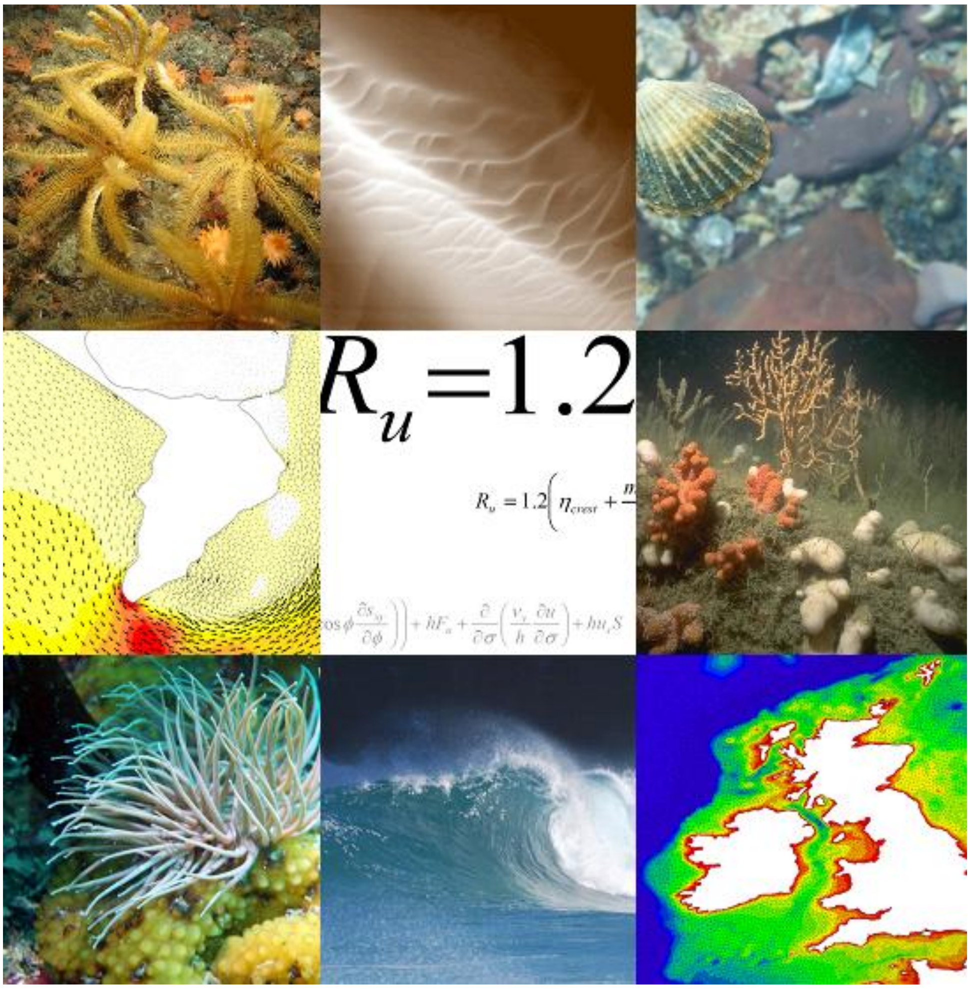
Accessing and developing the required biophysical data sets and data layers for Marine Protected Areas network planning and wider marine spatial planning purposes

Task 2F - Development of a marine diversity data layer: review of approaches and proposed method

16 September 2009



Proudman Oceanographic Laboratory
NATURAL ENVIRONMENT RESEARCH COUNCIL

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Project Title: Accessing and developing the required biophysical data sets and data layers for Marine Protected Areas network planning and wider marine spatial planning purposes

Report 2: **Task 2F - Development of a marine diversity data layer: review of approaches and proposed method**

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Executive summary

The UK is committed to the establishment of a network of marine protected areas (MPAs) to conserve marine ecosystems and marine biodiversity. MPAs are a valuable tool to protect rare and threatened species and the integrity and functioning of habitats. They can also be used to aid implementation of the Ecosystem Approach to management, which aims to maintain the ecosystem goods and services produced by the normal functioning of the marine ecosystem that are relied on by humans (Smith & Maltby 2003).

A consortium[1] led by ABPmer has been commissioned to develop a deliver a series of biophysical data layers to aid in the selection of a network of Marine Conservation Zones (MCZs) in England and Wales (and the equivalent MPA measure in Scotland) under the Marine and Coastal Access Bill (Contract Reference: MB0102). These data layers will also be of wider use for taking forward marine planning in UK waters.

The overall aim of the project is to ensure that the best available information is obtained for the selection of MPAs in UK waters, and that these data layers can be easily accessed and utilised by those who will have responsibility for selecting sites. The project has been divided into a number of tasks, one of which was to review and assess approaches for the development of a 'marine biodiversity' data layer[2]. The identification of areas of high marine biodiversity is important to aid the conservation of structurally and functionally important areas, but may also enable the cost effective prioritisation of areas for protection.

This report provides a critical review of approaches to identify areas of high marine biodiversity and how these can be used to inform the selection of MPAs. *Biodiversity area* is used here to describe areas of species and habitat diversity. The various measures to quantify marine diversity are critically reviewed (e.g. diversity indices, number of species, number of priority species and taxonomic distinctness). The review highlights the limits of data quality and coverage and considers techniques for effort standardisation and validation (assigning confidence) that are fundamental for interpretation of variable data. Particularly in the pelagic and offshore benthic environments appropriate data are so limited that proxy indicators of diversity are required, since data for directly assessing diversity do not exist. We also review past uses of the term *biodiversity hotspots* and explore issues involved with employing this approach to UK waters.

Based on the conclusions of the review, it is recommended that no single layer adequately represents marine biodiversity and it is proposed that a series of layers are developed. These are presented according to data availability, suitability to represent overall biodiversity and conservation management constraints, and cost effectiveness.

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[1] ABPmer, MarLIN, Cefas, EMU Limited, Proudman Oceanographic Laboratory (POL) and Bangor University

[2] The layer was originally to be called Biodiversity hotspot layer, however, because the it will be presented as a continuous scale of diversity, without predefined levels of what is diverse the layer has been renamed a 'marine diversity data layer'.

For the UK benthos, the most appropriate (suitable for variable data sets) and comprehensive measures (encompassing diversity at different organisational levels) are species and habitat richness, taxonomic distinctness and habitat distinctness. Species and habitat richness are the most commonly recorded units of diversity and do not require abundance data, which can add a significant bias when handling data from multiple sources. Similarly taxonomic distinctness can be calculated without abundance data and provides additional information on the phylogenetic diversity of a site which is arguably more meaningful in terms of maintaining ecosystem function.

Biodiversity assessment is arguably less developed in the pelagic realm; it presents different challenges to the benthos due its inherent mobility and variability over a range of spatial and temporal scales, and because data to directly assess diversity are scarce. A series of metrics spanning different levels of ecological organisation were examined encompassing direct measures of diversity for different ecosystem components, satellite earth observation surrogate measures and indicators such as pelagic megafauna. It was concluded that many of the measures previously advocated as indicators of pelagic diversity (e.g. productivity or single species distributions) have insufficient scientific evidence supporting their relationship with overall pelagic diversity at the scale under consideration. Thermal fronts data however, has good spatial coverage and has been correlated with pelagic top predator diversity (a large scale indicator of pelagic biodiversity) and is recommended as an appropriate surrogate.

We propose an approach for future work to assess the marine biodiversity of UK waters that considers the pelagic and benthic realms separately (as they are reviewed here), but entails a common set of steps (although individual data layers will require separate methodologies):

1. examining and collating the available data;
2. data quality assessment and filtering;
3. selection of appropriate spatial scale;
4. analysing the data;
5. standardising for sampling effort (Monte Carlo techniques and regression if appropriate); and
6. validation and confidence assessment.

For the benthos separate analyses for the intertidal and subtidal inshore are proposed at different grid scales. For these regions, the assessment will focus on all macrobenthic species (but excluding fish) and habitats data, and will utilise actual records of species and habitats (including data collated as part of tasks 2B and 2C). Data will be grouped into broad collection methodology following quality assessment and filtering, before calculating the diversity metrics and carrying out other standardisation techniques.

For the pelagic biodiversity surrogate data layer, the proposed approach is to exploit a long term time series of EO SST data to map persistently occurring thermal fronts in UK waters. Initially, monthly maps at 1km resolution would be generated, and the second stage would be to aggregate these into seasonal front climatologies to identify strong, persistent and frequently occurring features, which would be presented along with their confidence.

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Introduction

1.1 Biophysical Data layers Project

1.1 The UK is committed through international agreements and European obligations to the establishment of a network of Marine Protected Areas (MPAs) to conserve marine ecosystems and marine biodiversity. The UK Government has also made a commitment under the Marine and Coastal Access Bill to take forward a network of Marine Conservation Zones (MCZs) to conserve and promote the recovery of a wide range of habitats and species. The Scottish Government is also considering equivalent provisions for its waters out to 200nm.

1.2 A consortium[3] led by ABPmer has been commissioned to develop a deliver a series of biophysical data layers to aid in the selection of a network of Marine Conservation Zone (MCZ) in England and Wales (and the equivalent MPA measure in Scotland) under the Marine and Coastal Access Bill (Contract Reference: MB0102). These data layers will also be of use in taking forward marine planning in UK waters. The overall aim of the project is to ensure that the best available information is available for the selection of MPAs in UK waters, and that these data layers can be easily accessed and utilised by those who will have responsibility for selecting sites. New Geographical Information System (GIS) data layers to be developed included:

- geological and geomorphological features;
- listed habitats;
- fetch and wave exposure;
- marine diversity layer;
- benthic productivity; and
- residual current flow.

1.1 The current report provides a detailed review on approaches available for the development of a marine diversity layer, and recommendations for a preferred approach and methodology.

1.2 Aims and Objectives for Marine Diversity Layers Task

1.2 The aim of this task was to identify and review current approaches available for the development of a marine diversity areas data layer of UK waters. The key aims of this element of the contract were:

- To complete an objective review of the current approaches available for the generation of marine diversity layers, identifying their strengths and weaknesses and any refinements/modifications required; and

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[3] ABPmer, MarLIN, Cefas, EMU Limited, Proudman Oceanographic Laboratory (POL) and Bangor University

- To present the review in a clear report that includes an assessment of the value (and use) of creating a marine diversity data layer for MPA site selection.

1.3 It is important that the methods developed to identify areas of biodiversity are widely reviewed and agreed by the scientific community in order to add rigor and support to the identification of MPAs, and marine nature conservation in the UK. This was first achieved through a workshop held on the 8th January 2009 in London (see transcript in Appendix 1) where methods for identifying marine biodiversity with the data available were critically discussed, and subsequently through individual feedback with selected experts. In addition, this report has been subjected to both internal and anonymous external review.

1.3 Format of Report

1.4 This report is divided into two main sections:

- a review section, examining past approaches for defining and identifying areas of biodiversity; and
- a section proposing an approach for the UK.

1.5 The review first discusses the rationale for identifying areas of high diversity. We review methods used to define areas of diversity, by examining first the evolution of the term “biodiversity hotspots”, its definition and then questioning what is a representative measure of diversity. Following on from this is a section which examines past approaches to the identification of high diversity areas and which highlights methodological issues regarding the units of measurement (metrics) used to show diversity. The report investigates extensions of current methodologies to offshore, data-poor environments and the pelagic realm, and then, in the second section, proposes the most appropriate methods and data needs for identifying marine biodiversity in UK territorial waters (inshore waters of England, Wales, Northern Ireland, Scotland and UK Offshore waters).

2 Background: Defining Areas of Diversity

2.1 Biodiversity (originally “biological diversity”) is quite a recent term. It is thought to have been first used officially in the USA during the "National Forum on Biodiversity," which took place in September 1986 under the patronage of the National Academy of Science and the Smithsonian Institute in Washington DC (Wilson 1988).

2.2 "Biodiversity" gained political meaning in 1992 at the United Nations Earth Summit in Rio de Janeiro, where 150 states (including the UK) signed the Convention on Biological Diversity (United Nations Convention on Biological

Diversity, CBD). The CBD defined biodiversity as "the variability among living organisms from all sources, including, *'inter alia'*, terrestrial, marine, and other aquatic ecosystems, and the ecological complexes of which they are part: this includes diversity within species, between species and of ecosystems". This is, in fact, the closest thing to a single legally accepted definition of biodiversity.

2.3 Under this definition, biodiversity includes richness at all levels from landscapes to genes (Godfray & Lawton 2001, Gaston & Spicer 2004) . Within that range of ecological scale, species richness and variety of habitats tend to be the most common measures to identify high areas of diversity for conservation management (Ward et al. 1999).

2.1 Rationale for identifying areas of diversity

2.4 Biological diversity is central to the Ecosystem Approach[4], the integrated management of human activities, based on knowledge of ecosystem dynamics, to achieve sustainable use of ecosystem goods and services, and maintenance of ecosystem integrity (Convention of Biological Diversity 1992). It has been proposed that the identification and protection of areas of marine biodiversity can contribute to the Ecosystem Approach to management of our seas (Prendergast et al. 1993, Ward et al. 1999). Biodiversity is also, arguably, the ultimate measure of ecosystem health (Leonard et al. 2006). Identifying which areas are the most valuable for biodiversity may also help enable the cost-effective prioritisation of areas for protection.

2.5 Marine biodiversity is beneficial to the preservation of a wide spectrum of important ecosystem services, sustained through a number of ecological mechanisms which link biodiversity to ecosystem functioning (see review by (Palumbi et al. 2009). These include fisheries, water quality and recreation, but also the resilience of the ecosystem to continue providing these services under increasing human pressure (Costanza et al. 1997, Fisher & Kerry Turner 2008).

2.6 Greater diversity of species within a species pool is likely to result in a greater diversity of traits (for example different modes of feeding, reproduction, growth, survival etc.) and hence functional groups, which affects ecosystem processes through niche complementarity and dominance of particular subsets of complementary species (Loreau et al. 2001, and Figure 1)

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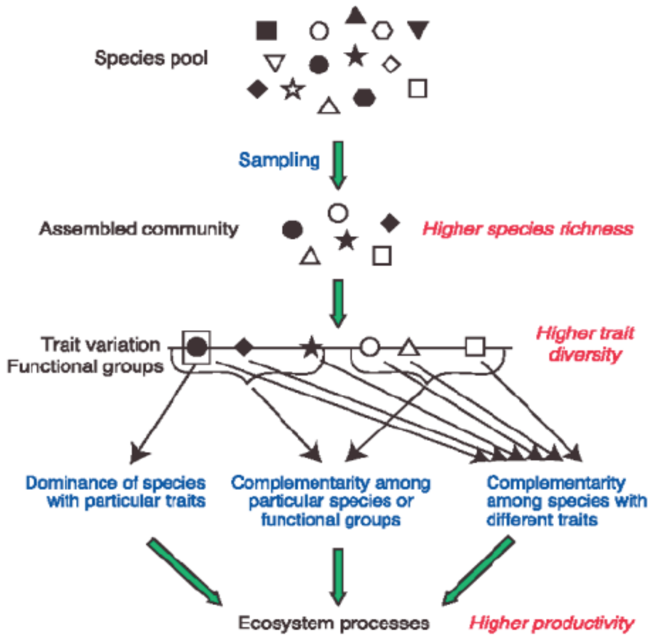
[4] The Ecosystem Approach is a strategy for the integrated management of land, water and living resources that promotes conservation and sustainable use in an equitable way. It was endorsed at the fifth Conference of the Parties to the Convention on Biological Diversity (CoP 5 in Nairobi, Kenya; May 2000/Decision V/6) as the primary framework for action under the Convention (IUCN, 2008).



Sampling in species pool assembly

→ more species likely to = more diversity in traits

→ trait diversity affects ecosystem processes through both niche complementarity and dominance

i.e. intermediate scenarios

[Complementarity may occur over larger spatial and temporal frames]

Figure 1 Hypothesized mechanisms linking biodiversity and ecosystem functioning (Source: Loreau et al. 2001)

2.7 Manipulative studies to address the impacts of reducing biodiversity suggest that a large pool of species is required to sustain the assembly and functioning of ecosystems subject to increasing human pressures (see review by Loreau et al. 2001). Whether dependence of ecosystem functioning on diversity comes from the need for recruitment of a few key species from the regional species pool (most productive marine ecosystems are typically characterized by low species diversity) or is due to the need for a rich assortment of complementary species within particular ecosystems (a detailed review of this is disputed, and beyond the scope of this study but see (Palumbi et al. 2009). Nonetheless there is broad agreement that diversity is important for reducing temporal variability in ecosystem functioning under changing environmental conditions (Kikkawa 1986, Schultze & Mooney 1993, Bengtsson 1998, Hooper et al. 2002, Bevilacqua et al. 2006). Diversity may also make a system less susceptible to invasive species because species-rich communities use available space, the limiting resource, more efficiently (Stachowicz et al. 1999).

2.2 Representative indicators of biodiversity

2.8 The Convention on Biological Diversity refers directly to ‘variability among living organisms’ and stresses that this includes diversity within species as well as between species. The relationship between variety within a species and the number of species in a genus was first identified by Darwin, and the rate at which species are formed and the relative abundance of species in ecological communities was made explicit within the neutral theory of biogeography (as cited by Magurran 2005). Research has continued over the decades to explore the relationship between genetic and species diversity and unravel the processes that underpin it (Vellend 2005).

2.9 At the other end of the scale, the relationships between habitat and landscape diversity (or heterogeneity) and species diversity have continued to be examined since Aldo Leopold first put forward his law of dispersion (principle of edge) in 1933 (Leopold 1933). Most studies have found a positive correlation between habitat heterogeneity and species diversity, although there is some dispute that empirical support is biased towards studies of vertebrates and habitats under anthropogenic influence (Tews et al. 2004). It could therefore be argued that whilst the most commonly accepted level for representing diversity are species, a measure of habitat diversity may be more representative of the whole community diversity of an area.

2.10 Species are by far the most common unit to represent biodiversity. In practice a convenient subset of the biota is usually assessed on the assumption that patterns in diversity of this subset correlate with overall biodiversity of the total species pool. This is conceptualized as surrogacy by Warwick & Clarke (2001) but we use the term surrogate measures later in this review to describe non-ecological physical surrogates. Apart from the obvious impracticalities of routinely sampling all species from microbes to mega fauna, it is also a reflection of management and conservation targets (i.e. few microbial or meiofaunal species appear on protected species lists).

2.11 A number of different multi-species surrogate measures for the total species pool have been proposed (**Table 1**). The correlation between these measures and total biodiversity however has only been tested in a few cases (Leonard et al. 2006).

2.12 Some studies have focussed on areas where the number of rare or declining species or habitats or other priority features is high; partly for cost effectiveness but also because it was assumed that by focusing on priority species there will be an effective umbrella for overall species richness area, which is not always the case (Bonn et al. 2002). Protecting structural or ecosystem engineer species may, however, be effective (Jones et al. 1997).

2.13 Additionally, biodiversity has been assessed using the biodiversity of certain groups (e.g. molluscs) as a proxy for the entire marine community diversity. This approach has the advantage that the group is stable taxonomically and fairly evenly recorded but they are not necessarily indicators of total diversity (Smith 2008). An extension of this approach is to use ‘death assemblages’ of shell-bearing molluscs, a technique often used to examine fossil records. In some cases a good relationship between the death assemblage and the diversity of the taxa in the area they originated from has been identified (Warwick & Light 2002), while others show inflated diversity compared with the living assemblage (Pandolfi & Greenstein 1997).

