



# Modelling benthic habitats and biotopes off the coast of Norway to support spatial management



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## ABSTRACT

Habitat conservation, and hence conservation of biodiversity hinges on knowledge of the spatial distribution of habitats, not least those that are particularly valuable or vulnerable. In offshore Norway, benthic habitats are systematically surveyed and described by the national programme MAREANO (Marine AREAL database for NORwegian waters). Benthic habitats and biotopes are defined in terms of the species composition of their epibenthic megafauna. Some habitats are of special conservation interest on account of their intrinsic value and/or vulnerability (e.g., long-lived species, rareness, to comply with international regulations such as OSPAR). In Norway, off Nordland and Troms, the following habitats of special interest can be found: *Umbellula encrinus* Stands, *Radicipes* sp. Meadows, Deep Sea Sponge Aggregations, Seapen and Burrowing Megafauna Communities, Hard Bottom Coral Gardens. In this paper, we used underwater video data collected within the MAREANO programme to define and describe benthic habitats and biotopes of special interest, and to map the geographic distribution thereof by means of habitat modelling.

We first evaluated the community structure of each habitat in the list using a SIMPROF test. We determined that the class Deep Sea Sponge Aggregations, as defined by OSPAR, had to be split into at least three classes. We then re-defined seven new types of ecological features, including habitats and biotopes that were sufficiently homogeneous. Then we modelled the spatial distributions of these habitats and biotopes using Conditional Inference Forests. Since the purpose of the distribution maps is to support spatial planning we classified the heat maps using density thresholds.

The accuracy of models ranged from fair to excellent. Hard Bottom Coral Gardens were the most rare habitat in terms of total area predicted (224 km<sup>2</sup>, 0.3% of the area modelled), closely followed by *Radicipes* Meadows (391 km<sup>2</sup>, 0.6%). Soft Bottom Demosponges (Geodid sponges and other taxa) represent the largest habitat, with a predicted area of 9288 km<sup>2</sup> (14%). Distribution maps of classes defined by habitat-forming species (Hard Bottom Coral Gardens) were more reliable than those defined by a host of species, or where no single species was a clear habitat provider (e.g. Seapen and Burrowing Megafauna Communities). We also put forward that a scale of patchiness larger than the scale of observation, and homogeneity of the community both play a role in model performance, and hence in map usefulness. These along with density threshold values based on observed data should all be taken into account in marine classifications and habitat definitions.

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## 1. Introduction

Concepts like that of habitat have risen above others (e.g. species) in political agendas primarily because habitats can be used as surrogates for species distributions (Lindsay et al., 2008; Mumby et al., 2008) which are the ultimate target of conservation efforts, while being more readily described and documented. In addition, patterns in habitat distribution can be observed at the scale where management occurs. Hence, most governments now have a mandate to protect habitats

and/or related biological features (e.g. biotopes, ecosystems). Protecting habitats is however conditional on knowing their spatial distribution; therefore mapping the distribution of habitats paves the road to preserving them, which in turn leads to conservation of biological diversity.

When survey data are costly to obtain, as is the case in seabed environments, insight into the spatial distribution of habitats can be gained by use of spatially-explicit modelling, particularly distribution modelling at the community level (Ferrier and Guisan, 2006). This approach is similar to Species Distribution Modelling (Franklin, 2009) except a suite of species are modelled collectively, and it is also known as habitat modelling. First, biota–environment relationships are derived from a set of observational data. These relationships can easily be used to make predictions about the biological properties (e.g., the species

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composition) of sites where no direct observation of the biota has been made. When environmental data are available as map layers (i.e., full-coverage and sufficient resolution) a prediction can be made for every single pixel across a study area. In this way, ‘wall-to-wall’ maps of biota can be cost-effectively generated.

In the benthic realm the species composition of the epibenthic megafaunal community, comprising all organisms living on the sediment surface which are large enough to be visible to the naked eye, can construe habitats and biotopes. Megafaunal habitats, or simply benthic habitats are defined by two components: (1) an environmental setting characterized by the presence of one or more habitat-forming species and (2) the whole host of species that co-occur with it. This acceptance of the word “habitat” is absolute rather than relative. In other arenas habitat is understood as the type of environment where an organism lives, usually an animal, and is defined relative to that organism (hence the use of phrases such as “spotted-owl habitat”, or “Essential Fish Habitat”). Benthic ecologists, instead, used the term “associated fauna” to refer to the biota that utilize the resources and space procured by the habitat-forming species. The terrestrial concept closest in meaning would be that of vegetation types.

The term benthic habitat, however, has also been widely used in reference to areas that are simply homogeneous in terms of their geophysical (abiotic) environment, particularly in the hydroacoustic literature (e.g. Brown and Blondel, 2009, Jordan et al., 2005). This sense of the word implies that to assign an area to a type of habitat no data on the biota present in that area may be required; for example, “rocky reef”, or “coarse unconsolidated substrate”. When this is the case another concept is usually employed as a modifier, that of biotope, to designate units that can be characterized by a typical species assemblage in addition to the type of substrate (e.g. “*Mytilus edulis* beds on sublittoral sediment”, “*Phragmatopoma lapidosa* reefs on high energy sand”).

