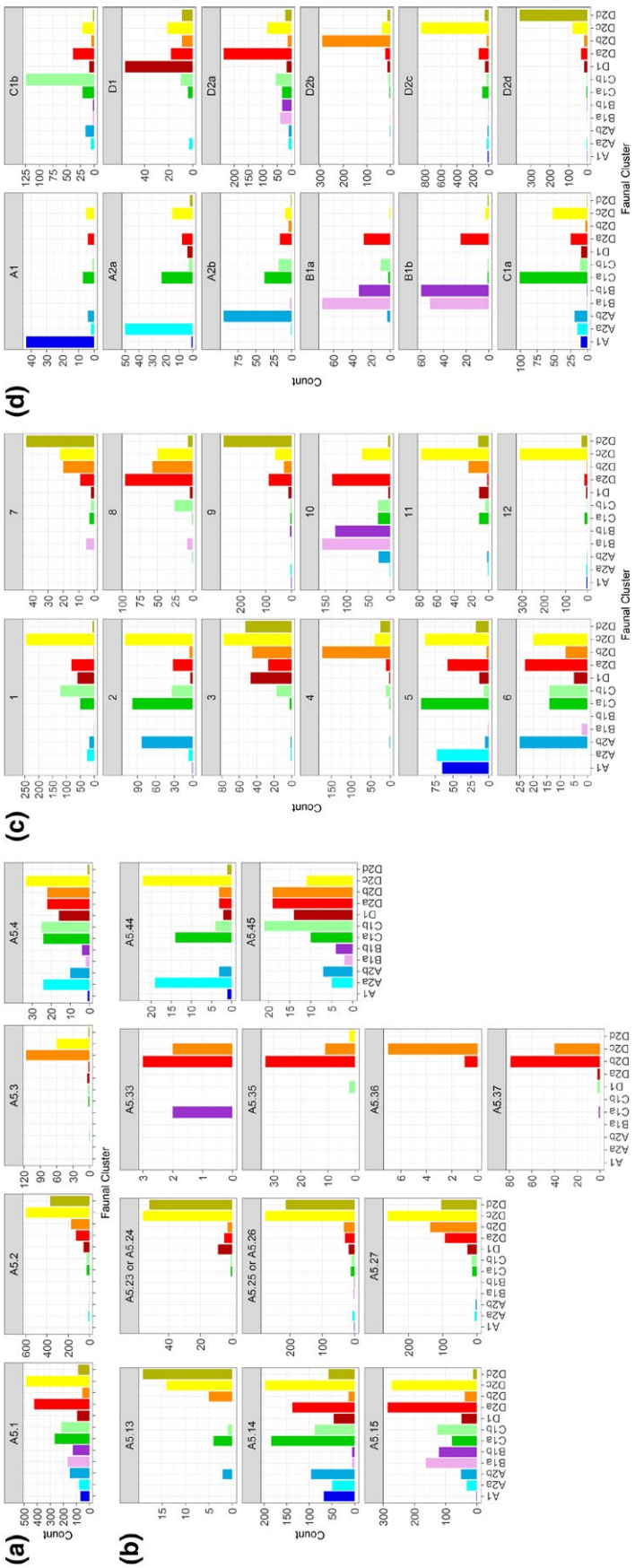

FIGURE 5 Faunal assemblage type (identified from clustering) by habitat class for: (a) EUNIS 3, (b) EUNIS 4, (c) Physical clusters (PHY) and (d) Faunal clusters (BIO). Note the dominance of a single assemblage type for most BIO classes. This contrasts to EUNIS and PHY where habitat classes often include multiple assemblage types

It is important to acknowledge limitations associated with this study. Firstly, the full coverage faunal assemblage habitat map produced here required significant quantities of suitable benthic data. While this is possible for the well-studied UK shelf, sufficient data are unlikely to be available for most regions of the world. It is likely therefore that traditional physical-based habitat maps will continue to be used to infer benthic faunal distribution patterns. The challenge therefore must be to find new ways of classifying the physical data such that identified "habitats" are more biologically relevant (e.g., Hill et al., 2017; Valesini, Wildsmith, & Tweedley, 2018). Secondly, we believe the macrofaunal model could be enhanced through improvement of the raster layers, particularly for sediments. An initiative to do this is already underway through the European Emodnet programme (see http://www.emodnet.eu/).

Findings from this study are important as they suggest that adopting a more biologically based habitat map could greatly improve our ability to detect change and significantly reduce the costs of ecological monitoring programmes. The biologically-driven habitat map could also assist with marine spatial planning (Douvere, 2008), environmental impact assessment and nature conservation efforts. For example, it will be much easier to gauge the likely significance of a development where there is a knowledge of spatial extent of communities and of how changes in physical metrics are likely to alter the biology (Cooper & Barry, 2017a). In addition, in the UK such a classification scheme may facilitate the development of a coherent network of marine protected areas that adequately represents the known faunal assemblages. Finally, results from power analysis can help identify which habitat classes (particularly for the biologically-driven habitat classification approach) are most efficiently monitored (i.e., those with the greatest chance of detecting change for a given sampling effort). In addition, the improved understanding of seabed faunal distribution presented in this study allows for monitoring of particular taxa or assemblages of interest. Clearly it will be important to consider implications for existing time series when deciding whether to adopt this new habitat map.

Despite the impressive model results with 59% of samples correctly assigned to macrofaunal cluster groups, and 71% to the correct or nearest group, the performance of the random forest biology model could be improved. Updating sediment raster layers with newly acquired data and incorporating measures of population connectivity and species interactions into spatial clustering are means of addressing this. Additionally, it would be sensible to assess whether the outcomes of the current analysis using taxon richness and total abundance applies to a wider suite of indicator metrics, particularly those used in monitoring programmes to assess assemblage status.

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AUTHORS' CONTRIBUTIONS

K.M.C. and S.G.B. conceived the ideas and designed the methodology, assisted by J.B. and A.-L.D.; K.M.C. collected the data; K.M.C., J.B. and A.-L.D. analysed the data; K.M.C. and S.G.B. led the writing of the manuscript. All authors contributed critically to the drafts and gave final approval for publication.

DATA ACCESSIBILITY

The dataset used in this study is available from the Cefas Data Hub https://doi.org/10.14466/cefasdatahub.34 (Cooper & Barry, 2017b). R script and supporting files are also available from the Cefas Data Hub https://doi.org/10.14466/cefasdatahub.56 (Cooper et al., 2019).

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SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of the article.

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