Table 1. Multi-species measures that have been proposed as surrogates for the biodiversity of the total species pool

Indicator	Comments	References
Selected taxa or taxon groups	Uses one or a subset of taxonomic groups (e.g. polychaetes, Malacostraca, sea birds, mammals, or sharks, that have well known taxonomy and are tractable to sample) to represent total biodiversity. This technique is well established in the terrestrial literature (e.g. Prendergast et al. 1993).	(Williams & Gaston 1994, Phillips 2001, Olsgard et al. 2003, Terlizzi et al. 2009)
Death assemblages	Use of the remains of shell-bearing molluscs (gastropods and bivalves) in sedimentary habitats to indicate diversity patterns in original living communities.	(Warwick & Light 2002, Smith 2008)
Gut contents of key predators	Uses the concept of predators as biodiversity collectors and assumes that their gut contents reflect the biodiversity of prey items available (unvalidated).	(Féral et al. 2003)
Large conspicuous species	Uses species that are conspicuous for visual census such as *Pinna nobilis* in *Posidonia* meadows, assuming a relationship between conspicuous and cryptic diversity.	(Féral et al. 2003)
Functional (e.g. trophic) diversity	Uses the diversity of functional groups to infer patterns in overall biodiversity. Functional diversity reflects the biological complexity of an ecosystem and it can be argued that functional diversity may in fact be the most meaningful way of assessing biodiversity while avoiding cataloguing all species in marine ecosystems. By focusing on processes, it may be easier to determine how an ecosystem can most effectively be protected and in the process of protecting biological functions, many of the species that perform them will also be protected.	(Steele 1991, Leonard et al. 2006)
Diversity of rare or endangered species	Uses the number of rare or threatened (priority) species or habitats as a surrogate for overall biodiversity. While this is not a true reflection of biodiversity, it can be a useful tool for managers to identify hotspots of priority features.	(Prendergast et al. 1993, Myers et al. 2000, Hiscock & Breckels 2007)
Endemic species	Due to fewer and weaker barriers to dispersal there are no marine species believed endemic to anywhere in the UK. It is therefore not an appropriate measure for assessing biodiversity hotspots in this instance	(Reid 1998, Myers et al. 2000, Phillips 2001, Hughes et al. 2002)

2.14 Genetic diversity is the variation in the amount of genetic information within and among individuals of a population, a species, an assemblage, or a community. It is reflected by the level of similarity or differences in the genetic makeup of individuals, populations and species. These similarities and differences may evolve as a result of many different processes e.g. chromosomal and/or sequence mutation, and physical or behavioural isolation of populations. Although genetic diversity is not always obvious, it is extremely important as it is a requisite for evolutionary adaptation to a changing environment. Genetic diversity can be thought of as an insurance, which allows adaptation to changing environmental conditions. Recently there have been concerns for the loss of genetic diversity in commercially important fish species could have an impact on fisheries (Smith 1994).

2.15 Microbial diversity on earth is estimated to be between 10^3 – 10^9 species (Pedrós-Alió 2006). In marine systems, the diversity of microbes is the key to their unique metabolisms that allow microbes to carry out many steps of the biogeochemical cycles that other organisms are unable to complete. The smooth functioning of these cycles is necessary for life to continue, not just in the oceans but on earth. While the diversity in taxonomy and function of marine microbes is recognised, little progress has been made to describe them formally (Pedrós-Alió 2006).

2.3 Metrics for measuring marine diversity

2.16 There is considerable controversy surrounding the most appropriate measure to identify areas of high diversity, both in terrestrial and marine systems (Possingham & Wilson 2005). Each metric has different data requirements and benefits and disadvantages for its use (Table 2) and we review the main ones here (see Magurran 2004, Gray & Elliott 2009 for more comprehensive reviews of measures of species diversity). Compounding this problem of selecting the most appropriate metric is the lack of similarity between different metrics (Orme et al. 2005).

2.17 Global taxonomic richness can be viewed at three different scales.

- Point diversity, which is the diversity of a single sample (Whittaker 1972).
- Within-community (α) diversity, which is the diversity of a particular area, usually expressed as the number of species in that ecosystem (Whittaker 1972, Hooper et al. 2002, Price 2002, Worm et al. 2003).
- β diversity is the comparison of diversity between ecosystems, often measured as the amount of species change (Whittaker 1972, Vanderklift et al. 1998, Hooper et al. 2002) and also known as turnover diversity (Magurran 2004).
- γ diversity is a measure of overall diversity within a large region (Whittaker 1972, Vanderklift et al. 1998, Hooper et al. 2002).

2.18 In addition, diversity can be measured at different levels of biological organization, from genes to landscape, although in practice, species and habitats are the most common units.

Table 2 Examples of the measures used to identify areas of biodiversity

Metric	Description	Strengths	Weaknesses	References
Species/ habitat richness	The number of different species / habitats in a given area.	• Low data requirements; easy to apply using presence absence data	• Does not convey spread in abundance. • Heavily influenced by sampling effort (a per-entity encounter rate) and will need to be standardised. • Relies on good species identification skills.	(Myers et al. 2000, Phillips 2001, Hughes et al. 2002, Price 2002, Worm et al. 2003, Hiscock & Breckels 2007)
Evenness	Conveys spread of dominance of species, so a site with one dominant species would be considered less diverse than one with more equal species abundance.	• Gives more information than species richness alone on how the community is structured.	• Requires abundance data which will be biased by sample size (area covered).	(Kati et al. 2004)
Diversity indices (e.g. H', Hills N)	Combines species richness and evenness.	• Many indices are sample-size robust beyond small numbers of samples.	• Require abundance data	(Kati et al. 2004)
Taxonomic or habitat distinctness	Represents phylogenetic or broad habitat diversity.	• Robust to sampling effort. • Ecologically meaningful and a potential proxy for ecosystem functional diversity	• Affected by scale and geographical scope.	(Clarke & Warwick 1998, Price 2002, Hiscock & Breckels 2007)

Metric	Description	Strengths	Weaknesses	References
Functional diversity	Currently no consensus on a measure to use for functional diversity. Taxonomic distinctness may be a useful approximation.	• Useful as meets a number of policy objectives	• No consensus on the measure to use.	(Leonard et al. 2006, Akpalu 2009)
Higher taxonomic diversity	Identification of individuals in samples to target taxon (phylum, class, order) and indices calculated from numbers of taxa and/or relative abundance.	• Quicker/cheaper to process samples to lower taxonomic resolution	• This technique has not been validated for biodiversity, only for environmental health.	(Heip et al. 1988, Williams & Gaston 1994, Gaston & Blackburn 1995, Roy et al. 1996)
Rarefaction/ Accumulation curves	Allows a comparison of samples containing different numbers of individuals or samples. Curves are produced by repeatedly re-sampling the pool of '*n*' individuals or '*n*' of species that would be found in samples containing fewer and fewer individuals than the total sample. Steep curves represent high diversity.	• A comparative measure that is sample size independent	• Assumes that the proportional composition of individuals from different species is the same across sample sizes. • Can only be used to compare taxon richness at comparable levels of sampling effort.	(Sanders 1968, Gotelli & Colwell 2001, Gray & Elliott 2009)

Turnover (beta) diversity	Represents between habitat diversity or extent of change in composition among the samples of a set.	• Useful when comparing regions that extend across different habitats • An alternative measure when taking a neighbourhood approach. • Can be applied to presence absence data	• This technique is primarily used for comparing diversity along transects. • Beta diversity will be high when differences in alpha diversity are large.	(Whittaker 1972, Koleff et al. 2003, Magurran 2004, Gray & Elliott 2009, Terlizzi et al. 2009)
Chao estimator	Based on the concept that rare species carry the most information about the number of missing ones.	• Robust to sampling effort. • A potential measure to examine sampling artefacts	• Sensitive to area and must limit spatial extent of samples used in its calculation. • Assume homogeneity of samples so not suitable for comparing samples across different sites	(Chao & Shen 2003, Foggo et al. 2003)

2.3.1 Direct measures of species diversity

2.19 Species richness, the number of species at a given location, is arguably the most widely used and simplest measure of diversity and does not rely on abundance data being recorded.

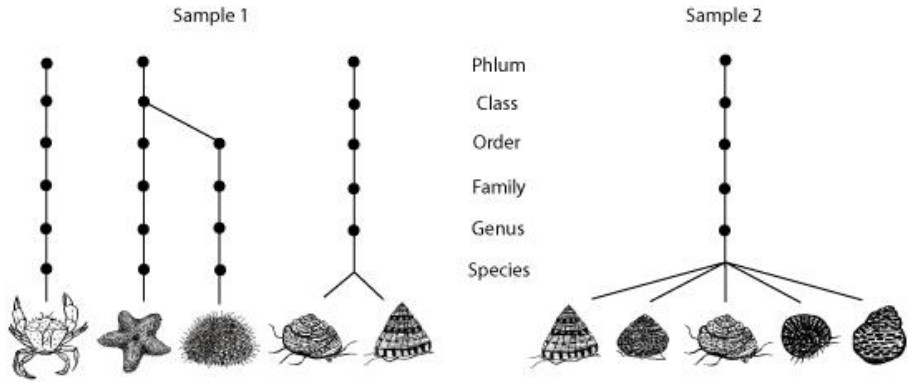
2.20 Species richness alone does not account for the spread in abundance between different species. For example, a site with ten species but with one species dominating would be classed as less diverse than one where all species were found in equal abundance. This information is captured in species evenness indices such as *Pielou's evenness* index (Purvis & Hector 2000).

2.21 Other indices widely used to quantify diversity include the Shannon-Wiener Index. The advantage of this index is that it takes into account both the number of species and their evenness. The value of the index is increased either by having additional unique species, or by having greater species evenness. The disadvantage is that the measure requires abundance data.

2.22 Average taxonomic distinctness is a diversity measure that reflects how different species are from each other at any given location (Warwick & Clarke 2001), representing the range of taxonomic groups that are present (phylogenetic diversity, see Box 1). For example, a sample consisting of ten species from the same genus would be seen as much less biodiverse than another sample of ten species, all of which are from different families. Unlike measures of species richness, the level of taxonomic relatedness is robust to variations in sampling effort and does not require abundance data.

Box 1. Average taxonomic distinctness

Average taxonomic distinctness calculates the average taxonomic distance apart of all the pairs of species in a sample, based on branch lengths of a hierarchical Linnaean taxonomic tree (Warwick & Clarke 2001). The illustration below shows the principle of average taxonomic distinctness. Both samples have the same species richness with five species present. However, sample 2 has five species from the same genus, whilst sample 1 has five species from four different genera and three different phyla. Therefore species from sample 1 are separated by longer branch lengths in the taxonomic tree and have a greater average taxonomic distinctness.



2.23 Another approach is to use higher (taxonomic) level diversity to assess biodiversity in marine ecosystems (e.g. family-level richness Heip et al. 1988, Williams & Gaston 1994). The rationale behind this is: 1) diversity at high taxonomic levels is much greater in the sea where nearly all known phyla are represented (there are 14 phyla found only in marine ecosystems (Clarke & Warwick 2001)) and: 2) identification of species only to higher taxonomic levels is quicker and cheaper (Féral et al. 2003). Legandre and Legandre (1998) make a case that “in principle, diversity should not be computed on taxonomic levels other than species” because the resources of an ecosystem are apportioned among the local populations (demes) of the species present in the system, thus each species represents a separate genetic pool.

2.3.2 Metrics for measuring habitat diversity

2.24 The variety of different habitats in an area is another way of expressing biodiversity. This is based on the link between species richness and habitat diversity that is found at a variety of scales (e.g. Izsak & Price 2001, Hewett et al. 2002, Tews et al. 2004, Thrush et al. 2006). While conceptually there is a good argument for considering diversity at the level of habitats, pragmatically this can also help to fill in gaps in data coverage in species records and explain patterns found in species diversity where data overlap.

2.25 Many measures developed for species can equally be applied to habitat diversity such as habitat richness (number of habitats at a location) and habitat distinctness. Locations with habitats from completely different habitat types can be considered more diverse than locations with similar habitats (i.e. from the same broad habitat group). Habitat distinctness was first applied in a UK wide assessment of marine benthic biodiversity by Hiscock & Breckels (2007). The measure works in the same way as average taxonomic distinctness (Clarke & Warwick 1998) to allow quantification of the variety of habitats present at any particular location, using the EUNIS hierarchical habitat classification (Box 2 and Box 3), which is similar in principle to the Linnaean tree for species taxonomy.

2.26 While a biotope is the smallest geographical unit of the biosphere or of a habitat that can be delimited by convenient boundaries and is characterized by its biota (Lincoln et al. 1998), it is arguably not the most suitable for quantifying habitat diversity from a practical viewpoint. This is because biotope classifications include information on the species assemblages present and the dominance of key species. Higher levels of the hierarchical classification (such as main habitat types, Box 2) may be more suitable in representing higher organisational levels of diversity without the bias of dominant species.

2.27 The different diversity metrics each have their own advantages, disadvantages and data requirements (Table 2). Furthermore, there is an observed lack of congruence between measures (Orme et al., 2005). No one measure provides a complete representation of biodiversity. This has led to the combination of a range of measures being used to capture patterns in biodiversity (e.g. Reid 1998, Myers et al. 2000, Hiscock & Breckels 2007).

2.28 Some studies that have combined different measures have incorporated direct measures of diversity with, for example, the number of endemic species[5] and areas of threatened or declining habitats (Myers et al. 2000). The advantage of these combined approaches is that the resulting score or rank of biodiversity importance is simple for marine spatial planners to visualize. However, with the ongoing technological development of GIS, different biodiversity metrics (e.g. species richness, biotope distinctness, seabed type diversity etc.) can be held as separate layers within a decision support tool. A disadvantage of combined scores is in determining the weighting of different metrics. Decision-makers may well require to see the information that the score was based on, which can be effectively 'lost' from the planning process when metrics are combined.

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[5] Endemism (where a species is restricted to a particular area) is an important criterion to identify hotspots on land and in fresh water but is an unusual feature in the marine environment of the north-east Atlantic due to fewer and weaker barriers to dispersal, and there are no marine species believed endemic to anywhere in the UK.

Box 2. Description of the EUNIS classification system

The EUNIS classification was developed for the European Environment Agency in order to standardize the description of habitat types across Europe. It allows for harmonization of a number of classification schemes (including the Marine Biotope Classification for Britain and Ireland). The classification allows the identification of both artificial and natural habitats in the terrestrial, marine and freshwater environments. For the purpose of the EUNIS classification a habitat is described as “Plant and animal communities as the characterising elements of the biotic environment, together with abiotic factors operating together at a particular scale” [http://eunis.eea.europa.eu/about.jsp].
As a hierarchical classification it can be used at various levels of detail (see below). The JNCC have produced translation tables that match habitat types in the EUNIS habitat classification to the following schemes:

the marine habitat classification for Britain and Ireland (v04.05);

EC Habitats Directive Annex I types;

OSPAR priority habitat types; and

UK Biodiversity Action Plan priority habitat types (Source: Joint Nature Conservation Committee, 2007)

Description of EUNIS classification levels

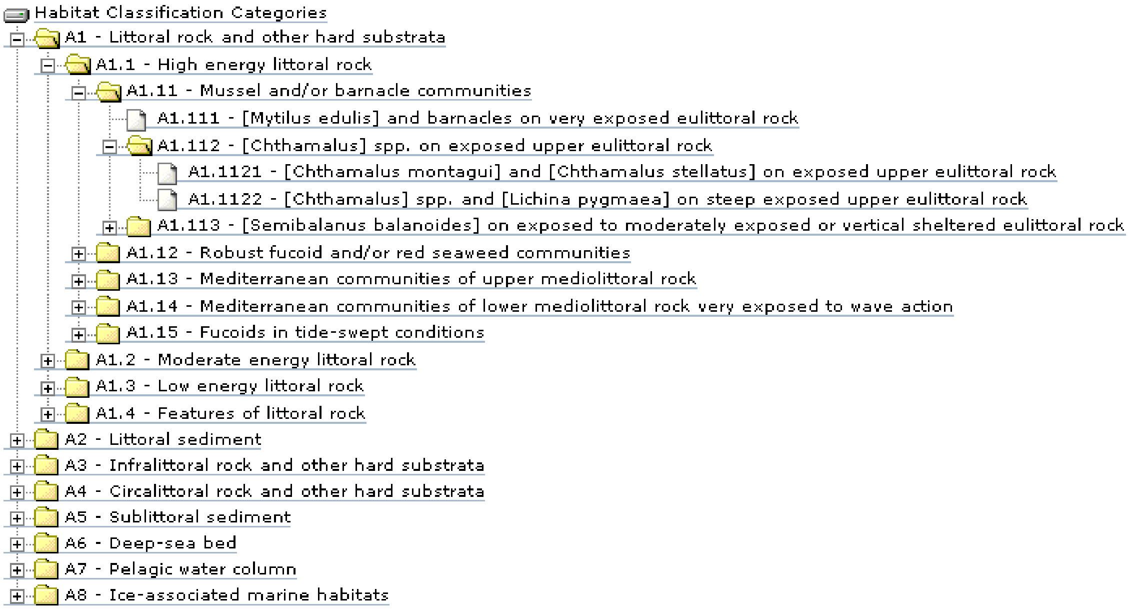
Level	Description
1	***Environment (marine):*** a single category is defined within EUNIS to distinguish the marine environment from terrestrial and freshwater habitats.
2	***Broad physical habitats:*** based on depth and broad substrata (e.g. rock or sediment) or water column e.g. littoral sediment.
3	***Main habitats:*** mainly physical based on energy regime but with some general description of biogenic habitat e.g. Littoral sediments dominated by aquatic Angiosperms, and Sublittoral macrophyte dominated sediment
4	***Dominant community type:*** community type described without specific reference to conspicuous species e.g. Fuciods in tide swept conditions
5	***Community:*** distinguished by their different dominant species or suites of conspicuous species e.g. *Chthamalus* spp. on exposed upper eulittoral rock.

2.3.3 Spatial considerations

2.29 The number of species, or even habitats, present in any given area is a function of the size of that area (McGuinness 1984). This is a limitation of most of the metrics outlined above and is especially true for species richness; they are highly dependent on spatial scale (and sampling intensity – this is dealt with in section 2.3.4). In order to make comparisons of the levels of biodiversity, data must be standardised for spatial scale so that locations with high diversity can be identified.

2.30 Several approaches have been taken to standardize the spatial scale in the area being assessed and these fall broadly into two types: 1) in some studies the area was broken down into even-sized grid units (grid size is generally dependent on resolution and coverage of survey data but management implications may also play a role in their spatial determination) to enable comparison across the area of interest (Worm et al. 2003, Orme et al. 2005, Langmead et al. 2008); and 2) other studies have used natural features as their sample units (e.g. Hiscock and Breckels 2007). In the latter approach, physiographic features were applied as the sample unit (islands, embayments, estuaries, linear coastlines and sea lochs). The main problem with this method is that some of these features may be substantially larger than others, meaning that diversity may be compared at a local level in some (α diversity) but regionally in others (β diversity), invalidating overall comparisons between areas.

Box 3. Example from the EUNIS hierarchical habitat classification system.



- Habitat Classification Categories
  - A1 - Littoral rock and other hard substrata
    - A1.1 - High energy littoral rock
      - A1.11 - Mussel and/or barnacle communities
        - A1.111 - [Mytilus edulis] and barnacles on very exposed eulittoral rock
        - A1.112 - [Chthamalus] spp. on exposed upper eulittoral rock
          - A1.1121 - [Chthamalus montagui] and [Chthamalus stellatus] on exposed upper eulittoral rock
          - A1.1122 - [Chthamalus] spp. and [Lichina pygmaea] on steep exposed upper eulittoral rock
        - A1.113 - [Semibalanus balanoides] on exposed to moderately exposed or vertical sheltered eulittoral rock
      - A1.12 - Robust fucoid and/or red seaweed communities
      - A1.13 - Mediterranean communities of upper mediolittoral rock
      - A1.14 - Mediterranean communities of lower mediolittoral rock very exposed to wave action
      - A1.15 - Fucoids in tide-swept conditions
    - A1.2 - Moderate energy littoral rock
    - A1.3 - Low energy littoral rock
    - A1.4 - Features of littoral rock
  - A2 - Littoral sediment
  - A3 - Infralittoral rock and other hard substrata
  - A4 - Circalittoral rock and other hard substrata
  - A5 - Sublittoral sediment
  - A6 - Deep-sea bed
  - A7 - Pelagic water column
  - A8 - Ice-associated marine habitats

2.31 Although there are no examples known to the authors, it is clearly possible to use different spatial resolutions for different areas or system components, driven again by data availability (sampling intensity). There are large differences in spatial and temporal resolution of data between the intertidal and subtidal, inshore and offshore, and the benthic system compared with the pelagic. Inherently there is a trade-off between using a small spatial unit (surveys so sparsely spread that many spatial units are empty) and using larger spatial units (losing resolution in the data), and determining the optimal grid cell size is for each type of data is an important step in biodiversity assessment (Stockwell & Peterson 2003), yet the reasoning for the choice of grid cell size is rarely given. General guidance from macro ecology promotes the use of re-sampling procedures to identify the optimal resolution (Rahbek

2005). It is clear that one size does not fit all with respect to the optimal spatial resolution for conducting biodiversity assessments, and consideration at different scales is particularly important when taking an integrated, multi-level systems approach to identifying areas of high diversity if important detail is not to be lost in 'scaling up'.