The biotope level is often the final (most-detailed) level available in marine classifications of ecosystems and communities (e.g. the Marine Habitat Classification for Britain and Ireland, Connor et al., 2004; the Coastal and Marine Ecological Classification Standard in the US, Federal Geographic Data Committee, 2012). Biotope is usually defined as the sum of habitat, which in this case is taken to be the abiotic component, and the species assemblage as the biotic component (Olenin and Ducrotoy, 2006). Note that if the habitat is best described by something of a biological, rather than geophysical nature (i.e., a habitat-forming species) the terms biotope and habitat become undistinguishable. In general, the term “habitat” can assume a wider range of meanings, including referring simply to a naturally occurring, relatively homogeneous type of nature.

Norway has a programme in place to systematically collect ecological data from the seabed and define, describe, and map the distribution of benthic habitats and biotopes beyond the continental platform: MAREANO (Marine AREAL database for NORwegian waters). Among other sampling tools the MAREANO programme operates an underwater video platform which yields geo-referenced, species occurrence data covering nearly the whole range of species of epibenthic megafauna. In this paper we use MAREANO video data to (1) test methods to define and describe benthic habitats and biotopes of management interest, and (2) map the geographic distribution of benthic habitats and biotopes by means of distribution modelling. The intended use of all the data products generated is to support spatial management of Norwegian offshore areas, with a view to conserving biological diversity rather than understanding patterns of distribution.

## 2. Material and methods

### 2.1. Biological data

Under the MAREANO programme Norway has conducted over 1300 video transects using the Campod and Chimaera platforms. On average the spacing between the video transects is 10 km (Buhl-Mortensen

et al., 2015, van Son et al., in preparation), although more complex areas can be sampled more densely. These transects are generally 700 m in length, occasionally longer. During each transect the video platform, carrying a forward-looking, high definition, colour video camera is towed behind the survey vessel at a speed of 0.7 knots, 1.5 m above the seabed. Laser pointers allow calculating the width of the field of view of every video frame. Navigation data is collected via a hydroacoustic positioning system and a transponder mounted on the video platform.

In the laboratory, video footage is translated into quantitative, species occurrence data. Every encountered organism is identified to the most-detailed possible taxonomical resolution (generally species level), and individually geo-referenced to approximately 5 m-accuracy. The abundance of each occurrence of megafauna is also quantified for the frame in view either as a count of individuals or percent cover, taxon by taxon. Following video analysis, data can be pooled into equal-length segments depending on the analysis scale of interest. Final abundance for all fauna of interest is reported as density, where area is calculated from the estimated values of field width and the length of the segment. Densities are standardized to numbers of individuals (or colonies, where relevant) per 100 m<sup>2</sup>.

In this paper we used data from video transects conducted off Nordland and Troms (Fig. 1) between 2006 and 2009. The area selection was dictated by management needs and is approximately 63,000 km<sup>2</sup>. The total number of video transects was 388. The species occurrence data was pooled at a 200-m scale. Each transect yielded 3–5 point-locality samples, and the total number of samples (*n*) was 1709.

Unfortunately, not all video data for the chosen area had been analyzed at the time of this study and a gap had to be filled in with spatial predictions larger than the general spacing between the video transects (see Fig. 1). The gap area is known to be similar in its biological composition to the adjacent areas and is not thought to contain any completely unsampled communities or landscapes. While representativeness is not believed to be compromised, predictions in that area will be affected by a larger degree of uncertainty.

### 2.2. Habitat selection and assessment of species structure

We used three commonly-used criteria to prioritize marine benthic habitats: being dominated by long-lived species, being unique in Norway, or simply, being included in the OSPAR list of Threatened and/or Declining Habitats (OSPAR, 2008). Habitat types used and the list of taxa whose presence prescribes the presence of the habitat (termed here “qualifying taxa”) are described in Table 1 and in the Supplementary material. They are all considered highly vulnerable to physical or mechanical damage by e.g. demersal fishing gear, and some host significant biological diversity.

After removing from the dataset all samples which did not contain any of the qualifying taxa we compared the species compositions between all pairs of samples within each class. We applied a SIMPROF (Similarity Profile) test (Clarke et al, 2008) to each subset. This test results in an assessment of whether there is any internal structure in a group of samples. When the test is not significant the group of samples is said to represent only one type of community (or is homogeneous in terms of its species composition) and further division is not warranted.

### 2.3. Modelling habitats

For each habitat that was deemed homogeneous we created a spatially-explicit dataset of the total abundance of all of the qualifying species pooled together, which was used as the response variable (total density of organisms/colonies of qualifying species). Samples where none of the qualifying species were found for each habitat were used as absence data. We reserved 677 samples for model evaluation.

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