2.32 Finally, different shaped spatial grids have been used for mapping diversity, with either rectilinear (Roberts et al. 2002) or hexagonal units. The latter are commonly used for spatial planning (Bassett & Edwards 2003, Worm et al. 2003, Oetting et al. 2006). The argument in favour of hexagonal units suggests that they offer the best alignment to complex features thus providing a better level of coverage. In addition techniques have been developed to counter the bias of placing grids over complex landscapes and spatially auto correlated data sets. Overlapping or roaming grid squares and neighbourhood statistics 'soften' the artificial edges and smooth errors which are an artefact of the grid placement, by taking adjacent cells into consideration in analyses (Dennis et al. 2002). Neighbourhood statistics involve combining data from surrounding cells into the central focal cell, thus the final value of each cell is influence not only by the data underlying that cell but also by its neighbours. This is important when you consider that species richness is not only influenced by the number of individuals but also by the species richness of the surrounding community.

2.3.4 Data quality and standardisation

2.33 Estimates of areas of diversity are extremely dependent on the state of current knowledge: data coverage (discussed above), sampling effort and also the age of data sets (Magurran 1996, Worm et al. 2003). For species richness there are clear relationships with the number of samples, or put simply, the more effort spent searching for species, the more will be found (species accumulation curves, Figure 2). Species accumulation curves generally rise very quickly at first and then level off towards an asymptote as fewer new species are found per sampling unit collected.

2.34 Different statistical techniques have been employed to compensate for variable sample intensity in order to give a comparable unbiased estimate of relative biodiversity. These include rarefaction (Worm et al. 2003), regression analysis (Hiscock & Breckels 2007, Langmead et al. 2008) and re-sampling techniques such as Monte Carlo analysis (Moulins et al. 2008). There is a limit to the success of these techniques when faced with extremely low sample numbers, and some studies have omitted areas with extremely low numbers of surveys by setting a lower limit to the number of surveys per spatial unit (Langmead et al. 2008). In addition, the Chao 2 estimator measure is based on the concept that rare species carry most information about the number of missing ones, and has been applied to look for artefacts in data sets caused by this (Foggo et al. 2003).

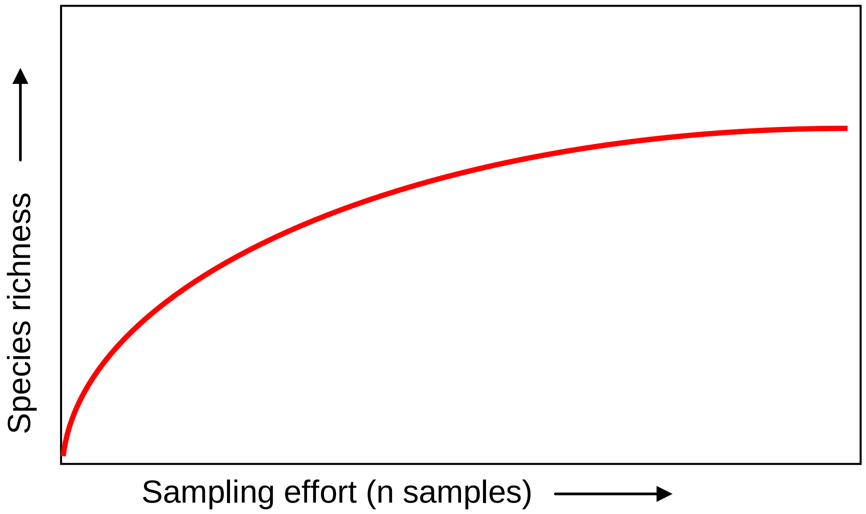


Figure 2 species accumulation curve showing relationship between the species richness and sampling effort.

2.35 With benthic marine data sets, the number of species can be closely linked to the type of habitat, and the sampling technique employed. Samples collected using a benthic core sample and sieved using a 0.5 mm sieve are likely to have greater diversity than samples collected using a trawl, drop down camera or diver surveys. Thus sub-setting data for standardization facilitates like-with-like comparisons of diversity that are not simply an artefact of the data collection technique. In a study by Langmead et al. (2008), data were split by physiographic type to account for such differences (e.g. rocky areas were only compared with other rocky areas) and sites of high and low diversity were identified for each main physiographic type. These estimations were combined for all physiographic types to build up a picture of benthic biodiversity (irrespective of habitat) for the entire Firth of Clyde. Building on this approach, further work has been carried out to classify the methods employed to collect benthic data into broad groups and compare diversity measures only within these groups to remove the bias inherent in the sampling methodology (Jackson et al. in progress).

2.4 Surrogate measures for marine pelagic biodiversity

2.36 All the measures in the previous section are more or less direct measures of the biodiversity of an area, and have mostly been applied to benthic systems. Measures previously proposed to indicate pelagic diversity reflect the fact that most marine pelagic ecosystems have a relatively simple structure, with energy flowing from phytoplankton primary producers, through zooplankton (often dominated by copepods) to pelagic schooling fishes, and finally to a variety of top predators including fishes, marine mammals and seabirds (Jennings et al. 2001). These were:

i. Diversity measures for different system components including phytoplankton, zooplankton, fish, cetaceans and seabirds;
ii. Satellite earth observation (EO) surrogate measures (thermal fronts, sea surface temperature (SST) and ocean colour);
iii. Indicators such as pelagic mega fauna (e.g. basking sharks).

2.37 Earth Observation data (SST, thermal fronts and ocean colour) have high spatio-temporal coverage and fine spatial resolution, which is lacking for most other pelagic measures (apart from Continuous Plankton Recorder data on plankton). In addition, EO data has been correlated with overall pelagic diversity, whilst others are restricted to being measures of specific system components and as such are not reviewed here (but see Appendix 3).

2.4.1 Thermal fronts

2.38 The influence of oceanic fronts on biological productivity has long been studied. Pingree (1977) noted that the stratified side of tidal fronts could support dense phytoplankton blooms throughout the summer due to the rare combination of high nutrients and light. Further into the stable stratified region nutrient levels remain depleted after the spring bloom; and on the well-mixed side of the front the plant cells receive a much lower mean light level which outweighs the relatively high nutrient levels. Bakun (1996) identified fronts as important structures that could result in the ‘triad’ of enrichment, concentration and retention of nutrients.

2.39 Relationships have been established between fronts and fish abundance, for instance swordfish (Podesta et al. 1993), tuna and billfish (Worm et al. 2005). In addition, Worm et al. (2005) determined a global correlation of predator diversity with fronts. Although no studies have found a correlation between fronts and overall diversity, higher predator diversity has been linked to biodiversity in the open ocean (Worm et al. 2005).

2.40 Fronts that extend to the sea surface may be observed by satellite if the water masses differ in temperature or colour. This remote sensing of fronts has enabled a process-based understanding of mesoscale population dynamics capable of explaining regime shifts (Bakun 2006, ICES 2006). Remote sensing of fronts is promoted as a key tool in determining marine habitat hotspots (Palacios et al. 2006, Sydeman et al. 2006). Since identifying fronts in satellite images manually is a tedious and subjective task, several researchers have proposed image processing algorithms to do this semi-automatically (e.g. Simpson 1990, Bardey et al. 1999), or entirely automatically (Cayula & Cornillon 1992). A few authors have superimposed the locations of all fronts detected on a sequence of images to produce a single combined map (e.g. Podesta et al. 1993, Ullman & Cornillon 1999). Miller (2004, in press) extended this methodology to visualise both dynamic and stable fronts, generating metrics to indicate their temperature gradient, persistence and proximity to other observations.

2.4.2 Sea Surface Temperature (SST)

2.41 Apart from the use of EO-derived SST for locating oceanic fronts, the range of SST values has also been applied as a surrogate for fish abundance. Most species have a preferred temperature habitat, so this can help define their spatial distribution e.g. for tuna (Zainuddin et al. 2008), or represent coastal retention events for pilchard, sardine and anchovy stocks (Cole 1999). The most generic relationship between SST and fish abundance is that caused by coastal upwelling, bringing nutrient-rich deep water to the surface. Upwelling zones can support much greater biodiversity. Upwelling zones are a regionally important feature with small zones around the south west of the UK (off Cornwall) influencing productivity. EO SST time-series data of upwelling events have been related to studies of zooplankton and fish larvae in Galicia (Tenore et al. 1995), Portuguese swordfish, tuna, sardine and mackerel (Santos et al. 2001, Santos et al. 2006), but few studies have correlated SST or upwellings with levels of diversity.

2.4.3 Ocean colour

2.42 Chlorophyll-*a* is a good estimator of phytoplankton abundance. Various EO models can be used to estimate primary production. EO models using chlorophyll-*a,* light (photosynthetically active radiation (PAR)) and SST can quite accurately estimate surface primary production, and these are well summarised by (McClain 2009). Higher productivity may support high pelagic diversity; this may also impact on benthic productivity and biodiversity.

2.43 However, there are issues with this technique since standard algorithms for chlorophyll-*a* retrieval from EO ocean colour, while accurate for the open ocean, suffer errors in turbid shelf seas where suspended sediment and coloured dissolved organic matter mask the chlorophyll signal. This can result in exaggerated chlorophyll-*a* values near estuaries, reducing the value of standard chlorophyll-*a* maps for monitoring phytoplankton in shelf seas. Several algorithms have been proposed to tackle this problem: the empirical OC5 algorithm (Gohin et al. 2002) corrects the chlorophyll-*a* signal by estimating and removing the radiance contribution from suspended sediment, significantly reducing these errors in turbid water.

2.5 Predictive techniques

2.44 Biological survey data is relatively sparse, particularly in inaccessible and offshore areas, and different approaches to the ‘data-hungry’ measures outlined above have been researched. One possibility is the use of predictive maps of broad scale habitats and environmental parameters to identify potential areas of high diversity where survey data do not exist.

2.45 For the terrestrial environment there are well established theoretical reasons why environmental variables should be good estimators of the spatial distribution patterns of species richness, supported by empirical studies (Austin 1985, Austin et al. 1990, Prendergast & Eversham 1997, Margules & Pressey 2000). Models and statistical techniques developed in terrestrial ecology to compare how well different environmental surrogates reflect diversity (Margules & Austin 1994, Gioia & Pigott 2000, Elith et al. 2006) are applicable to the marine environment, where theories on why high diversity areas occur where they do are beginning to emerge from analyses of data on global and continental scales. Orme et al. (2005) argue that the ecological, evolutionary and human effects that underlie the origin and maintenance of biodiversity are largely associated with large-scale topography.

2.46 A number of projects to map marine species distributions by modelling relationships with marine habitat and environmental information (e.g. Sandman et al. 2008, Vaz et al. 2008 and HabMap, http://habmap.org). The obvious extension to modelling individual species distributions is to combine them to create maps of richness (Stockwell & Peterson 2003). Predictive species maps are however only possible for species with a clear relationship to certain environmental characteristics and aggregations of species maps do not account for density dependent factors and other species interactions.

2.47 Developments in satellite remote sensing and a geographic information system (GIS) coupled with spatial statistical software allow the efficient characterization of biodiversity at landscape level using geospatial techniques. Roy & Tomar (2000) predicted biological richness at landscape level as a function of habitat, biogeographical setting, disturbance regime and environmental complexity. Top-down rule-based approaches, which combine environmental variables, such as depth, productivity, seabed type and current speed, can be used to classify areas of the seabed into different broad habitat types. This technique has been used for broad scale national and international projects such as UKSeaMap (Connor et al. 2006) and MESH[6]. Such predictive seabed habitat maps could be used to look at landscape diversity. However, the quality of predictive seabed habitat maps (or model that underpins it) is related to the data used to construct it.

2.48 Problems with data availability and a lack of robust relationships between species and environmental conditions, particularly at larger spatial scales have led researchers to examine alternative approaches. For example modelling and predicting potential underlying drivers of high diversity, e.g. productivity and disturbance regimes (Loreau et al. 2001, Chase & Leibold 2002).

2.49 Comparisons of different predictive methods have shown divergent results (Stockwell & Peterson 2003) attributable to differences in analytical methods, geographical scales and biogeographical histories of the study areas.

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[6] Mapping European Seabed Habitats (MESH) - http://www.searchmesh.net/

Reliable generalizations and an understanding of how such factors affect taxonomic surrogacy are still developing for the marine environment.

2.50 In summary, predictive methods have the potential to identify important areas of diversity where survey data is limited or absent. However, any predictive method requires substantial validation and with an uncertainty still surrounding the reliability of predictive approaches conservation managers are unlikely to base decisions on the location of MPAs on predicted map layers without considerable validation and resurvey.

2.6 Hotspots of biodiversity

2.51 In 1988, the British terrestrial biologist Norman Myers initiated the use of the term "biodiversity hotspot" as a biogeographic region characterized both by exceptional levels of plant endemism and by serious levels of habitat loss (Myers 1988). Since then the term “biodiversity hotspot” has been used to describe the relatively high occurrence of a single species, diversity of species within a certain group (realm, trophic level, size class), of ecosystem services or of productivity.

2.52 In an assessment of biodiversity hotspots carried funded by WWF, Breckels and Hiscock (2007) used the definition:

“Marine biodiversity hotspots are areas of high species and habitat richness that include representative, rare and threatened features”.

2.53 The main drawback with the hotspots approach is that the threshold at which a location is identified as a “hotspot” is often subjective or ambiguous, and can be related to 1) conservation objectives and 2) the area of search, which limits the range of diversity for example the number of species within the species pool increases with area of search making a local hotspot *cooler*. In addition there can be confusion in the use of the term ‘hotspots’ with other types of hotspot, such as hotspots of productivity (Valavanis et al. 2004) and single species abundances (Sims et al. 2003, Evans & Wang 2008), which may be unrelated to biodiversity *sensu stricto*.

2.7 Summary and conclusions

2.54 The preceding sections provide a critical review of approaches for identifying areas of high marine biodiversity in both the benthic and pelagic realms. The review identifies various measures to assess marine diversity (e.g. diversity indices, number of species, number of priority species and taxonomic distinctness) and highlights the importance and limits of data quality and coverage. The review also identifies the necessity, not only to employ effort standardisation techniques, but also to validate and present the level of confidence given to the layer.

2.55 Due to the inherent patchiness and variability in data availability for assessing biodiversity no single layer represents marine diversity adequately and it is concluded that a series layers are developed representing different zones and realms (for example inshore offshore, pelagic and benthic) with biodiversity measured using a suite of metrics that together provide a more comprehensive view of the range of biodiversity. Presenting the layers separately allows the individual biodiversity measures (e.g. species richness, biotope distinctness, EO thermal fronts etc.) to be used separately or in combination as part of the MPA selection process. Splitting the analyses this way should help to overcome a large portion of the variability (which may lead to spurious comparisons of biodiversity) resulting from major differences in data availability, methods of collecting data and variations in scale dependent factors.

2.56 Our knowledge regarding diversity patterns of pelagic organisms is scarce and mostly restricted to the assessment of individual components of the system. The inherent mobility of the pelagic ecosystem also means that it is constantly changing at a variety of spatio-temporal scales. Benthic environments have the advantage that species and habitats tend to be more static in time and space than those in pelagic environments. This has advantages in terms of mapping and recording data for use in biodiversity assessments (although the resolution and coverage may still vary, particularly between inshore and offshore areas). These inherent differences necessitate the employment of very different approaches in identifying areas of biodiversity in the pelagic and benthic realms. Assessing biodiversity patterns of pelagic organisms will require the use of a surrogate, which must be shown to be correlated with biodiversity over large scales and have good spatial coverage (e.g. thermal fronts).

2.57 The biodiversity layers generated in the proposed study would need to be considered within the context of expert knowledge. The resultant maps will be based on available data reflecting current availability and may miss important sites that have not been formally surveyed, particularly offshore. As such, they can never be a definitive representation of regional patterns of biodiversity, only what is quantitatively known. Gaps in the data can exist because of the availability or accessibility of data, but true data gaps also occur where no survey work has been carried out. In some cases, locations may be identified by experienced marine biologists as ‘rich’ or including special features but survey results have not been recorded and should be considered a priority for future survey effort. Diversity layers produced in this project should not be static but should continually evolve as new data become available.

2.58 Predictive modelling would be a valuable tool in identifying potential areas of high biodiversity in extremely data poor offshore areas and fill the survey gaps in the inshore areas by relating patterns of benthic biodiversity to environmental parameters (such as seabed type, depth, wave stress, productivity etc.). However, the use of these areas in identifying MPAs would be of limited value without additional survey. Also such modelling could only be undertaken after identifying patterns in the current known distribution of diversity (and all the steps related to standardizing for issues of scale, sampling method and heterogeneous spatial spread of samples) had been undertaken. It is therefore recommended that such a modelling approach be considered in any projects building on from the current work.

2.59 The use of marine diversity area data layers to inform nature conservation should be supported by other aspects of the Ecosystem Approach, especially the development of management measures that take account of species biology and the maintenance of ecosystem structure and functioning. This work should however be viewed within the context of the larger project that includes the development of a number of other data layers including benthic productivity and vulnerability mapping and the identification of areas of high biodiversity will form one of many tools for designing and managing a network of MPAs. For example, taking an Ecosystem Approach to represent marine biodiversity requires all species and habitats to be represented within protected areas and in sufficient amounts (area and population size) to allow the ecosystem to function “normally”.

2.8 Selection of diversity layers to be developed

2.60 The conclusions of the review and additional views from the workshop (see transcript in Appendix 1) were presented to the MPA Data Layers Project Steering Group and an independent reviewer. Due to resource limitations, not all data layers could be developed, and a prioritisation of these data layers was undertaken (see Table 3).

2.61 Potential layers were prioritised according to data availability, the suitability of indicators to represent overall biodiversity and conservation management constraints, and for cost effectiveness. Decisions about the location of marine conservation areas need to be evidence based. Predictive modelling approaches based on the environmental data sets could provide full coverage maps in data poor offshore areas and even identify previously unknown areas of potentially high diversity but a lack of adequate validation data means that potential areas identified through modelling would require significant ground truth survey prior to inclusion in the MPA design process. Additional survey falls beyond the scope of this work. Some indicators (e.g. the numbers of top predators) have been used in the past and have been put forward as indicators of areas of high pelagic diversity but there is insufficient scientific evidence supporting their relationship with overall pelagic diversity at the scale under consideration (these relationships have only been confirmed at local scales) (see Section 2.4). Proposed methods for the lower priority measures which were considered can be found in Appendices 2 and 3.

2.62 The following section provides details on the recommended approach and methods for developing a marine diversity areas data layer for the UK using the following representative measures:

- Benthic species richness.
- Benthic biotope richness.
- Benthic taxonomic distinctness.
- Benthic biotope distinctness.
- EO – thermal fronts.

Table 3 Summary of proposed measures for the production of a biodiversity data layer and prioritisation

	Measure /layer	Assumption(s)	Strengths	Weaknesses	Data requirements	Data availability	Priority (1,2, 3)
Benthic	Species richness	Sampled species richness is indicative of the overall species diversity of that area	Robust over large spatial scales, easy to obtain from wide data sources; fulfils criteria for protecting high numbers of species within an MPA	Very sensitive to sampling effort/method; does not convey spread in abundance or higher level diversity	Generally low - requires presence/ absence data and some measure of sampling effort	Species records widely available from national data sets and specific surveys	2
	Habitat richness	Richness of habitats in an area is indicative of species richness.	Representative of assemblages under different abiotic conditions and therefore potential to be more ecologically relevant. Linked to environmental conditions and therefore potentially easier to model.	Poor coverage. Combination of polygon and point data which must be handled separately. Point data often centroid which may bias spatial analysis.	Habitat records/maps - limited primarily to conservation agencies surveys. Low academic buy-in and this is reflected in data availability.	Not widely recorded	2
	Taxonomic distinctness	Assumes representative samples (and accurately identified). Assumes that taxonomic path lengths between successive taxonomic levels are equal and robust to variation in the definition of step length.	Captures the phylogenetic relatedness of an assemblage and therefore more representative of higher taxonomic diversity and possible proxy for functional diversity; Robust to sampling effort (especially at large scale); more robust for comparisons of diversity between sites	Certain phyla are underrepresented/ recorded and have to be excluded	Generally low - as a minimum (for Δ^{+}) requires presence/absence data	Same as species richness + phylogenies	1

	Measure /layer	Assumption(s)	Strengths	Weaknesses	Data requirements	Data availability	Priority (1,2, 3)
Benthic	Habitat distinctness	As for taxonomic distinctness	Representative of higher level habitat diversity; Robust to sampling effort (especially at large scale); reflects higher habitat diversity; more robust for comparisons of diversity between sites	See data availability	Habitat records/maps - limited primarily to conservation agencies surveys. Low academic buy-in and this is reflected in data availability.	Habitats are not widely recorded and biotope matching is very time consuming	2
	Predictive model-derived diversity	Biological diversity is related to physical and environmental parameters	Predicting biodiversity hotspots in data poor areas (e.g. offshore); Full (modelled) coverage and the potential to identify unrecorded areas of high biodiversity	Model would be based on modelled data (with poor validation). Research based and therefore unable to guarantee level of confidence in predictions before undertaking the work. Potential hotspots would require significant ground truth survey prior to inclusion in the MPA design process.	Dependent on the prior production of other data layers (e.g. benthic productivity, UKSeaMap 2, wave stress, and measures of diversity)	Many information layers that such a model would be dependent on will not be available until September; therefore this work may need to be considered as a second phase to avoid duplication of effort and cost.	3
Pelagic	EO - Fronts	Fronts are an indicator of pelagic diversity	Full spatial coverage	Inshore areas have lower confidence; the value of these measures as surrogates for biodiversity needs to be tested	High	Satellite data	1
	EO - SST	Upwelling zones support high diversity					2
	EO - Chl-a	Diversity is related to productivity					1
	Phytoplankton species richness	Sampled species richness is indicative of the overall species diversity of that area	Plankton are the foundation of the pelagic marine food web.	Not all taxa identified to species level. No evidence that plankton diversity is linked to overall biodiversity of the area.	High	Data available through SAHFOS. The CPR data set is the most spatio-temporally comprehensive plankton data set in the world	1
	Zooplankton species richness						1

	Measure /layer	Assumption(s)	Strengths	Weaknesses	Data requirements	Data availability	Priority (1,2, 3)
Pelagic	Pelagic fish[7]	Patterns in commercial species are reflected across the pelagic fish community	Key pelagic components, highly mobile and linked with the plankton; Reliable distributions can be generated from acoustic data for herring and possibly other species	Data available for few pelagic species, reliance on commercial landings data that would only comprise UK ports	High	Spatially patchy	2
	Seabirds	Seabirds, while not spending all their lives in the sea, are a part of the pelagic system because they are important predators	Good spatial coverage	Data collected in several ways depending on species	JNCC provide effort corrected densities	Available from SAST Team (JNCC)	3
	Cetaceans	Cetaceans as top pelagic predators are a key component of the pelagic realm and sampled species richness is indicative of the overall species diversity of that area	Good spatial coverage - the Joint Cetacean Database is the most important effort-standardised resource for cetaceans in NW European waters	Data maybe at too high a resolution to identify hotspots and further processing may be necessary	High	Data available through Joint Cetacean Database (JNCC)	3
	Basking shark	Basking shark are indicators for areas of high pelagic biodiversity	Basking sharks could be a cost effective indicator for pelagic biodiversity; Charismatic, widely observed species	Spatially restricted to frontal areas in WEC and Irish Sea, data collected in several ways and not easy to aggregate	Moderate	MBA holds a database of shark observations	3

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[7] Task 2B is mapping the distributions of some pelagic fish species; this can feed into this work if the timescales for delivery allow.

3 Proposed approach for the UK

3.1 Following the selection of appropriate indicators for the production of diversity data layers a series of steps will need to be undertaken to control quality and standardise effort. Firstly the available data will be collated and the data sets reviewed to identify adequacy and quality and filtered to remove inappropriate data and section areas of the UK territorial sea which may require different approaches due to data availability. The next step will involve the selection of appropriate spatial and temporal scales, and appropriate diversity measures and their analysis (including methods for standardising sampling effort). Finally, a validation and confidence assessment step will be required. The following section details the proposed approach for each of these steps in the production of the diversity data layers common to both benthic and pelagic realms.

3.7 Dividing up the sea

3.2 **Figure 3**There are a number of reasons for splitting up regions of the sea prior to any assessment of high biodiversity areas, primarily due to the importance of comparing ecologically similar systems (and this is reflected in the methodologies used to gather data). In addition, there are inherent differences in data availability between different zones or regions of the sea and in the way that areas are, or will in the future, be managed. Data on pelagic species, which tend to be more mobile and show greater temporal/spatial variability, are often recorded at larger spatial scales to benthic data. There is also an observable decline in benthic data availability for analysis with distance offshore.

3.3

3.4 Figure **3** illustrates the separation of areas of the UK territorial waters, the proposed measures applicable to each and the priority measures. Such a division will result in a minimum[8] of five priority marine diversity data layers (benthic species richness, habitat richness, taxonomic distinctness, habitat distinctness and pelagic thermal fronts.

3.5 For the purposes of this work it is recommended that the sea is split into pelagic and benthic, both inshore and offshore. The benthos should be further split into intertidal, subtidal and the deep-sea region (>200m) which is likely to be different from that on the continental shelf and inshore regions. A number of pelagic diversity measures will not be available for inshore waters due to:

i. decreasing confidence in measurements (e.g. Earth Observation surrogate measurements for frontal detection are not reliable <6km from the coast); or

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[8] Assuming that equal grid sizes are used for the inshore and offshore, which may not be appropriate.

ii. data are not gathered in inshore waters (e.g. commercial fish catch data are from >6nm offshore, as are research trawl data for the most part).

3.6 Deep-sea areas (depth >200m) represent another distinct area where sampling effort is very patchy. Recent research indicates that benthic diversity is strongly influenced by depth (Weaver et al. 2004) and by the presence of certain geomorphological features (e.g. sea mounts and canyons). With very poor data availability for the deep sea, taking an approach based on actual records may miss important areas. It is therefore proposed that the deep sea is left out of the marine diversity data layer and incorporated into the MCZ process in another way, in discussion with deep-sea ecologists.

3.7 For each of these regions a grid of equally sized cells will be overlaid to provide units for analysing the underlying data. Due to differences in spatial resolution of data it will be appropriate to utilise different sized spatial units for different areas, for example using a sub-km scale for the inshore compared to the offshore (where some pelagic data sets are recorded at the 0.5-1 degree scale) and a finer scale for certain fine scale physiographic features, e.g. lochs and estuaries and the intertidal. In addition to spatial unit size, the methods used to identify levels of diversity in each region will differ due to the differences in the underlying data. The following sections separately address the approaches and issues for the benthic and pelagic realms.

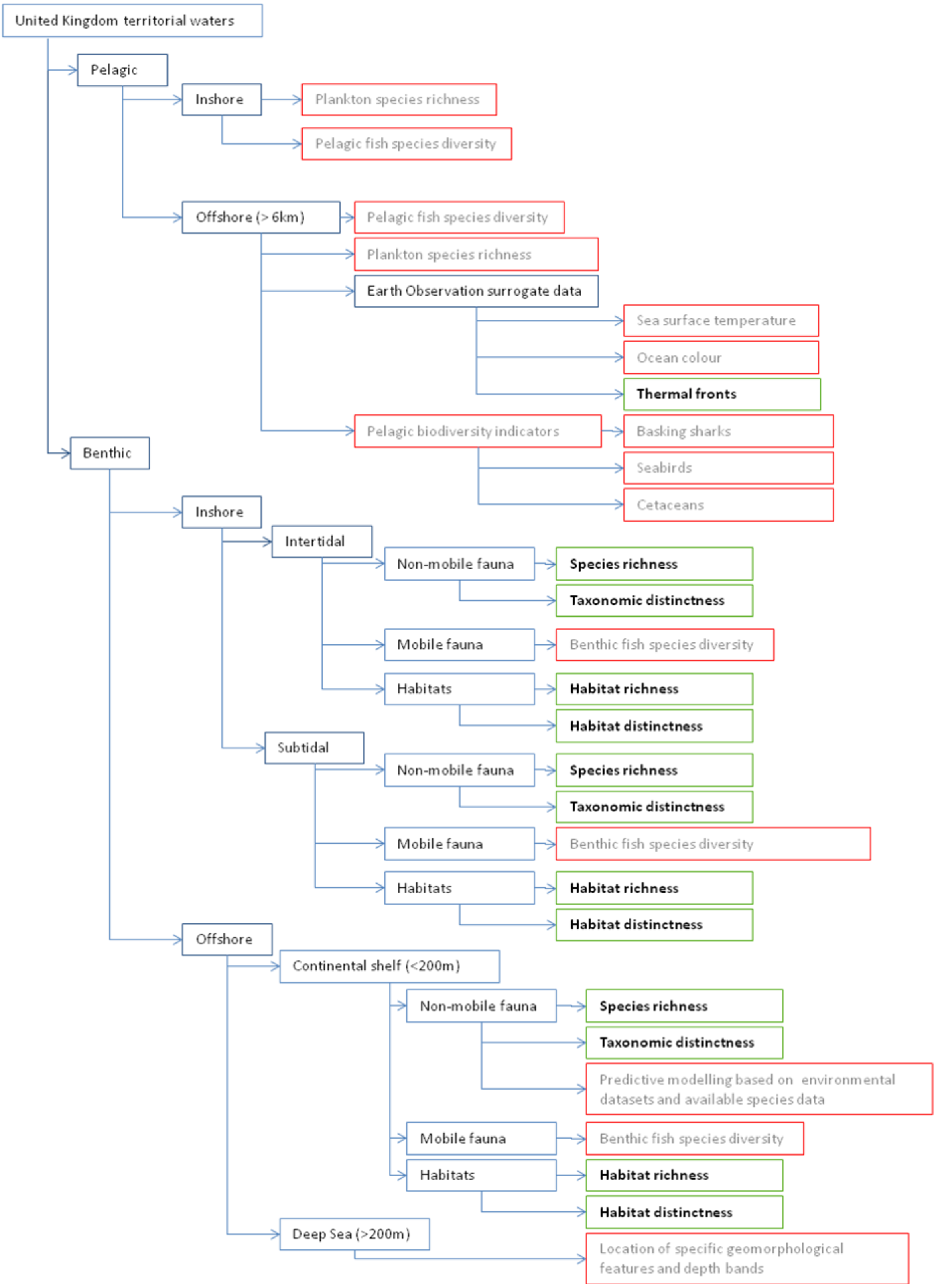

Figure 3 Tree diagram showing the proposed division of the UK territorial seas for the purpose of producing the diversity area data layers.

3.8 Benthic diversity area data layers

3.8.1 Data availability and gaps

3.8 The assessment of benthic biodiversity will focus on all non-mobile macro benthic species[9] and habitats. In the inshore area (and particularly in the intertidal) there are detailed data available both from national databases and other sources, for example the Marine Recorder database, which is maintained by the UK National Biodiversity Network and Data Archive for Seabed Species and Habitats (DASSH). Figure 4 shows the locations of survey data sets which had been collated for the purposes of the marine diversity layer, at the time of the production of this report.

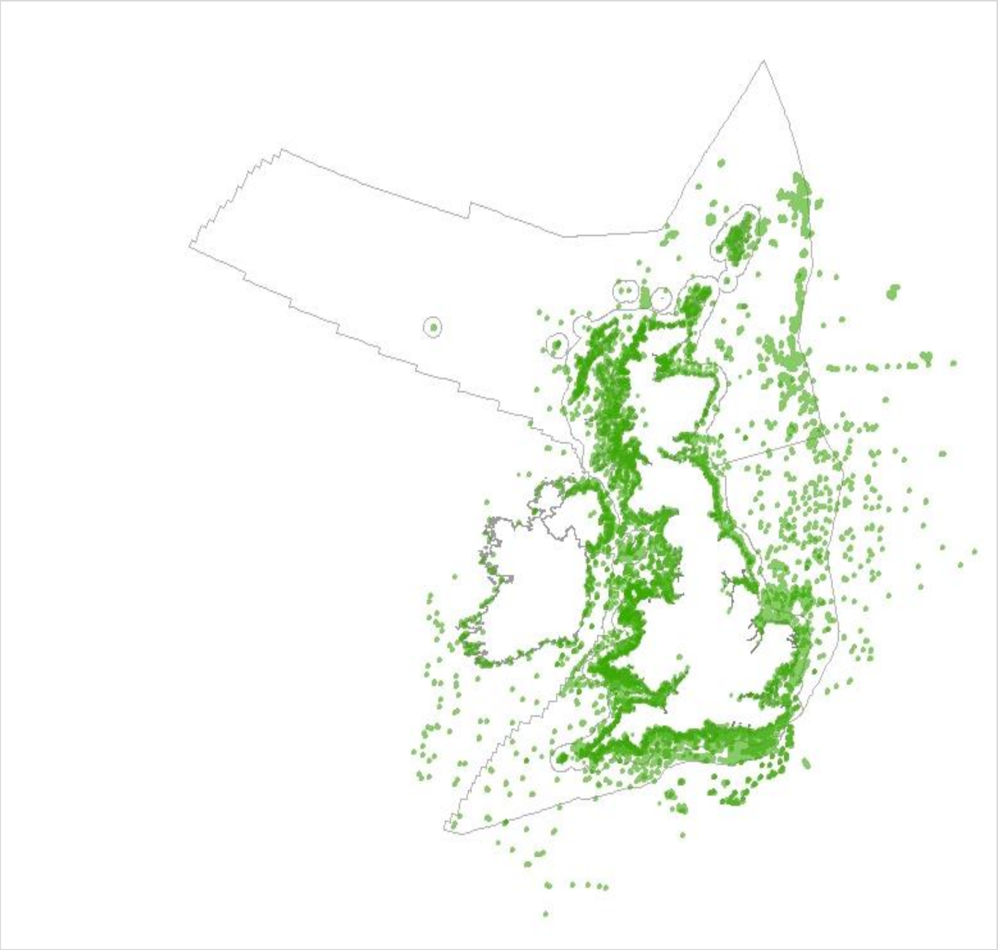

Figure 4 Locations of marine survey data collated (at the time of production of the current report) to support the production of the Biodiversity data layer. Grey lines illustrate UK marine administrative regions.

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[9] A proposed approach for incorporating demersal fish data (which was considered to be lower priority) is given in Appendix 2

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3.9 Figure 4 illustrates the decline in survey density with distance from the shore and also the disparity in data availability between different regions of the UK. There are also data available from various surveys related to academic research, monitoring and planning activities; however the time frame available for the production of the data layer and the difficulties in mobilising these data will limit their collation.

3.8.2 Quality assessments and filtering

3.10 The seabed and associated benthic data will be divided into subtidal/intertidal, inshore/offshore, based on wave stress models if the data layer is available within the timeframe. Species and biotope information collected, collated and catalogued during the production of the priority species and habitats layers (Task 2B and 2C) will be combined with any additional data sets that can be acquired in the timeframe. Each data set will be reviewed against quality criteria and assigned confidence rating to assess suitability, taking into account the source of the data, its age (older data sets may be removed from analyses), spatial, taxonomic and methodological accuracy. Derived confidence ratings will be recorded in the metadata and low quality data will be flagged and may be removed from subsequent analyses. The assessment of the quality of the data will be made based on criteria set out in the ISO 19115 standard for geospatial metadata. To ensure all species names are standardized in terms of spelling and synonyms the recorded species names will be checked against the World Register of Marine Species database (WoRMS 2007).

3.11 Data will be subjected to a series of temporal and spatial filters to remove low quality or inadequate information. For monitoring data, only the most recent surveys at each location will be included in analyses. This is due to much of the data originating from impact assessments; the survey sites may have changed over the course of the monitoring period, either becoming degraded or recovering. For similar reasons it will be important to set a date limit on the age of the data used in analyses, which will be defined by the available data. Many old data sets will be removed during the quality assessment phase but in the absence of any recent records for an area it might be worth using high quality old records but flagging them as such (e.g. within a confidence layer). This will identify the need for up-to-date survey information at specific localities and help to inform stakeholders about the quality of the data.

3.8.3 Selection of spatial units

3.12 The identification of suitable spatial units or cell sizes for analyses will be dictated partly by region (inshore and intertidal will have finer resolution than offshore due to the greater habitat variability in these regions) but also by the sample/survey coverage. It is possible that intertidal and inshore data can be analysed at a smaller spatial scale or that spatial scale is adapted to reflect the inherent spatial heterogeneity of different regions (to minimise the inclusion of numerous different broad habitats or topographic features occurring within one grid cell). An analysis to determine the optimal spatial unit size for each region (e.g. inshore/offshore) will be undertaken, for example, by considering the frequency distribution of sampling and examining the move from a logarithmic to Poisson distribution (Foggo, pers. comm., 2009). Essentially this is the optimal point in the trade-off between using a high resolution small cell size (where surveys are so sparsely spread that many spatial units are likely to be empty) and using larger spatial units (that are likely to have lost resolution in the data).

3.13 Whatever the final spatial scale it is likely that the some grid cells will not include any data. No interpolation of data for these cells will be carried out. Instead, the cells will be displayed as “no data” in order that the layers represent the underlying data.

3.14 The shape of the grid will also be taken into consideration. Hexagonal units are commonly used for spatial planning (Bassett & Edwards 2003, Worm et al. 2003, Oetting et al. 2006) and because they offer the best alignment to complex features, such as the UK coastline, ensuring a better level of coverage. Since the size, shape and the actual position of the grid can influence the way in which point data are analysed within a grid, the use of neighbourhood statistics or roaming windows are a necessity (Zhang et al. 2007). Neighbourhood statistics, coupled to a GIS are an effective way of quantifying and visualizing spatial variation.

3.8.4 Sample standardisation

3.15 Since biodiversity measures are a function of sample size (sampling effort), data will be standardized for variance in sampling intensity using two possible methods depending on suitability (rarefaction or regression techniques versus re-sampling methods such as Monte Carlo techniques). The aim will be to have a minimum of five samples per sampling unit. For each unit these data would then be summed or averaged, or if there are more than five samples per unit, repeat samples of 5 would be taken (e.g. using Monte Carlo resampling methods). Rarefaction techniques would be employed to examine whether, for example the number of species found at that level of sampling is significantly higher or lower than expected. Other sources of variability, such as spatial patchiness, will be accounted for in the designation of spatial resolution of spatial units and in the use of neighbourhood statistics.

3.16 Survey method can add significant bias to measures of diversity. Differences in sampling method are strongly related to the type of habitat being surveyed (e.g. grab sampling or coring for soft sediments versus diver observation surveys for reef habitats). In soft sediment post sampling methods can also significantly influence recorded species diversity, for example the size of sieve mesh used or the time allocated to sort samples (Schlacher & Wooldridge 1996). To account for this bias, diversity will be standardised by an appropriate level of method type within a spatial unit and then aggregating within each grid cell to give a final measure of diversity.

3.8.5 Biodiversity measures

3.17 In order to adequately represent marine biodiversity for the benthos we recommend the assessment of species richness, habitat richness (number of habitats/ biotopes[10] per unit), taxonomic distinctness and habitat distinctness as the four main measures. Considered together these measures give an indicative picture of ecological diversity, and enable assessment of the conservation value of a potential site. The data will be presented as continuous values (i.e. these will not be binned into categories relating to ‘hot-‘ or ‘cold-spots’) and the different measures will be presented as separate layers and not combined into a single measure, following discussions from the workshop, and in order to provide a flexible product which can be adapted for subsequent use by stakeholders.

3.18 For species richness calculations, species lists will be compiled for each sampling method type within each grid cell, and the total number of samples that yielded these lists aggregated. Regression techniques will be employed to standardise species richness (i.e. total number of species) for sampling effort, for each sampling method. Regression will be performed with $\log_{10}$ transformation of both axes (transformation of the y axis to straighten the curve, and of the x axis to spread the samples, since most will be at the lower end of the scale) and 95% confidence intervals. Each data point (corresponding to the number of species and sampling effort by method in a specific grid cell), will be assigned a value based on value of residual (distance from the regression line) divided by the 95% confidence interval. This gives a statistically robust indication of whether the data point (grid cell) has a higher or lower than expected diversity for that particular sampling method and number of samples. In the event that large numbers of samples are found within a grid cell, Monte Carlo techniques will be employed to reduce bias incurred by large sample size.

3.19 In order to examine habitat richness, an assessment at a similar level of classification is required. The available habitat data include sub-biotope codes and, in some cases, levels broader than biotope. In the current study we will base the analyses of habitat richness on the EUNIS classification throughout, and where possible will use EUNIS Level 4. Level 6 and Level 5 biotopes will be reduced to Level 4. Any habitats classified at EUNIS Level 3 and above will only be included in the analyses if they represent a distinct biotope within the grid cell (i.e. have no hierarchical children in the same cell).

3.20 Taxonomic distinctness will be calculated only on species from seven phyla/groups will be analysed (Cnidaria, Crustacea, Annelida, Mollusca, Porifera, Bryozoa and Echinodermata). This is because these phyla are widely distributed and have full taxonomic classifications. Master species lists for these seven phyla will be compiled for each broad method type occurring

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[10] Where available (e.g. for the intertidal and inshore areas) biotope level data will be used, for all data a minimum of Level 4 will be employed.

within each grid cell. Master species lists for each broad method type will then be used to calculate the average taxonomic distinctness, using PRIMER-E version 6. Funnel plots will be generated for each method type, indicating the 95% confidence intervals for random ‘expected’ distinctness based on 1000 random permutations of the same number of species from a master list for each method type (i.e. all the species from the UK records found by that method type). The funnel plots can be used to assess statistical departures from the expected levels of average taxonomic distinctness for that sampling method. Residuals can then be used to provide a value on a continuous scale that indicates the unusualness of each grid cell.

3.21 Similarly to habitat richness, habitat distinctness requires measures to be analysed at a comparable level of habitat classification. As previously, EUNIS level 4 will be used, and any Level 5 or 6 biotopes will be reduced to level 4. Any habitats classified at EUNIS Level 3 and above will only be included in the analysis if they represent a distinct biotope within the cell (i.e. have no hierarchical children in the same cell). Funnel plots will be generated as for taxonomic distinctness and values for habitat distinctness will be calculated on a continuous scale.

3.8.6 Validation and confidence layers

3.22 A number of techniques (known as estimators) exist for extrapolating species richness from limited numbers of samples (Foggo et al. 2003) and these will be used to check for artefacts in the diversity analyses. For example the Chao2 estimator is based on the concept that rare species carry most information about the number of missing ones, and looks at species that occur only in one or two samples within a set area (Foggo et al. 2003).

3.23 An analysis of concordance (using Cohen’s Kappa statistic) between measures will be used to quantify the independence of different measures, for example, whether areas of high habitat diversity match up with those for species. Previous work carried out at a local scale (Firth of Clyde, Langmead et al. 2008) found that no single measure captured all aspects of benthic biodiversity, but it is important to ask this question at the regional (UK-wide) scale. Carrying out an assessment of concordance would show whether it is possible to use one or two of the layers as indicative of areas of high biodiversity (which may be easier for stakeholder interpretation) or whether all the layers are necessary to illustrate different aspects of biodiversity.

3.24 In addition to the quality criteria applied to the collated data sets, confidence ratings based on the quality and quantity of data used in the final analysis will be calculated for each grid cell to provide users with a view of the underlying data when examining the occurrence of high levels of diversity. The confidence map layer will also flag where invasive species and very old data have contributed to the area of diversity. Task 1C is examining the confidence of broad-scale habitat maps that will be used as the basis for assessing biodiversity areas in the offshore benthic areas. The output of this task will be incorporated into the confidence map for offshore biodiversity layers.

3.9 Pelagic diversity data layer

3.9.1 Identifying thermal fronts: pelagic diversity surrogate

3.25 The proposed approach is to exploit a long time-series of EO SST data to map frequently occurring, persistent thermal fronts within UK waters. Algorithms developed by Plymouth Marine Laboratory (PML) enable fronts to be located accurately and objectively. The composite front map technique combines the location, gradient, persistence and proximity of all fronts observed over a given period into a single map (Miller in press). This often achieves a synoptic view from a sequence of partially cloud covered scenes without blurring dynamic fronts, an inherent problem with conventional time-averaging methods (

3.26 Figure **5**).

3.27 The first output would be a 10-year sequence of monthly front maps at 1 km resolution. This high spatial resolution is necessary to resolve mesoscale fronts, some of which may only exist close to the coast. These monthly maps would enable tracking of dynamic and mobile fronts that would not be represented in the subsequent stable front analysis.

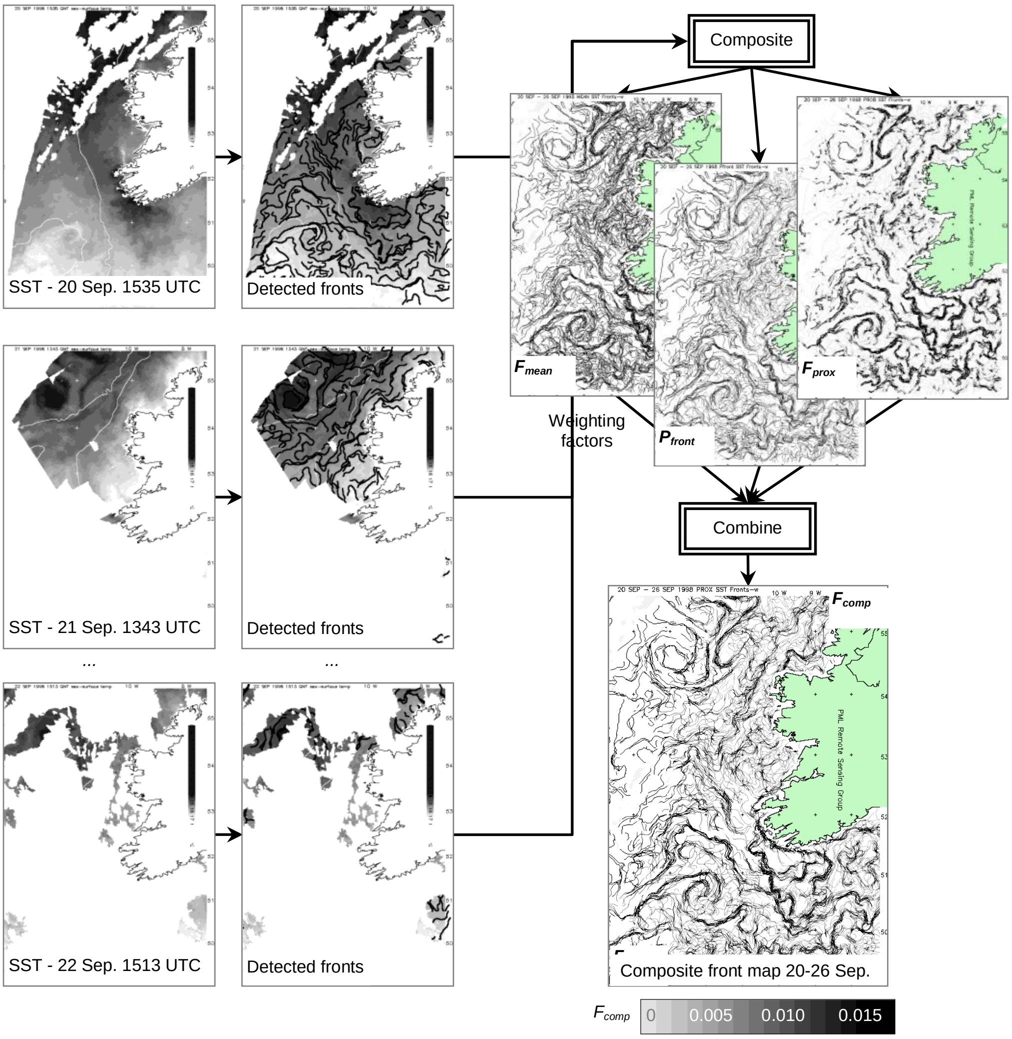
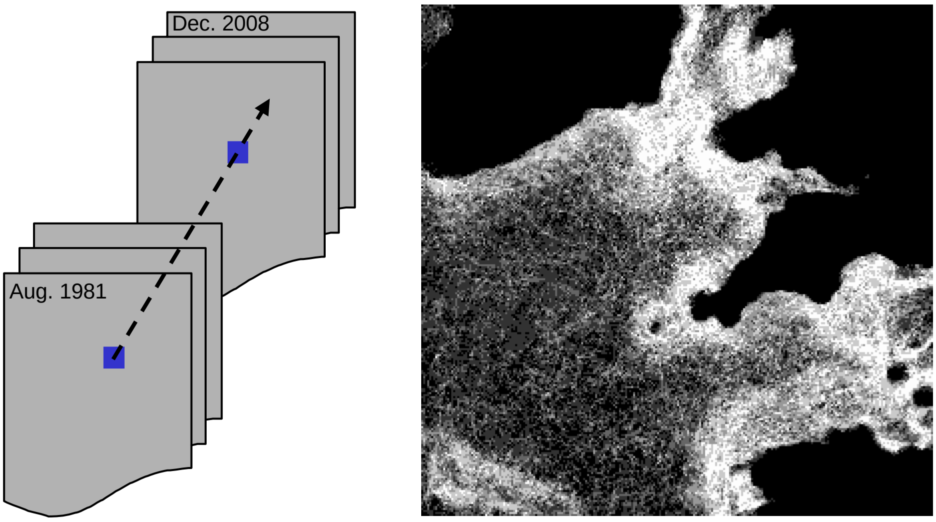


Figure 5 Schematic diagram of composite front map technique. 30 AVHRR SST maps (three shown) of the Irish shelf within a 7-day window are processed to detect front locations, which are then composited to calculate the mean frontal gradient Fmean, the probability of detecting a front Pfront, and the evidence for a feature in proximity Fprox. These weighting factors are combined as the composite front map Fcomp to provide optimal visualisation of all oceanic features observed during the period.

3.28 The second stage of analysis would be to aggregate the monthly maps into monthly and seasonal front climatologies to identify strong, persistent and frequently occurring features (Figure 6). Such frontal systems would be key factors influencing the distribution of productivity and diversity. An algorithm has been developed and tested to perform this aggregation, and estimates the percentage of time a strong front is observed within each grid location.



(a) (b)

Figure 6 Front aggregation method. (a) Each grid location is analysed through the time-series of monthly fronts to calculate the percentage of months in which a strong front was observed. (b) Example front climatology map for June for UK SW area using 2003-2007 data.

3.29 The source of data for this frontal analysis is the AVHRR archive acquired by Dundee Satellite Receiving Station, several passes per day over UK continuously since August 1981. This covers UK waters at the 1 km resolution necessary for detection of all scales of fronts relevant to biodiversity areas. PML have developed automated processing systems to allow AVHRR infrared data to be calibrated into SST values, navigated, cloud-masked and mapped consistently for the UK region (Miller et al. 1997). It is recommended that at least 10 years of data are used to encompass the inter-annual variability; though the entire 28 year archive could provide greater confidence in describing this variability.

4 Time-tabling issues and estimated costs

4.1 Production of the marine diversity area layers as discussed at the workshop, project steering group meeting and proposed here are dependent on data being collated as part of other tasks within the MPA data layers project. Tasks 2B and 2C, are collating available species and habitat data and extracting priority species and habitats, however the data collated can be used in its entirety to identify biodiversity patterns.

4.2 In order to deliver the diversity areas layers based on the best available information we are proposing a timetable which delivers draft biodiversity layers and a report on the 29th January 2010 (see Table 4 and Table 5). In

Table 4 we have presented an adaptation of the timetable illustrating when the data, on which the biodiversity analysis will be based, will be available and the subsequent time taken to carry out the analysis. This is a preferred option because it is based on the best available data for the time and allows the biodiversity analysis to be carried out properly, once, thus reducing costs.

Table 4. Costs for carrying out Task 2F Biodiversity areas layers. Deliver all layers by 29th January 2010

Task	**Sub-contracts**	**MarLIN/ ABPMer Costs**	**Total Costs**
1. Collect and collate existing marine biodiversity data for UK waters			
1.1 Benthic - Use draft species and habitat data from MPA data layers (all data to be supplied by external parties by the 14th of September 2009 in order to keep to schedule).		£1,300	£1,300
1.2 Pelagic – Data collated and quality assessed for: Earth Observation data: Fronts	£21,440	£130	£21,570
1.3. Collate available species and biotope information into geodatabase		£910	£910
2. Pre-analysis			
2.1. Review data sets to identify adequacy, comparability and appropriate spatial scales based on data and ecological relevance		£2,090	£2,090
2.2. Apply methods for minimizing impact of variability in data sets (divide by sampling method, set up neighbourhood queries)		£3,560	£3,560
2.3. Run geo database queries		£1,510	£1,510
2.4. Estimate for reruns of geo database queries following PSG review		£860	£860
3. Conduct diversity analyses and generate maps			
3.1. Conduct diversity analyses for each region at each appropriate scale (including running Monte-Carlo simulations, Primer analysis and rarefaction techniques, neighbourhood methods). Benthic – Species Richness Biotope/habitat richness Biotope/habitat distinctness Taxonomic distinctness		£2,520	£2,520
3.1. Generate GIS data layers		£1,210	£1,210
3.2. Review of the layers with PSG and estimated reanalysis costs		£1,410	£1,410
3.3. Estimate for generation of GIS layers following PSG review		£235	£235

Task	Sub-contracts	MarLIN/ ABPMer Costs	Total Costs
4. Validation			
4.1 Benthic – Concordance between measures (including predictive data versus actual – where overlaps exist), Chao estimator.		£630	£630
4.2 Pelagic – concordance with pelagic fish distributions produced by task 2B	£2,000	£630	£2,630
4.3 Production of GIS confidence layers.		£1,030	£1,030
5. Project reporting and management			
5.1 Project meetings			
Planning meetings		£480	£480
Progress meeting		£1,110	£1,110
T&S (1 trip Southampton for 2; 1 trip London for 2)		£650	£650
Video conference meetings		£420	£420
5.2 Draft report		£2,470	£2,470
5.3 Revise and finalise report based on comments received		£1,580	£1,580
Printing costs (estimated)		£800	£800
Consultancy – advise and expertise Dr Keith Hiscock (2 day), Dr Andrew Foggo (2 days)	£1,950		£1,950
Equipment – Processing computer (64-bit dual processor workstation. 16GB RAM, 600GB HD and high-end graphics card)		£4,000	£4,000
Staff cost		£24,085	
Overheads (at 100% staff cost)		£24,085	
Total cost	**£25,390**	**£53,620**	**£79,010**
+ VAT 15%			£11,852
Total cost inc VAT			**£90,862**

Table 5 Indicative timetable for carrying out Task 2F Biodiversity areas layers: Deliver draft 29th January 2010

Task	May	June	July	Aug	Sept	Oct	Nov	Dec	Jan
1. Collect and collate existing marine biodiversity data for UK waters									
1.1 Benthic - Use data already collated as part of 2B and 2C Collate surrogate data (all data to be supplied by external parties by the 14th of September 2009 in order to keep to schedule).				■	■				
1.2 Pelagic – Data collated and quality assessed for:									
EO	■	■	■	■					
1.3. Data to geodatabase	■	■	■	■	■				

Task	May	June	July	Aug	Sept	Oct	Nov	Dec	Jan
	▨	▨	▨	▨	▨				
2. Pre-analysis (will be carried out as and when data become available)									
2.1. Review data sets to identify adequacy, comparability and appropriate spatial scales.					▨	▨	▨		
2.2. Apply methods for minimising impact of variability in data sets					▨	▨	▨		
2.3. Run geo database queries					▨	▨	▨		
3. Conduct diversity analyses and generate maps									
3.1. Conduct diversity analyses for each region at each appropriate scale (including running Monte-Carlo simulations, Primer analysis and Rarefaction techniques, neighbourhood methods).						▨	▨	▨	
Benthic – Species Richness						▨	▨	▨	
Taxonomic distinctness						▨	▨	▨	
Biotope/habitat richness						▨	▨	▨	
Biotope distinctness						▨	▨	▨	
3.1. Generate GIS data layers					▨	▨	▨	▨	▨
4. Validation									
4.1 Benthic							▨	▨	▨
4.2 Pelagic					▨	▨			
4.3 Production of GIS confidence layers.						▨	▨	▨	▨
6. Project reporting and management									
6.1 Project meetings									
Planning meetings			▨		▨			▨	
Progress meeting			▨	▨	▨	▨	▨	▨	
6.2 Draft report – 20/12/09								▨	
6.3 Revise and finalise report based on comments received									▨

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Appendix 1 Biodiversity Hotspots Workshop Transcript by Justine Saunders, ABPMer

Date: 8th January, Time: 10 am – 4 pm
Venue: Associated British Ports, 150 Holborn, London, EC1N 2LR

Organisers: Justine Saunders (ABPmer) jsaunders@abpmer.co.uk 02380 711 840 Emma Jackson (MarLIN) Olivia Langmead (MarLIN) Heidi Tillin (ABPmer)
Attendees: Kirsten Ramsay (CCW) Michel Kaiser (University of Wales, Bangor) Leigh Jones (NE) Beth Stoker (JNCC) Keith Hiscock (Associate of MBA) Julie Bremner (Cefas) Andy Foggo (University of Plymouth) Louise Lieberknecht (Finding Sanctuary) Nick Polunin (Newcastle University) Abigail McQuatters-Gollop (SAHFOS) *Contributors to Workshop material:* Peter Millar Clive Fox *Note: Comments by individual attendees are represented by their initials*

WORKSHOP NOTES

These notes represent the issues discussed and comments raised during the workshop. Presentations that supported the discussions are attached separately to this report.

Introduction and Background

JS outlined the approach for the day and then gave a background into the project including the tasks associated with other data layers and collaborators associated with the project (see attached presentation).

In particular, it was noted that the purpose of MCZs (as specified in the Marine and Coastal Access Bill) is to conserve or aid the recovery of:

- rare or threatened species and habitats;
- globally or regionally significant areas for geographically restricted habitats or species (e.g. estuary habitats and the spiny lobster);
- important aggregations or communities of marine species where a large number of species occur in one area, particularly hotspots;
- areas representing a range of biodiversity in UK waters;
- areas important for key life cycle stages of mobile species, including habitats known to be important for reproduction and nursery stages;
- areas contributing to the maintenance of marine biodiversity and ecosystem structure and functioning in UK waters; and

- features of particular geological and geomorphological interest.

In order to support the identification and management of MCZs the following tasks (contributors in brackets) are specified within the overall project:

Task 1 – Improve existing habitat maps - biotope tagging, translation and confidence assessment mapping (EMU, ABPmer, MarLIN + independents)

Task 2 – Data layer development:
  2A: Geological and geomorphological features (ABPmer)
  2B: Species data (MarLIN, Cefas)
  2C: Habitats data (MarLIN)
  2D: Non native species (MarLIN)
  2E: Models of fetch and wave exposure (ABPmer, POL)
  2F: Biodiversity hotspots (MarLIN, ABPmer)
  2G: Residual current flow (ABPmer, POL)
  2H: Benthic productivity (ABPmer)

Task 3 – Sensitivity mapping (ABPmer, MarLIN)

Task 4 – Data management – maximising access and use (ABPmer)

It is important to note that biodiversity hotspots will be just one of many data layers used to inform the MCZ process and that there is potential for inputs from other tasks into this one.

Biodiversity data layers approach

Emma Jackson from MarLIN then gave an overview of approaches to identifying hotspots and an introduction into the various issues.

LL made the comment that the approach taken is dependent on:
what is possible with the data available and
how the data is to be used

LL provided insights into the MCZ planning process where ‘stakeholders’ will have an active involvement in site selection. They will be given data layers or maps of relevant information (collated into Regional Profiles) and asked to provide feedback on where they think sites should be. This process would have to conform to guidelines set out by the Scientific Advisory Panel (SAP) in terms of targets for representivity and replication, size and priorities for protection etc. LL also said that hotspot layers would be more useful if provided separately rather than pre-aggregated into one score.

Emma Jackson suggested that we clarify our working definition of Biodiversity hotspots for the purposes of the MPA data layers project.

Definition of biodiversity hotspots

Biodiversity of what?

We could consider:

- A focus or weighting on priority species (part of tasks 2B/2C)
- Pre-selected representative or indicator species and habitats
- All species and habitats (where records allow)

KH suggested that we should identify the 'best' sites but this would leave us open to interpretation of 'best' which should be up to the Scientific Advisory Panel to decide or provide a steer on.

Distributions of priority species and habitats are being investigated as part of task 2B/2C in the project and include those on the OSPAR and BAP lists. Nationally Important Marine Features (NIMFs) are not included in this current project. A priority species hotspot layer could be an add on to task 2B/C using methods identified in 2F, as stakeholders may find it difficult to view 50 or so species and habitat distribution maps. A combined map may facilitate the consultation process (LL) but may also be redundant if rare and scarce species are limited to a single record (MK).

Biodiversity as a whole is the criteria, not single species or species group hotspots and the data layer should provide a clear guide to a unique characteristic, e.g. not priority species which is a separate data layer. Ultimately the group decided that it would be good to investigate numbers of both priority species and all species or habitats within a 'sampling unit' but to keep these layers separate as this will provide the SAP with flexibility in the management and consultation process.

There are problems with setting criteria to define 'hot' and it was generally agreed that the term 'hotspots' is somewhat misleading (what about lukewarm?).
It would be better to investigate producing a range of biodiversity levels mapped on a continuous scale. This would also allow a common base between different countries who may wish to display the information differently.

At what stage in the MCZ process should we apply a hotspots layer?

EJ suggested that it be used to prioritise sites which have already met other criteria in terms of representativity, replication, connectivity.
LL and BS advised that it would be one of many information layers used by stakeholders in the consultation and planning process to ID sites.

A suggestion was made to use Marxan to identify sites from the variety of data layers but BS commented that different Devolved Administrations and the associated Statutory Nature Conservation Agencies may use the data differently or use alternative decision support software and that we should aim to keep the data as flexible as possible in terms of format.

Furthermore, ranking of data layers has not yet been decided. It is likely that some data layers will be mandatory, and others optional (BS). It was repeated that we should just be providing a scientifically robust information layer and not provide advice on what sites are 'best' nor how the data should be used.

Metrics

EJ introduced a number of different metrics, which have been utilised in past studies and comments were collated about them in the form of discussion and post-it notes (see Table

A1 below). It was agreed that we should also take care over whether we’re measuring alpha or beta diversity

Table A1 List of potential metrics and comments

Metric	**Description and workshop comments**
Species/habitat richness	doesn't convey spread in abundance, but is easy to apply and less sampling bias easy for non-specialists to understand but influenced heavily by sampling effort richness is ? for number of entities sampled so it is actually a per-entity encounter rate; use "number of different species/biotopes" the most appropriate for our data what about higher phylogenetic level "diversity" (genetic correlate?) consider a per sample rarefied measure work on presence/absence data due to data inadequacies? and different sampling systems?
Chao 2 estimator	*based on the concept that rare species carry most information about the no. of missing ones* use to look for artefacts also incidence coverage estimators other chao estimators must limit spatial extent of samples used in calculation of estimator alpha not beta diversity effectively consider ICE estimator as well
Evenness	*conveys spread, but requires abundance data* if you plan to use evenness, why not use parametric diversity estimator like H' which incorporates it and species richness anyway requires abundance data which will be biased by sample size (area covered)
Diversity indices (e.g. H')	*a combination of the above that does not adequately represent either?* Many are, to me, pretty sample-size robust beyond quite trivial numbers of samples
Taxonomic or Biotope distinctness	*represents phylogenetic or broad habitat diversity and robust to sampling effort, but may not be appropriate as a relative measure* affected by scale and geographical scope fairly robust to sampling effort compared to other metrics quite robust and hopefully more ecologically meaningful than some of the others? Taxonomic distinctness is sample size independent (AF) since the geographical scope of the study determines the branch length
Surrogates	Look at inputs from the biomass data layer (Task 2H) For offshore and data poor areas we have to investigate the use of surrogates, both for benthic and pelagic biodiversity. This may be for benthic productivity, biomass, topographic complexity etc. For pelagic this may be planktonic, chl a or

Metric	Description and workshop comments
	upwelling information. KR mentioned that Ireland have an example where researchers used the biodiversity of molluscs as a proxy for the entire marine community.
Others	Expert opinion - needs appropriate documentation (KH) and should be applied in the stakeholder process (LL, BS) not in the data layer itself. Validate by analysing deviation from nestedness at an appropriate scale? Indicates “different” or unique assemblages (AF - this can be successfully calculated from presence/absence data)

Metrics and maps should inform the identification of MCZs/HPMRs but not determine them – important to use professional knowledge and commonsense.

Functional diversity

Although not the main focus of the MCZ study, measures of functional diversity may also be very useful as there is a strong focus on this in other policy areas (e.g. ecosystem approach).

However, there are complex issues over what metric to use (AF).
Furthermore, taxonomic distinctness (see above) may capture this to a certain extent (EJ)

Although the data may not yet exist or be robust enough to support the data layer (LJ, JB), there is a lot of good work being done that we can use to provide some recommendations from (e.g. approx 250 species in the BIOTIC database www.marlin.ac.uk/biotic).
AF has found good correlations between measures of functional diversity and taxonomic distinctness.
However, other work by HT (unpublished), has found that indices of taxonomic distinctness do not correlate well with functional diversity.
JB commented that since there is no consensus on the measure used for functional diversity, if some people consider taxonomic distinctness to be a useful approximation to functional diversity and they have evidence to support their assertion, it may be appropriate to use it.

Sampling issues

A number of points were made in regard to spatial scale as follows:

MK – important to analyse at the regional level although there was discussion over what regions – draft Regional Seas boundaries are currently being updated?
MK - scale determines whether α or β diversity is assessed.
A benthic/pelagic split was generally accepted however there was much discussion over an inshore/offshore split and where this boundary might be.
The ‘offshore’ region will be highly dependent on modelling approaches therefore needs to be considered/analysed separately. See outputs from the Productivity Task 2H. Kerry Howell’s work in the NW offshore region was noted. Surrogates such as sediment data will be useful. BS mentioned that some data from the NOC will be available in April.
MK – Try linking to underlying mechanisms behind biodiversity, e.g. ecological factors such as wave stress, 25 m depth contour, etc. or other indicators of the influence of land (KH).

Use different planning units for different areas, e.g. for the inshore (sub km scale) compared to the offshore (AMG used 0.5-1 degrees) and also for different physiographic features, e.g. lochs and estuaries.
Dividing the analysis over management or political boundaries (e.g. 6 or 12nm, Wales, Scotland England) was considered to be unnecessary.
Interpolation of data – recognise that there are issues with the use of gridded cells, polygons and physiographic features, but that some unit is required for analysis.

Some site-specific issues with the way data is collected but MNCR data are mostly vector/point data.
There are some issues with the way you might select a site/region/ physiographic feature, e.g. Menai Strait? Perhaps it might be useful to apply the methodology to a pilot area first.
Neighbourhood statistics – combine data only choose those neighbouring polygons of a similar physiographic type (e.g. estuarine).
Use of POLCOMS data was mentioned – this is modelled physical data from The Proudman Oceanographic Laboratory Coastal-Ocean Modelling System
Sub-setting the data by sampling method for the analysis, e.g. use of cores, grabs, trawls, can minimise variability and account for differences in physiographic type.
There are also temporal issues in terms of the seasonality of the data, the age of data that has been used (e.g. no older than 50 yrs?)

There is a potential issue relating to species/regime shifts over the time period of assessment (AMG). For example, if the community has shifted for some reason such as climate change, then the assessment would count species recorded before the change as well as those new species recruited after, leading to incorrectly high estimates of biodiversity. It will be useful to look at a time series of data if possible.

Issues relating to quality of data, age of data and method of sampling highlight the necessity to provide some underlying confidence assessment of the data layer. The methodology for this might be drawn from Task 1C.

Finally, discussions regarding the techniques for minimising sampling effort bias (e.g. rarefaction, monte carlo, sample independent metrics) highlighted the importance of these and the need for subsectioning data poor regions and using different methods. The point was also raised that individual records should be left out of analyses which incorporate some statistical techniques for minimising sampling bias (another advantage of splitting data by collection method).

Benthic Breakout Group

Quality Control Issues

Marine Recorder database and MESH has some confidence information associated with data.
ISO data quality criteria applied to the data and low quality removed.
Additional decisions regarding criteria for inclusion/exclusion of data will depend on expert judgement when the data is queried.
A confidence map should be produced with each hotspot map (link to methodology being developed in 2C).

What metrics to use?

As above, use a range of metrics to depict species and habitat diversity and to best represent the available data within each region or realm, but do not use a combined hotspot scoring approach, keep all layers separate.

What to measure?

Benthic biodiversity should include fish species with a benthic association. KR raised the point that records for territorial fish are poor.
Invasive species should be included but to tag those areas that have an invasive species component.
As above, focus should be on ALL species where possible but a summary diversity distribution map of priority species could be added as a useful layer for Task 2B.
The lists to use should be consistent across the study, i.e. the OSPAR and BAP species included in Task 2B but not NIMFs (these will be captured in the data layer of all species)
MK made the point that a diversity data layer of rare and scarce species may be somewhat redundant when you could be restricted to a single record and when you're restricting the species counted in the measure of diversity.

Data availability and gaps

There are two aspects to data gaps: data available but not accessed and true data gaps (EJ).

Sources through MARBEF and DASSH: In some cases data may be extracted in some form even though the entire data set is not released, i.e. species presence but not abundance. These effects may lead to loss of information and influence the diversity metrics that can be used.

There is a lot of unreleased data (e.g. MK's benthic data) and lots of 'grey' data held in academic or industry records (e.g. Oil and Gas – see John Hartley from Hartley Anderson Associates and The Crown Estate, Marine Aggregates Levy Sustainability Fund reports - JS). Also suggestions for data not held on national databases (e.g. CEFAS data, Irish Sea data held in the Isle of Man).

Hotspots of 'data' are likely to occur around the NW Seamounts (BS), Rockall Trough (SAMS). There was also a suggestion to use VMS data intensity as a proxy for offshore diversity (MK).

Spatial scales

How do we divide the seabed for analysis?

Intertidal/Subtidal
Inshore/Offshore
Data rich/Data poor
Physiographic features

General agreement to divide into four areas, coastal, inshore, offshore and deep-sea.

A suggestion was made to divide seabed according to management scales, e.g. 1 nautical mile limit of Water Framework Directive. 3 nm would separate the area under most coastal influence (KH) 12 nm territorial limit. However, for the analysis itself it's not so important how the data is to be used/managed. Therefore management boundaries are less important in producing the data layer.

MK noted that it was more important from an ecological sense to focus on drivers of diversity, e.g. wave stress for inshore areas, 25m depth contour.

Important to define deep-sea region as input of food sources is likely to be different from that on the continental shelf and inshore regions (>200m?)

You may also want to measure biodiversity differently in the different areas.

What scale should we use?

Largely agree that the data itself will define this.
There may be differences in the way that you analyse different habitats (e.g. intertidal vs subtidal) and also data collected using different methods, e.g. consistency in sampling and gear used.
Dependent on inshore (sub km) vs offshore (0.5-1 degree lat and long)
You could do a sensitivity analysis of the effect of using different scales. AF proposed that by plotting the average number of species per grid versus effort for each grid size, a move from a logarithmic to Poisson distribution could be taken as indicative of appropriate unit size for a grid based method.
Use of neighbourhood statistics or roaming windows are a necessity.

Temporal issues

Date limit for data?

EJ raised the issue of repeat surveys and very old data for discussion.
LL – Important to have a date limit but the data may define this.
LL – used 20 years, any less than this and lost too much data
AMG – as with plankton there may be issues with regime shifts
Perhaps use time series data for areas of concern
In the absence of any recent records for an area it might be worth using old records but flagging them as such (as suggested for invasive species). This will therefore identify the need for up-to-date survey information at that locality and help to inform stakeholders about the quality of the data (EJ).
EJ commented that some older data would be removed during quality assessments but not all.
Many agreed that a confidence layer will be important to capture this information (e.g. age and quality of data).
Based on long-term observations many places remain the same (KH)
Need to be aware of changes in taxonomy over time (KR).
There will be positioning errors between data sets of different ages.
Marclim have some evidence for changes along the south coast and, possibly up the North Sea coast. Marclim cover mainly key intertidal species. Speak with Nova Mieszkowska at the MBA (JB)
There are climate-related temporal changes in the North Sea from subtidal studies of soft sediments (JB)
Don't add two data sets together (KR)

General data issues

Some data sets are limited to specific taxonomic groups (KR)
Consideration required for treatment of mobile species that form part of the biodiversity but are not always present.

Effort bias

MK provided a useful approach:
Ensure that you have at least 5 samples per sampling unit
Sum or average this data
If more than 5 samples per unit take repeat samples of 5 (e.g. using Monte Carlo statistical sampling methods)
Rarefaction is problematic – incorporates modelling error
If you have actual samples and data, use them.
Assess sampling effort by considering the frequency distribution of sampling and the move from a logarithmic to poisson distribution (AF)

Pelagic Breakout Group

Olivia gave presentations on existing data holdings from
Peter Miller (PML) on existing Earth Observation data (e.g. SST fronts and chlorophyll a measurements)
Clive Fox (SAMS) on existing fish diversity and spawning grounds data

Physical predictors and surrogate measures

Use all data that you have, e.g. fronts, SSTs, Chl a, fish data.
It would be good to have use of the mobile fish species data (including spawning grounds) from Task 2B but this won't be delivered within the timeframes for use in this project and only focuses on priority species (e.g. OSPAR and BAP species lists)
MK – the consistency and persistency of oceanic frontal systems is supported by a number of studies.
What about estuarine mixing fronts (JS)?
Note that surrogate measures such as frontal systems and spawning grounds also highlight ecosystem functioning, i.e. feeding and spawning.

Spatial and temporal scales of analysis

The key frontal systems to focus on will be those that are persistent on a seasonal basis. The analysis is best carried out from monthly climatology over a set time period, e.g. 10 yrs (BS - noted that the MCZ reporting cycle outlined in the Marine and Coastal Access Bill would be every 6 yrs from 2012).

More mobile features could be assessed in real time and could feed into seasonal and adaptive management measures. Difficult to identify hotspots for highly mobile species although there are some well known single species megafaunal hotspots, e.g. basking sharks. David Sims has done some tagging work on them and the MBA holds a database on their sightings (volunteer records but not effort corrected).

Other comments included the following:
There are regional considerations (E different to W)
BS – Callum Roberts has reviewed connectivity and adequacy for MPA sites in a contract for NE, but this is not publically available yet
There should be an overall consistency in layers: the same cut off between inshore and offshore should be used for the pelagic and benthic studies.
Divide into four areas, intertidal, inshore, offshore, deep sea. Deeper waters only have EO data (OL).

Links between pelagic productivity and diversity

Links are generally very good, supported by a number of studies (MK)
The shape of this relationship could be used to model the biodiversity.
Use of Earth Observation data requires support from groundtruthing exercises (AF).
There may be timelags between an increase in diversity in relation to blooms and ‘snapshot’ approaches may miss this (AF)
Theoretically higher productivity will result in higher diversity due to an increase in ecological niches (JB), but need shape of productivity/diversity relationship, would predict this to be unimodal (AF).
KH advocated the use of proxy indicators for pelagic biomass such as porpoises, dolphins and seabirds.

Data availability and gaps

Some data on fish species but mostly commercial – demersal data is good, pelagic isn’t (mackerel, herring and sprats only and these are acoustic data restricted to Scottish waters, collected by FRS) - remove pelagic species from samples collected using bottom gears
Risk that just relying on commercial fish species will be contested, therefore need to support with other data as noted above. Possible data sources are: Atlas of Cetacean distribution in north-west European waters; SCANS 2 cetacean data; European seabirds at sea; etc. (BS)
Data from commercial catch species will reflect quota limits set for these species (HT)
MK - Issues of catchability addressed by Simon Greenstreet (FRS)
MK – Fisheries data is limited in that it samples on a species by species basis; there is no measure of community structure, but commercial data is all that we have for pelagic species
MK – GOV data samples all demersal species, approx 8m off the seabed but doesn’t include the English Channel or Irish Sea)
MK - Distribution of fishing vessels (from VMS data) overlaps with the location of ocean fronts. Bycatch data may give an insight as well, but is hard to obtain.
MK - Stuart Rogers (Cefas) ran inshore juvenile fish surveys up until 1999 – see technical reports by Cefas. The bottom trawl surveys were run at least twice a year
MK – Andy Brierly from St Andrews looked at jellyfish distributions
Use GOV trawl data to validate predictions from sea surface temperature and other EO data (AF)
Take maps of beam trawling into account, these are unable to fish in some areas (JB)
Use cetacean and seabird occurrence data to validate (KH)
Including fish spawning areas is a thorny issue (AF) data may only exist for 1-2 commercial species (OL).

Management Issues

Protecting breeding areas is key to conservation of species (AF).
Issues around including commercial species as these populations face different pressures
Managing fisheries could have noticeable effects in trophically linked areas (JB)
Confidence in data, to use or not? If data is used it may promote conservation in the wrong area, but if it is not used then there may be no conservation at all (AF).

Plankton

There are two different regimes in the North Sea (AMG) but we should focus on what areas have high levels of plankton (biomass) irrespective of species identity. However, it will still be important to set the time period for assessment carefully so that species from both regimes are not included in the analysis, i.e. before or after the regime shift.
AMG – Plankton data do not identify species of fish larvae and eggs. However FRS do identify species in some of their sampling for toxic plankton.

Other issues

The point was made that there should be the ability to update data layers at a later point and the importance of adaptive management.

Overall Summary

Key points were made as follows:

- Investigate other approaches but generally there was consensus with the overall one presented.
- Definition of biodiversity hotspots should refer to all species (not just priority ones) and a range of levels (i.e. not just ‘hot’).
- Present separate maps of
- The number of species in a sampling unit
- The number of pre-identified rare and scarce species in a sampling unit
- Aim is to present a scientifically robust information layer that is unbiased and flexible, i.e. can be used in the planning process in a number of different ways by a number of different agencies
- Use and combine a number of different metrics.
- Investigate functional diversity and make recommendations
- Investigate the issues with making different divisions (e.g. inshore/offshore) and make recommendations
- Try linking to underlying mechanisms behind biodiversity, e.g. ecological factors
- Use different planning units for different areas, e.g. for inshore vs offshore and also for different physiographic features.
- Investigate a time series of data to look at temporal issues, i.e. regime shifts
- Provide a confidence assessment of the data layers

Appendix 2 Proposed approaches for non priority measures/ indicators for the Benthic diversity data layers

Incorporating demersal fish data

In general more mobile species such as demersal fish are under-represented in most benthic data sets, due to difficulties in observation, in-situ identification and/or catchability (Rozas & Minello 1997). Additional data sets showing the distributions of demersal fishes would need to be incorporated but this data would need to be handled separately due to the focus of the survey on only one group.

Demersal fish data are available from commercial data. Commercial fishers are required to record their catch by ICES rectangle[11]. The logsheets are handed in at the port of landing and the data aggregated to produce annual statistics by the Marine and Fisheries Agency. Enquiries are being made as to whether the agency can supply the raw data. However, commercial fisheries data will only record commercial species whilst the gears used usually have too large meshes to retain the full range of fish species in the area. Vessels from other nations fishing in UK offshore waters will hand their logsheets into the port of landing. Therefore records from the UK will be incomplete for the sea area and the range of species reported will be affected by fleet characteristics e.g. traditionally the Dutch fleet targets more flatfish. If commercial catch data can be obtained to ICES rectangle level it may give some indication of overall diversity patterns but is unlikely to be sufficiently taxonomically resolved to generate useful biodiversity indices and research survey data is likely to be much more suitable, and is therefore proposed for use in this work.

The fisheries agencies have conducted regular research surveys covering most of the UK offshore waters. Internationally these surveys are co-ordinated through ICES (International Bottom Trawl Working Group and Working Group on Beam Trawl Surveys). The gears and tow criteria are standardised between participating countries although some changes in gear have occurred over time. However, for the last decade, gears have been standardised. Generally on research surveys all fish caught are identified to species level. Abundance is usually expressed per hour of towing. The timing of surveys has varied but generally at least quarter 1 and quarter 3 data are available although in some areas only a summer survey is undertaken e.g. the western Channel.

Recent work on using the North Sea Q1 GOV survey data to map fish biodiversity (Figure 7) shows the importance of (a) Need to clean raw data for non-standard tows, the information required for this may not be available in the DATRAS database[12] (b) Need to aggregate at least 20 tows to reduce variability (c) Need to correct the raw data for catchability before computing diversity indices which take account of abundance as well as species presence/absence (Fraser et al. 2008).

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[11] ICES rectangles recorded to 4 figures are boxes of 1 degree of longitude x 0.5 degree of latitude

[12] ICES database of trawl surveys (http://datras.ices.dk/Home/Default.aspx)

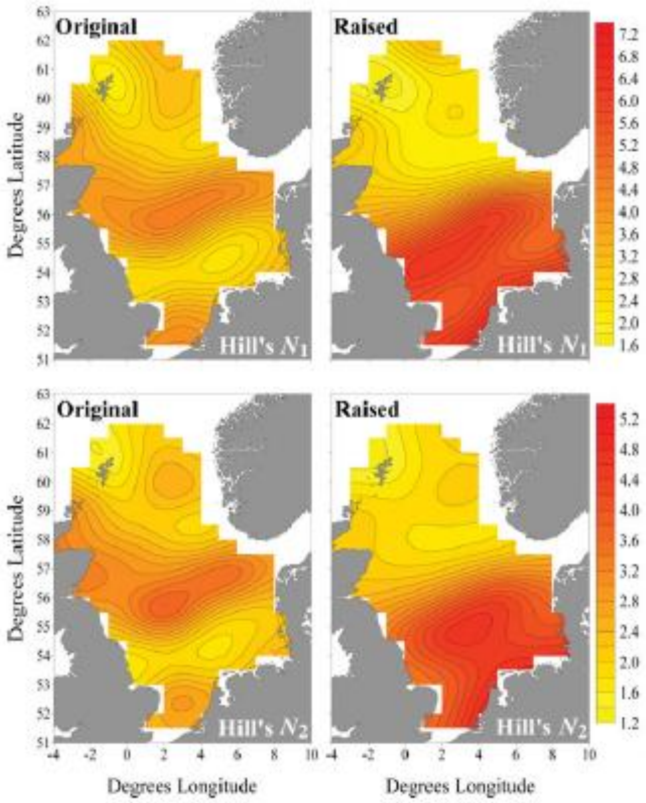

Figure 7 Spatial variation in Hill's N1 (exponential Shannon Weiner) and Hill's N2 (reciprocal Shannon Weiner) across the North Sea based on the ICES International Bottom Trawl Survey using GOV TV3 trawl (IBTS GOV) data set, illustrating the effect of taking into account species- and size-related catchability in the GOV trawl data (Fraser et al. 2008).

Predictive modelling of diversity areas

Predictive modelling offers a method to counter the extremely data poor offshore areas and fill the survey gaps in the inshore areas by relating patterns of biodiversity to environmental parameters. Predictive modelling could only be undertaken after the proposed work mapping the current known distribution of diversity (and all the steps related to standardizing for issues of scale, sampling method and heterogeneous spatial spread of samples) had been undertaken.

The known distribution of benthic marine biodiversity would comprise the first step of the process. Environmental data sets would then be acquired. For the MESH EUNIS Model, these included:

- substrate;
- depth;
- tidal bedstress;

- light reaching the seabed; and
- wavelength.

This would be considered the minimum requirements for predicting biodiversity. Additional measures could include suspended particulate matter, chlorophyll a concentrations and a measure of benthic productivity (e.g. secondary production) if this data layer were available for entire UK waters.

Two modelling approaches would be contrasted to evaluate the best technique to apply to predicting biodiversity: 1) generalized additive modelling approach (GAMs) and 2) Bayesian belief networks (BBNs) (Guisan & Zimmermann, 2000; Sandman et al., 2008). While both of these techniques rely on statistical relationships, the latter is a stochastic approach that describes relationships as probability density functions. These act as a common metric, allowing the integration of quantitative and qualitative information, including discrete and continuous data (Langmead et al., 2008). In addition, BBNs do not require specific understanding of the complex systems linking two causally-related variables because changes are represented as probabilities and uncertainties are implicit in their distributions. Using this technique, sensitivity analyses can be carried out to assess the importance of the environmental variables. Both models would be developed using the mapped biodiversity layer in combination with environmental data. To maximise the use of data for model construction and avoid partitioning data sets for validation purposes, cross validation would most likely be used (such as leave-one-out cross validation).

Finally, we believe that caution needs to be extended when relating biodiversity to productivity (or other measures of EF); the relationship is complex (Seoane et al., 2005) and factors such as habitat complexity (arising from structural biogenic species) are likely to play a role in determining diversity but not necessarily productivity . In pelagic systems it cannot be assumed that high productivity is associated with high diversity (hence the need for both plankton diversity and chlorophyll measures), certainly this is not the case for pelagic fish communities that are dominated by few species such as herring and sandeel.

Appendix 3 Proposed approaches for non priority measures/ indicators for the Pelagic diversity data layers

Pelagic diversity measures: Plankton

Available data

The Continuous Plankton Recorder (CPR) has monitored the North Atlantic marine ecosystem for > 75 years using a largely unchanged methodology (Batten et al. 2003). Sampling is carried out by a high-speed plankton recorder that is towed behind ships of opportunity in the surface layer of the ocean (Batten et al. 2003). The CPR records > 400 plankton taxa as well as the Phytoplankton Colour Index (PCI), a measure of phytoplankton biomass.

The CPR is one of the most spatio-temporally extensive marine ecological data sets in the world (**Figure 8**), and its comprehensive approach enables the unique documentation of ecological effects caused by both hydrometerological change (i.e. phenological changes (Edwards & Richardson 2004), biogeographical shifts (Beaugrand et al. 2002), changes in species distribution (Beaugrand et al. 2002), changes in functional group distribution (Leterme et al. 2005), regime shifts (Reid et al. 1998), Harmful Algal Bloom dynamics (Edwards et al. 2006), jellyfish dynamics (Attrill et al. 2007), non-native species (Ibaibarriaga et al. 2007)) and anthropogenic pressures [i.e. eutrophication (McQuatters-Gollop et al. 2007b), and fishing (Lehodey et al. 2006)]. It must be noted however that conversion of CPR data to species abundance is complicated by the different catchability for different species related both to their size and behaviour (Pitois & Fox 2006). In addition spatial coverage of certain areas around the UK such as the west of Scotland is limited (**Figure 8**).

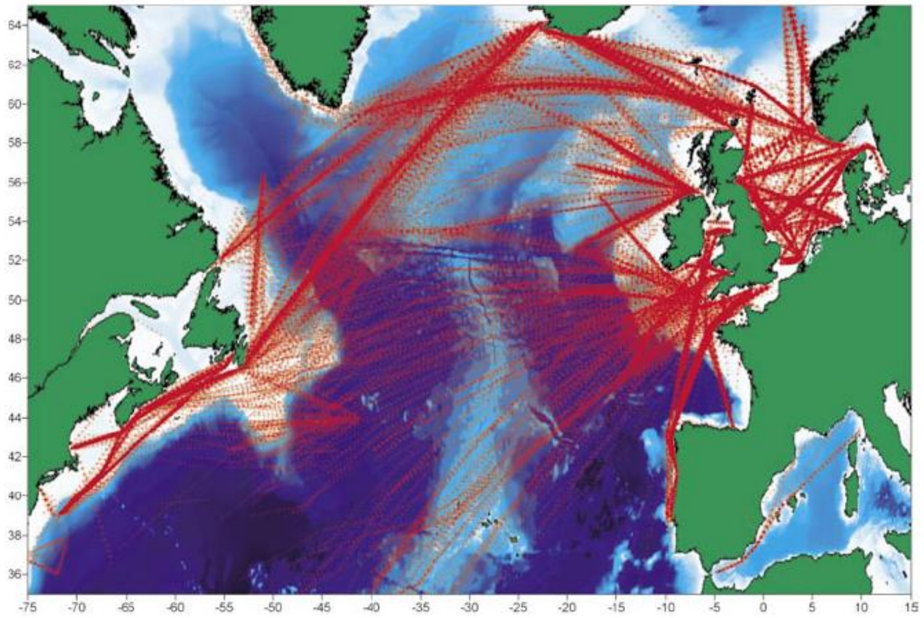

Figure 8 CPR samples collected in the North Atlantic since 1948.

Proposed approach and issues

Plankton abundance and distribution are primarily influenced by climatic factors with temperature being the most important; therefore plankton diversity in a region can be expected to change with long-term changes in climate and short-term changes in weather. Plankton distribution is spatially patchy and its dynamics are temporally variable with a prominent seasonal cycle and succession pattern; fortunately the CPR provides a sufficient amount of data (approximately 50,000 samples around the British Isles since 1948) with a spatial coverage which allows for effective interpolation for most sea areas although other areas are more poorly covered e.g. northern Irish Sea to the west of Scotland (
Figure **8**).

The proposed method for assessing plankton biodiversity is to calculate and then spatially map the diversity index selected for the project for each CPR sample in the study area for the defined time period chosen for the project. This will be done separately for each calendar month to reflect seasonal variability; a quarterly mean (for the defined time period) could then be calculated. The procedure would be performed separately for phytoplankton diversity, zooplankton diversity and phytoplankton biomass (PCI). CPR data will be gridded on a 0.5 or 1 degree grid scale and then interpolated with the Inverse Distance Weighting technique. Due to the large scale nature of CPR data Inverse Distance Weighting interpolation is a valid method for assessing areas with low sampling, such as the coastal zone and has been used in peer-reviewed publications (McQuatters-Gollop et al. 2007a).

CPR samples are analyzed to the species level where possible. However, some taxa are actually groups of species; in many cases this is because identification of species is not possible with an optical microscope. Regardless, changes observed in CPR data have been found to accurately reflect changes in the plankton population (Batten et al. 2003).

Pelagic diversity measures: Pelagic fish

Data and surrogates

While there is data available for mapping the biodiversity of marine fish in offshore waters around the UK, each data has known limitations (discussed here). Furthermore, much of these data are for commercially important species: it is assumed that these data will need to be combined to generate a limited number of diversity maps (possibly by season and regional sea area).

Local inshore data sets are specifically excluded here (such as the Thames Estuary time-series (Attrill & Power 2002) and data sets held by individual marine laboratories and university departments). These data sets, although valuable, generally only cover small sea-areas e.g. the Western Channel Observatory Data set of the Marine

Biological Association (Genner et al. 2004). Such data sets are however invaluable for cross-checking the range of species recorded in wider surveys. Other exclusions are data from the deep-sea and mega fauna such as the basking shark (covered separately as an indicator of pelagic biodiversity).

The areas utilised by pelagic species are likely to change significantly from year to year (Bellido et al. 2008) complicating the identification of high biodiversity. Because of their motility, pelagic species may be especially responsive to climate change e.g. the abundance of anchovy in the North Sea appears to be increasing (Beare et al. 2004). Data sets are available from two distinct sources: commercial catches and research surveys.

Because of the smaller range of pelagic species compared with demersal fish assemblages (the main ones being herring, sprat, mackerel, horse mackerel and offshore species such as blue whiting), commercial catch data may be of some value in showing pelagic fish diversity ‘hotspots’. For mackerel, total catch data at ICES statistical rectangle resolution appear to be available and are shown in the Working Group on Mackerel and Horse-mackerel and Sardine Assessment reports. For the remaining species data would have to be requested from the Marine and Fisheries Agency but this only records landings into UK ports. Because much of the pelagic landings are made by other countries e.g. most of the North Sea herring catch is caught by German vessels, available spatially resolved commercial landings data may not be comprehensive and complete which will complicate interpretation.

From research surveys, there are four potential sources of data available. Each have their own spatial and temporal constraints (to the authors’ knowledge there are no standardised mid-water pelagic trawl surveys (comparable to GOV demersal trawls) conducted except for juvenile fish (Herring MIK-net survey and Northern Irish AFBI juvenile gadoid survey):

i. Although the GOV trawl used in the North Sea and west of Scotland does catch some pelagic fish in International Bottom Trawl Surveys it is not designed to target them, so any use of this data would have to be treated with some caution (Figure 9 shows an example of the distribution of North Sea herring from the ICES DATRAS database).

ii. Most of the North Sea is also covered by an annual acoustic survey (Figure 10) which produces biomass and abundance distribution maps for herring. This clearly shows that the distribution of immature and mature herring is different and explains the high abundance of herring in the southern North Sea (Figure 9).

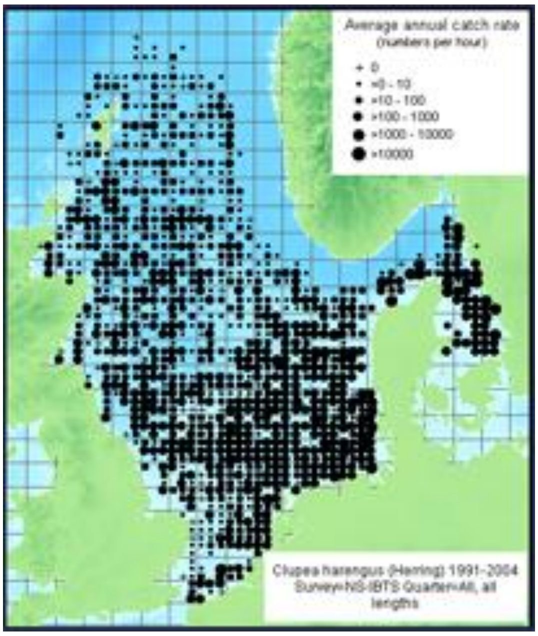

Figure 9 Distribution of herring in the North Sea from the IBTS GOV trawl survey.

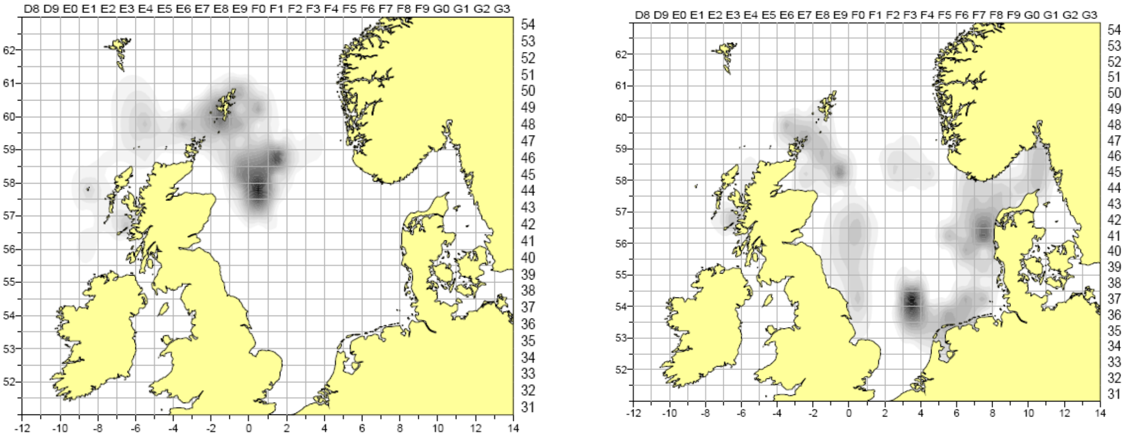

Figure 10 Biomass of mature (left panel) and immature (right panel) herring in the North Sea in 2006 from the combined acoustic cruises (source:(Herring Assessment Working Group for the Area South of 62° N 2007b).

iii. In the Irish Sea, an annual acoustic survey has been conducted in recent years targeting mainly herring but also providing data on distributions of sprat. However the Irish Sea herring stock structure is complex with known exchanges of fish between the Celtic Sea and Irish Sea. Spatial coverage is relatively course except for the area around the Isle of Man (Figure 11 Irish Sea herring **VIIa(N). (**A) Density distribution of 1-ring and older herring (size of ellipses is proportional to square root of the fish density (t n.mile-2) per 15-minute interval). Maximum density was 1100 t n.mile-2. (B) Density distribution of 0-ring herring. Maximum density was 100 t n.mile-2. Note:

same scaling of ellipse sizes on above figures (source: Herring Assessment Working Group for the Area South of 62° (2007a).

iv.

v. An annual acoustic survey is conducted by FRS covering the West of Scotland and waters around Shetland. This is combined with an acoustic survey conducted by the Dutch in the central western North Sea. The acoustic surveys provide an assessment of herring biomass and the data could be used to produce maps of distribution. However, interpretation of acoustic data is a specialised area and additional expertise would need to be contracted to undertake this task.

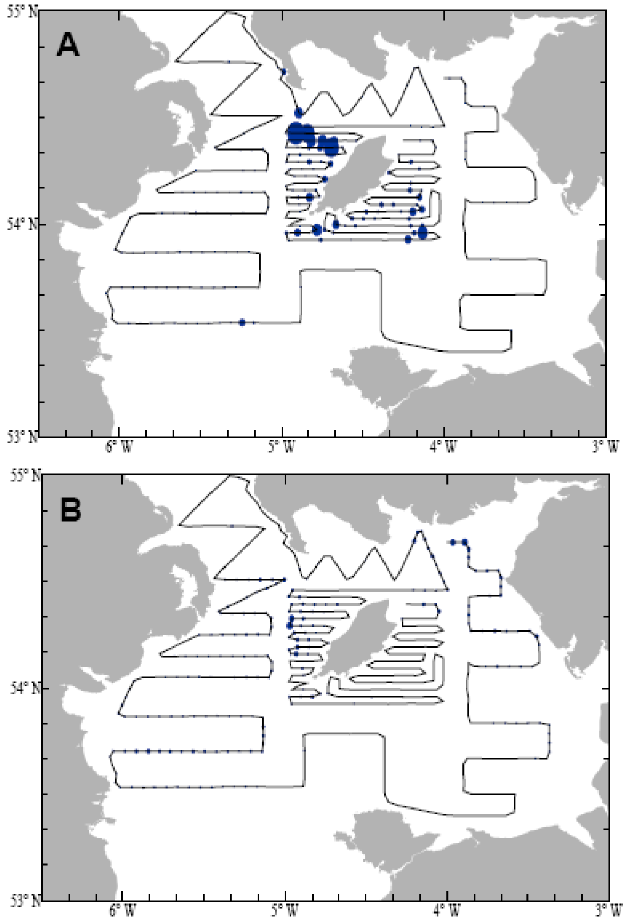

Figure 11 Irish Sea herring VIIa(N). (A) Density distribution of 1-ring and older herring (size of ellipses is proportional to square root of the fish density (t n.mile-2) per 15-minute interval). Maximum density was 1100 t n.mile-2. (B) Density distribution of 0-ring herring. Maximum density was 100 t n.mile^{-2}. Note: same scaling of ellipse sizes on above figures (source: Herring Assessment Working Group for the Area South of 62° (2007a).

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By combining the data sources described above the broad distribution of pelagic species can be described. Because acoustic data are collected continuously the spatial resolution achievable may be finer than the ICES Statistical Rectangle level.

Proposed approach and issues

To our knowledge robust methods to combine pelagic fish data and to generate pelagic biodiversity indices are not well developed and any work on this would have to be regarded as a piece of research. We propose a three-step approach (1) Explore the commercial landings data availability for pelagic species in collaboration with the Marine Fisheries Agency (it may be possible to corroborate these data with fishing pressure data layers) (2) Data-mining of the available acoustics data. This would need to bring together acoustics experts from each of the UK government fisheries laboratories, a representative from the ICES IBTS (International Bottom Trawl Working Group) and one or two experts in geostatistics. The amount of work required to generate defensible maps from the herring acoustic data for herring for additional species such as sprat might be considerable, but because acoustic data are collected continuously the spatial resolution achievable may be better than from trawl survey data e.g. it may be possible to identify associations between pelagic species and oceanographic fronts (3) Having mined the acoustics survey data the next step would be to combine it with additional data for species such as mackerel from the IBTS surveys. Given the large known changes in distribution over time, data would have to be analysed by season and by longer term time trends (probably decadal) since 1970. By comparing results from the different data sets an evaluation of confidence could be produced.

Validation, confidence layers and caveats

Available research trawl survey data provides useable data for biodiversity analyses for most areas around the UK but there are differences in gears between regions, problems of ground-type bias and relatively coarse spatial coverage. All these factors will limit the construction of a complete data layer for fish species diversity for UK waters, and it is likely that there will be significant gaps in spatial coverage. Species diversity metrics are very dependent on sample size, and it is recommended to use > 20 hauls (although pooling hauls limits spatial resolution). Furthermore, species diversity metrics are strongly affected by size and species catchability, changes in sampling gear, taxonomic skill, fishing skill etc. Simpler metrics such species richness in an area may be more robust than diversity measures as long as corrections are applied for differential sampling intensity (rarefaction or MCMS techniques).

Pelagic diversity measures: Seabirds

The relationship between top predators (including fishes, marine mammals and seabirds) and the lower trophic levels appears to function bilaterally, manifest both as ‘top down effects’ of predators on prey species abundance but also predators can be themselves regulated by prey abundance (e.g. seabird reproductive success is highly sensitive to changes in sandeel abundance; Frederiksen (2007)), highlighting the tight trophic linkage between seabirds and the pelagic ecosystem. If seabirds are considered to be a pelagic ecosystem component, then their diversity may be considered as a biodiversity layer (in the same way as other fully pelagic groups such as plankton or fish).

The JNCC Seabirds-At-Sea Team (SAST) has carried out a programme of survey and research on seabirds and cetaceans in the marine environment in the North-East Atlantic since 1979. These surveys have been conducted at sea from ships and aircraft using standard methods (Stone et al. 1995). The distribution of each species is mapped in one of three ways:

i. As birds.km^{-2} (common species);
ii. As birds.km^{-1} (less common species); and
iii. As sightings (rare species where all sightings of individuals are recorded).

These data are available effort corrected, and presented as densities of species in ¼ ICES (International Council for the Exploration of the Sea) rectangles (c. 25 x 25 km – 625 km^2) on a monthly basis (

Figure **12**).

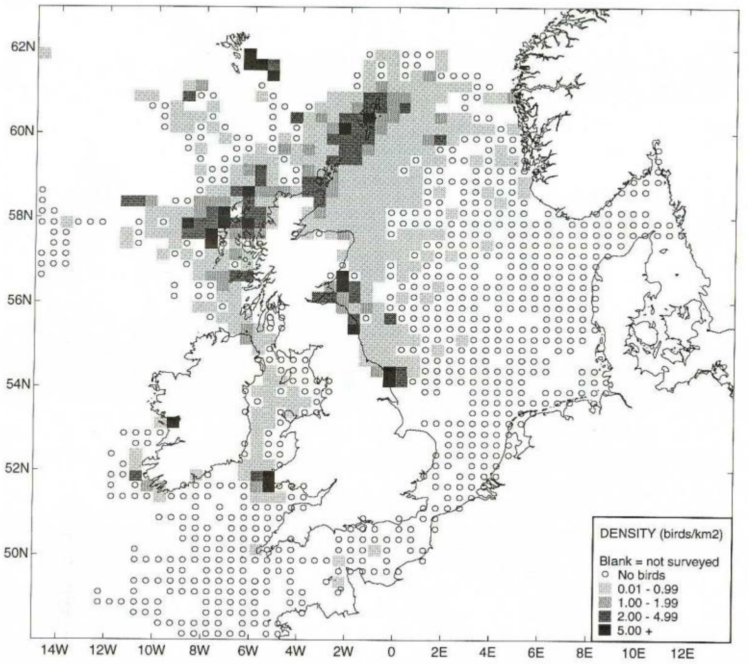

Figure 12 Puffin distribution in North-East Atlantic waters.
Source: Stone et al. (1995).

Pelagic diversity measures: Cetaceans

Diversity of cetaceans, another top predator group in the pelagic environment, could be considered as another layer to identify pelagic biodiversity hotspots. Twenty-eight species of whales, dolphins and porpoises are known to occur in north-west European waters with varying degrees of frequency and regularity.

Available data

The Joint Cetacean Database is an amalgamation of the three large data-sets on cetacean dispersion in UK and surrounding seas. The data sets are from:

i. Joint Nature Conservation Committee (JNCC) have collected data on cetaceans since 1979 during their at-sea surveys of seabirds in UK waters.
ii. Sea Watch Foundation (SWF) data are available from 1980 from both land based observations and ship surveys.
iii. Sea Mammal Research Unit (SMRU).

This database represents the most important resource of effort-related cetacean data for North-West European waters and has been used to produce maps of cetacean distributions for North-West European waters for a Cetacean Atlas at the scale of ¼ ICES (International Council for the Exploration of the Sea) rectangles (c. 25 x 25 km – 625 km^2) (Reid et al. 2003) (Figure 13).

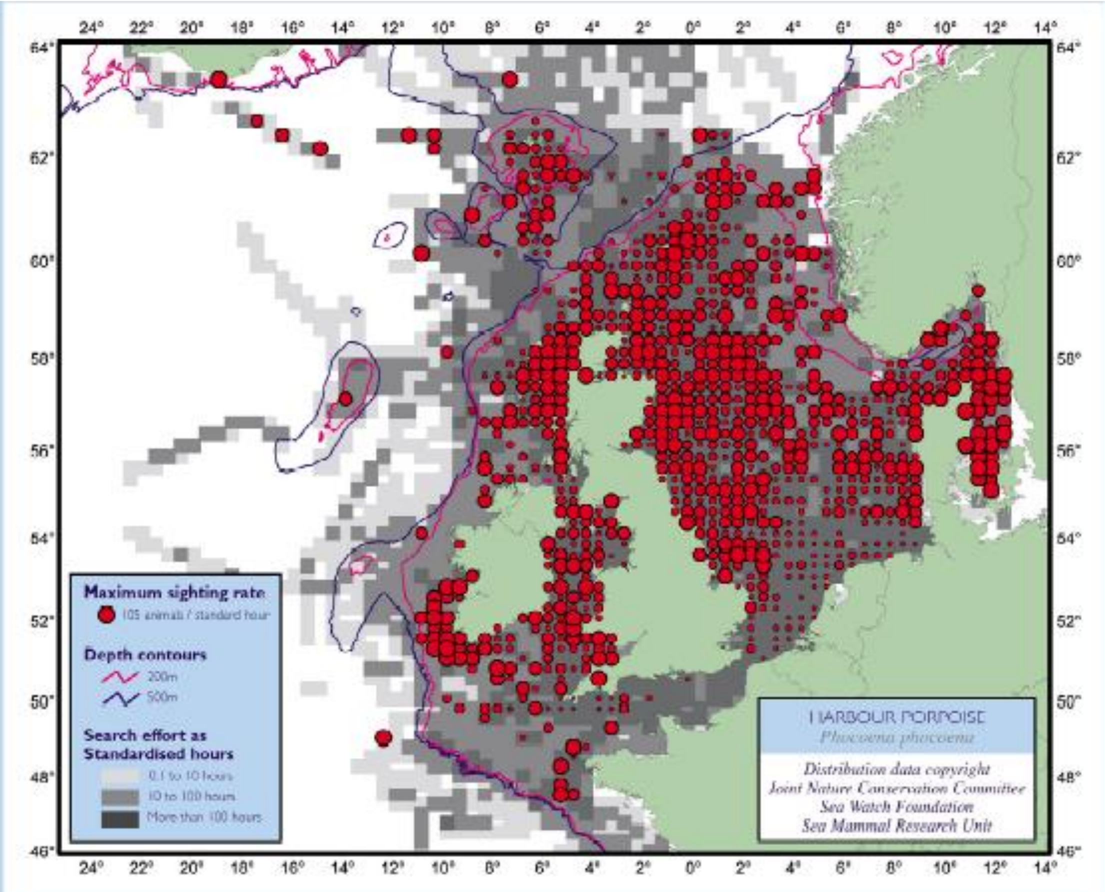

Figure 13 Distribution of sightings of harbour porpoise (*Phocoena phocoena*). Source: North-West European waters for a Cetacean Atlas (Reid et al. 2003).

Proposed approach

The spatial resolution of data from the Joint Cetacean Database was found insufficient to pick up single species density 'hotspots' in a study by Evans & Wang (2008). They increased the spatial resolution from c25 x 25 km to 1 x 1 km using a spatial modelling approach for mapping the distribution and abundance of harbour porpoises (Evans & Wang 2008). During analysis, search effort was corrected for sea state (effective effort) and sightings rates calculated as sightings per unit area divided by effective effort and displayed as monthly aggregates over the 22 year data set (Figure 14).

We propose to extend this approach to other cetacean species in UK waters. However, because of issues with low numbers of sightings for some species (sperm whale, northern bottlenose dolphin, selected beaked whales *Mesoplodon spp.*, common bottlenose dolphin, striped dolphin and killer whale (Reid et al. 2003)), additional techniques such as Monte Carlo methods would need to be employed to standardize for effort (Moulins et al. 2008).

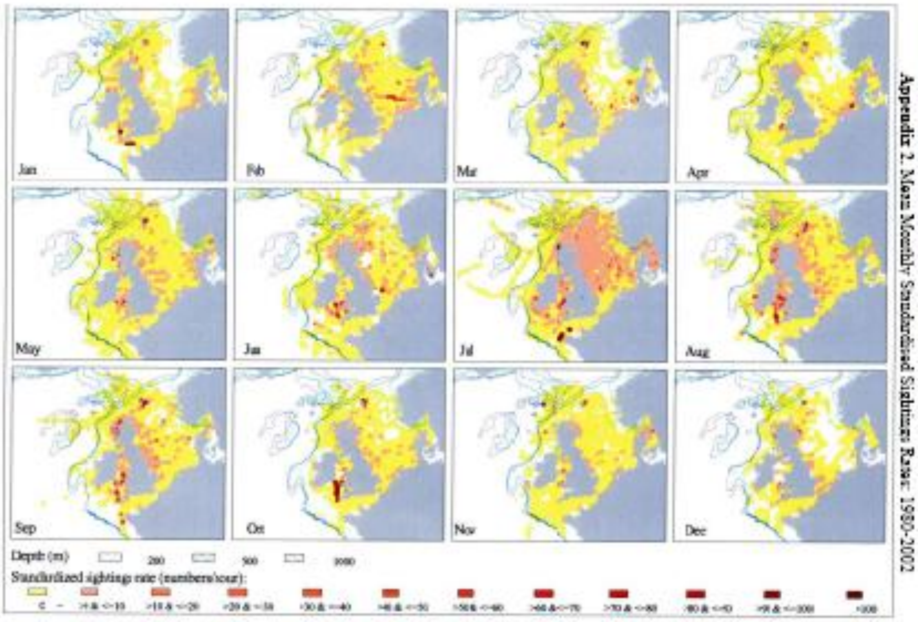

Figure 14 Mean Monthly Standardised Sightings Rates of Harbour porpoises (1980-2002). (Source: Evans & Wang 2008)

Pelagic diversity surrogates: Sea surface temperature

In order to generate useful metrics from EO SST data, these would first be composited into median value monthly maps. Monthly and seasonal climatologies (mean and standard deviation) would then be calculated to characterise the typical SST distribution, for example to indicate the extent of coastal upwelling and tidal mixing. Data layers could be provided at various resolutions from 1 km to 1° to be agreed within the team.

The same AVHRR data from Dundee Satellite Receiving Station would provide the best input data for the SST metrics, with coverage at 1 km resolution and a consistent 28 year time-series. In addition, lower resolution data sets may be helpful for validation or to fill gaps, e.g. NOAA Pathfinder at 4 km and NCOF OSTIA at 5 km resolution (which incorporates passive microwave data allowing SST sensing through cloud).

Pelagic diversity surrogates: Ocean Colour

The proposed approach for describing the surface productivity around the UK shelf is dependent on an algorithm for estimating chlorophyll-a concentration which deals effectively with turbid water. The OC5 algorithm corrects for the influence of suspended sediment on the water-leaving radiance (Gohin et al. 2002), and has been shown to provide more realistic and accurate chlorophyll-a retrievals in turbid shelf seas than standard chlorophyll-a algorithms provided by NASA and ESA (Figure 15).

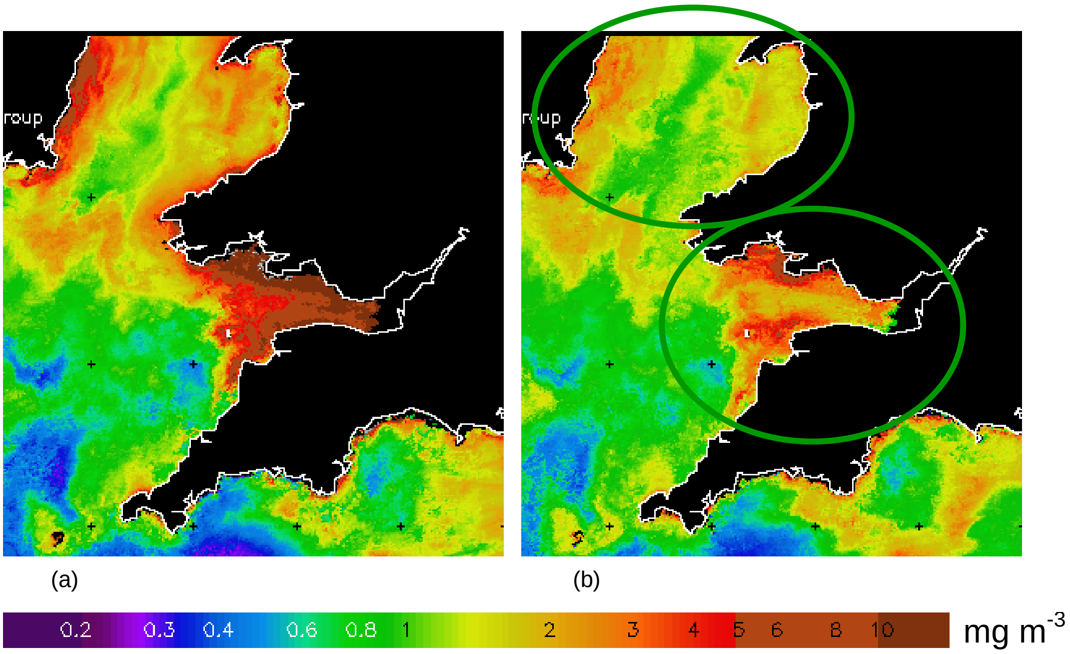
(a) (b)

Figure 15 Illustration of improvement to chlorophyll-a estimation in turbid shelf-seas using OC5 algorithm. Aqua-MODIS 7-day chlorophyll-a maps for UK southwest region on 12 June 2008: (a) standard NASA OC3 algorithm; (b) turbid water OC5 algorithm with rings indicating areas where errors due to suspended sediment were significantly reduced.

There is now an 11-year time-series of EO ocean colour data at 1 km resolution from SeaWiFS (Sep. 1997 to 2004) and Aqua-MODIS (Jul. 2002 to date) that would be applied to characterise the phytoplankton abundance within the UK waters. PML have automated systems that would allow these data to be reprocessed into chlorophyll-a using the turbid water OC5 algorithm. Then an optical model would be applied to estimate primary production of carbon based on chlorophyll-a, SST and PAR (Smyth et al. 2001).

Monthly and seasonal climatologies (mean and standard deviation) would then be calculated to characterise the typical chlorophyll-a distribution. Data layers could be provided at various resolutions from 1 km to 1° to be agreed within the team.

Validation, confidence layers and caveats

All EO products are validated prior to publication of the algorithms. However, additional validation of these products is proposed in comparison with related data layers. For example, selected in situ SST or chlorophyll-a samples could be matched up with EO data to provide cross-validation. In particular additional validation of the OC5 chlorophyll-a algorithm would be performed, probably using regular in situ samples taken for the Western Channel and Liverpool Bay observatories.

Most EO data are limited by cloud cover, which prevents infrared and visible sensing; this can be lessened using the compositing techniques proposed above. The cloud cover limitation is only avoided using passive microwave sensors of SST, though currently this is limited to a resolution of 25 km. Cloud cover may lead to biases in data analysis, for instance where phytoplankton blooms, upwelling or stratification fronts might appear to be more frequent than expected, if such events are correlated with clear skies.

Pelagic biodiversity indicators: Basking shark

There is potential to use megafaunal species such as basking shark (*Cetorhinus maximus*) and seabirds as indicators of pelagic biodiversity hotspots. These groups are monitored because of their conservation importance, thus data exist on their distributions. Spatial distributions in UK waters may be used to identify biodiversity hotspots based on the assumption that they aggregate in areas of high pelagic biomass which coincide with areas of high pelagic biodiversity. A relationship between top predator diversity (large pelagic predatory fish) and the diversity of lower trophic groups (zooplankton) has been established for the Pacific (Worm et al. 2005), and was positively correlated with thermal fronts, however this relationship needs to be tested for UK waters.

Data and surrogates

Methods for assessing patterns of spatial distribution for basking shark range from tracking individual movements through to large scale surveys. A major problem associated with visual surveys for basking sharks (e.g. ship, aerial or land-based) is that these methods rely on individual sharks spending sufficient time at the sea surface where they can be observed. Because it is not known whether all individuals within a population ‘bask’, how often this behaviour is exhibited, or whether they undertake it in all habitats occupied, may be a significant bias associated with such assessments of distribution pattern. Three key data sets exist (Figure 16):

i. Individual shark geolocations determined from satellite-linked archival telemetry (8 sharks tagged between May 2001 and December 2002 (Sims et al. 2003);
ii. Effort-corrected counts from ship surveys conducted by four organisations: MBA (1994-2004), UK Wildlife Trusts (1994-2004), Hebridean Whale and Dolphin Trust ((2003) and International Fund for Animal Welfare (2002-2003); and
iii. Sightings of sharks reported by the UK public over a 15 year period through the Marine Conservation Society’s Basking Shark Watch (since 1987).

Figure 16 Distributions of basking sharks determined using the three methods of (a) tag geolocations (2001–2003), (b) survey sightings (1994–2003) and (c) public sightings (1987–May 2004) (Source: Southall et al. 2005).

Archival telemetry theoretically provides a non-biased, independent means of assessing spatial distribution patterns, whereas public sightings and survey data may be biased towards identifying basking shark habitat only where sharks occur on the surface in areas accessible to study (Southall et al. 2005).

Proposed approach and issues

Concordance between basking shark data collected using the methods outlined above has already been assessed (Southall et al. 2005). A standard grid comprising 0.5 x 0.5° grid cell was used to map the data and generate the frequency of occurrence of shark distribution 'hotspots' (contour plots of high spatial density, Figure 17). The consistency of hotspots was examined by determining the frequencies with which the top five shark density 'hotspots' for each method used to assess the distribution occurred in each of the other methods top 25 density hotspots. There were differences in the distributions between the methods suggesting that the data cannot readily be combined and should be treated separately. In addition, the above data sets will be updated with new records where possible.

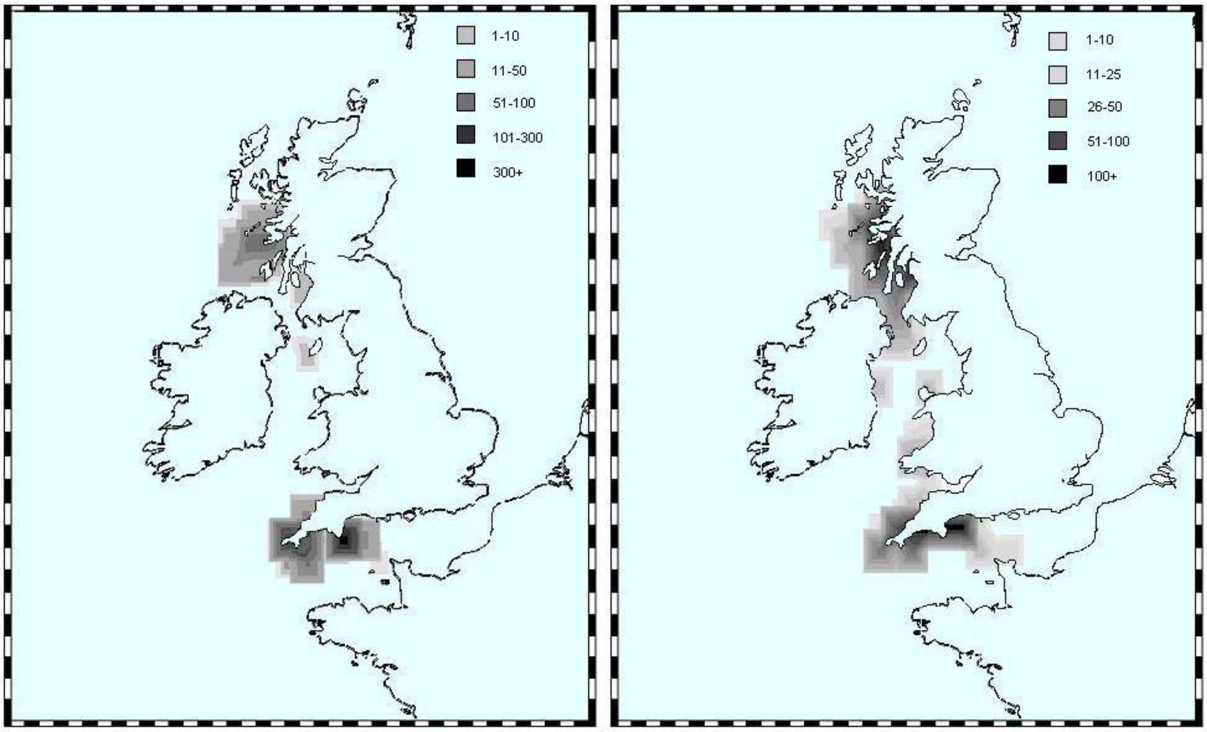

Figure 17 Contour plots showing (a) the total number of basking sharks sighted per 0.5 x 0.5^o (latitude/longitude) grid cell and (b) total amount of time (h) searched per grid cell (Source: Southall et al. 2005).

Validation, confidence layers and caveats

It does not appear to be possible to combine the data sets due to the differences in collection method and this is the main issue with these data. In addition, the temporal variability of these data are unresolved and although these animals have strong seasonal behaviours (Sims et al. 2003), this is not captured in these data sets, neither are longer term distributional changes (e.g. in response to climate). It is suggested that these data are interpreted in conjunction with the EO and plankton layers.

Pelagic biodiversity indicators: Seabirds

Many seabirds feed on a narrow range of prey items: thus their spatial distribution may be indicators for pelagic productivity but not necessarily pelagic diversity since they may be targeting a single prey species. An example are sandeel-dependant seabirds (such as black-legged kittiwake (*Rissa tridactyla*), Atlantic puffin (*Fratercula arctica*), razorbill (*Alca torda*), European shag (*Phalacrocorax aristotelis*) and common guillemot (*Uria aalge*)) whose reproductive success has been related to sandeel abundance (Frederiksen et al. 2007, Daunt et al. 2008). For this reason, they are arguably not appropriate indicators for pelagic biodiversity (Steven Votier, pers. com.) and are not explored further in this review